

STIC-Biotech/ChemLib

176081

From: Seharaseyon, Jegatheesan  
Sent: Tuesday, January 10, 2006 9:20 AM  
To: STIC-Biotech/ChemLib  
Subject: Re: 10/007270

CFF

Importance: High

Hi,  
Please search in the commercial and interference databases for  
1. Nucleotides encoding SEQ ID NO: 2.  
2. Nucleotides of SEQ ID NO: 1 and a word search of atleast 12 nucleotides.

Thanks.

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Art Unit 1647  
Remsen 4C61  
Mailbox 4C70  
Phone: (571)-272-0892  
Fax: (571)-273-0892

1-3330 NA  
2-797 aa  
LB

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

Searcher	1-3330 NA	STIC	IG
Searcher Phone		CM-1	STN
Date Searcher Picked up		Pre-S	Dialog
Date completed		Type of Search	APS
Searcher Prep Time		N.A. Sequence	Geninfo
Online Time		A.A. Sequence	SDC
		Structure	DARC/Questel
		Bibliographic	Other CGN

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PS Claim 1; Page 77; 105bp; English.  
XX The present sequence is that of cDNA encoding isoform A of novel human  
CC interferon receptor matrix 150 (IPM 150), a member of the newly identified  
CC interferon receptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or IPM2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polypeptides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing the photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression  
XX

Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;

Query Match 100.0%; Score 3330; DB 9; Length 3330;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TGTATCTTTTATAGATTTTGAAGGTTGTTCTGTGATTTTATCAAGATTAACAATGAC 120  
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Db 121 AAAAGCAGAAATGTATTTGAAAAGTGAAGAGCTATTTTGTGATTTTCTCA 180  
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Db 181 AGTTCAAGGAAACCAAGATATCTCCATTAATATATCAATTCGAAATCAAGACATAGA 240  
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Db 481 CCTGTGACAGGGGAATATCAGAGCTGGGTCAAGCATCTGCAGCAGGAACCTTCTGCT 540  
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Db 541 CTTTGACATTTGAAAAAAGCTTCAGCAATTCCTCCAGGACCTGGATCTTCCAGAGAG 600  
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Db 601 AATTAACAAGAGAGTTTCCCTGACAGAAAAGATGAATATCTGCAGAGAAGCATTTGGG 660  
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Db 661 AGAGCTGTGGAACCATTTGTCAATTCACAGCAATCTAATTCAAAAGCTTGGGAGCT 720

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Db 3301 GCGGAAGTTGTACTATATGACATTAATCAAT 3330

RESULT 2
ADA14840
ID ADA14840 standard; cDNA, 3330 BP.
XX
XX ADA14840;
XX
DT 06-NOV-2003 (first entry)
XX
Db Human interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX
XX ss: gene; human; IPMC 150 isoform A; gene therapy;
XX interphotoreceptor matrix component; IPMC; ocular disorder;
XX macular degeneration; photoreceptor death; retinal detachment.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 131..2586
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XX FT /product= "IPMC 150 isoform A"
XX FT /transl_except= (pos:689..756,aa:Thr-Asp)
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XX FT /*tag= a
XX FT /label= Signal_sequence
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XX FT misc_feature 692..753
XX FT /*tag= d
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XX US2002160954-A1.
XX
XX 31-OCT-2002.
XX
XX 08-NOV-2001; 2001US-00007270.
XX
XX 29-OCT-1998; 98US-00183972.
XX
XX 29-OCT-1999; 99US-00430195.
XX
XX (IOWA ) UNIV IOWA RES FOUNO.
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XX Hageman GS, Kuehn MH;  
 XX MPI: 2003-238235/23.  
 DR P-PSDB; ADA14841.  
 XX  
 PT New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.  
 XX  
 PS Claim 3; Page 29-30; 76pp; English.  
 XX  
 CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform A.  
 CC  
 XX Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;  
 8Q

Query Match 100.0%; Score 3330; DB 10; Length 3330;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCAAGAGGTTATCTCAATCATCTGTATCATATATATATATTTTTCACATTTTC 60  
 DB 1 TAAACCAAGAGGTTATCTCAATCATCTGTATCATATATATATATTTTTCACATTTTC 60  
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 DB 481 CCTGACACAGGGGAAATATCAGAGCTGGGTCAAGCATCTCCAGCAGAGACCTTCTGCT 540  
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 DB 541 CTTTGCATTTGAAAAAACTTCAGCAATTCACAGAGACCTGGAATCTTCTCAGCAGAG 600  
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 DB 601 AATTAACAGAGAGATTTCTTGAACAGAAAGATGAATATCTGACAGAGACATTTGGG 660

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 DB 2221 CTCACATTTGAACACAGCTGATCAAGAGATTCCTGTGAAGTCTGTGCGTGGCGGAATTT 2280  
 QY 2281 GCCCAATGTTTAAAGAACAGAGCTGAGAGAGCGGAGTTCCTGTGCAAAACCAAGATAT 2340  
 DB 2281 GCCCAATGTTTAAAGAACAGAGCTGAGAGAGCGGAGTTCCTGTGCAAAACCAAGATAT 2340  
 QY 2341 GACAGCCAGGGAGCTGTGACCGGTCTGGAACAGGCTCTGTGCGCCCTGTGCAAAAGAA 2400  
 DB 2341 GACAGCCAGGGAGCTGTGACCGGTCTGGAACAGGCTCTGTGCGCCCTGTGCAAAAGAA 2400  
 QY 2401 TGGGAGTCTCTCCAGGAAAGGAGCTCCATGACAGGTCCAGATCACTCTGAAATCA 2460  
 DB 2401 TGGGAGTCTCTCCAGGAAAGGAGCTCCATGACAGGTCCAGATCACTCTGAAATCA 2460  
 QY 2461 GCAATCAAAACTAGTCTTAAAAAGTTCCAAAATCAAAAATTAACAAAGTAAATCACTTAA 2520  
 DB 2461 GCAATCAAAACTAGTCTTAAAAAGTTCCAAAATCAAAAATTAACAAAGTAAATCACTTAA 2520  
 QY 2521 AGAAATTTCTGAATTAAGACCGTAGAATATGAAGAAATTTAACATCAAGATTGGGAAGA 2580  
 DB 2521 AGAAATTTCTGAATTAAGACCGTAGAATATGAAGAAATTTAACATCAAGATTGGGAAGA 2580  
 QY 2581 AATTAATACTGAAATGTACATTAATCACTTAAGGCTATCTCAGAGAGATGATTTGGCT 2640  
 DB 2581 AATTAATACTGAAATGTACATTAATCACTTAAGGCTATCTCAGAGAGATGATTTGGCT 2640  
 QY 2641 TCTCAAGGAAATGAGACAGGCAATTTCAATGGGTATCAAAAATCAGACATACAGTCAA 2700  
 DB 2641 TCTCAAGGAAATGAGACAGGCAATTTCAATGGGTATCAAAAATCAGACATACAGTCAA 2700  
 QY 2701 CACTGAGATCAGACACACATTAATTTAGAAAGTCAATGATCTTGGCAACGAG 2760  
 DB 2701 CACTGAGATCAGACACACATTAATTTAGAAAGTCAATGATCTTGGCAACGAG 2760  
 QY 2761 TAAATTTCTGAAAAAAGACACTTACTTAATTAACCCCAATGCAATCAGCGAAAC 2820  
 DB 2761 TAAATTTCTGAAAAAAGACACTTACTTAATTAACCCCAATGCAATCAGCGAAAC 2820  
 QY 2821 AATATTTTACTATCTTGATGATAGTCAAAATGATCATTAAGCAGGTTTGTCTCCACT 2880

DB 2821 AATATTTTACTATCTTGATGATAGTCAAAATGATCATTAAGCAGGTTTGTCTCCACT 2880  
 QY 2881 TCCCTGAAATTTTACTCAGACATCAATTTGCAACAAGATAGTACTTATTTGTTAGGG 2940  
 DB 2881 TCCCTGAAATTTTACTCAGACATCAATTTGCAACAAGATAGTACTTATTTGTTAGGG 2940  
 QY 2941 ACTGAACAATTTATTTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 3000  
 DB 2941 ACTGAACAATTTATTTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 3000  
 QY 3001 CTACTTAGCAGGAGATGACAGTCTCTCTAAAGCATGAATGTATGATGTAGAGCA 3060  
 DB 3001 CTACTTAGCAGGAGATGACAGTCTCTCTAAAGCATGAATGTATGATGTAGAGCA 3060  
 QY 3061 CTGTAGTAGTATATATATGCTCCACACTAGCTGTATTAACAAACCTCAGTATTCAG 3120  
 DB 3061 CTGTAGTAGTATATATATGCTCCACACTAGCTGTATTAACAAACCTCAGTATTCAG 3120  
 QY 3121 TTATTAAGCACATAGTTTATATCCCACTACTGCTTACATGATGACTGTTTGTGCGC 3180  
 DB 3121 TTATTAAGCACATAGTTTATATCCCACTACTGCTTACATGATGACTGTTTGTGCGC 3180  
 QY 3181 AATATCTTTGAATGTTCTTTAAAGAACTGAGGTTCAAGTACATACATACAGGAA 3240  
 DB 3181 AATATCTTTGAATGTTCTTTAAAGAACTGAGGTTCAAGTACATACATACAGGAA 3240  
 QY 3241 ATCTTACTTTTCTTGTACTACACAACCTATTTTAAAGAGATCTATGTTGGAGAA 3300  
 DB 3241 ATCTTACTTTTCTTGTACTACACAACCTATTTTAAAGAGATCTATGTTGGAGAA 3300  
 QY 3301 GGCGAAGTTGTACTATATGACATTAATCAAT 3330  
 DB 3301 GGCGAAGTTGTACTATATGACATTAATCAAT 3330  
 RESULT 3  
 AAA46205  
 ID AAA46205 standard; cDNA, 3263 BP.  
 XX  
 AC AAA46205;  
 XX  
 DT 04-SBP--2000 (first entry)  
 XX  
 DE cDNA encoding an Interphotoreceptor matrix proteoglycan (IPM150).  
 XX  
 KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 KW chromosome 6q13-q15; ocular disease; retinal detachment;  
 KW choriorretinal degeneration; retinal degeneration; cone degeneration;  
 KW age related macular degeneration; photoreceptor degeneration;  
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KW rod - cone dystrophy; cone-rod dystrophy; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 128..244  
 FT /\*tag= a  
 FT /transl\_except= (pos: 2411..2414, aa: Lys)  
 FT /product= "interphotoreceptor matrix proteoglycan IPM150"  
 PN WO200026367-A2.  
 PD 11-MAY-2000.  
 PF 29-OCT--1999; 99WO-US025440.  
 PR 29-OCT-1998; 98US-00183972.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Hageman GS, Kuehn MH;

DR WPI; 2000-365616/31.  
DR P-PSDB; AAY93336.

XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
PT preventing, diagnosing and treating ocular disorders such as retinal  
PT detachment and choriorretinal degeneration.

PS Claim 2; Fig 3; 183pp; English.

XX The present sequence encodes an interphotoreceptor matrix (IPM)  
CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).  
CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
CC is located on chromosome 6q13-q15, between markers CHC.GAT11F10 and  
CC D6S284. The IPM proteins may be used to supplement a patient's own  
CC production of the protein or to rectify alterations in their nucleic  
CC acids that result in expression of an inactive protein. The IPM nucleic  
CC acids may be used in this way to treat ocular diseases such as retinal  
CC detachment, choriorretinal degeneration, retinal degeneration, age related  
CC macular degeneration, photoreceptor degeneration, RPB (retinal pigment  
CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
CC also be used to assay for other modulators of IPM proteoglycan expression  
CC and activity that may be used to treat ocular diseases. The nucleic acids  
CC and proteins may also be used as diagnostic reagents to detect the  
CC presence of IPM nucleic acids and their products in samples from patients  
CC according to standard methodologies

XX Sequence 3263 BP; 1040 A; 721 C; 663 G; 838 T; 0 U; 1 Other;

Query Match 93.9%; Score 3125.6; DB 3; Length 3263;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 3257; Conservative 0; Mismatches 5; Indels 69; Gaps 6;

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QY 1 TAAACCAAGAAGTTTCTCTCATCTCGTATCATATATATATTTTTCACATTTC 60
DB 1 TAAACCAAGAAGTTTCTCTCATCTCGTATCATATATATATATTTTTCACATTTC 58
QY 61 TGTATCTTTTATGAGATTGAGTTGTTCTGTGATTTGTAACAAATTACCAATGCAC 120
DB 59 TGTATCTTTTATGAGATTGAGTTGTTCTGTGATTTGTAACAAATTACCAATGCAC 117
QY 121 AAAAGCAGATGTATTTGAAAATGAAAGCTATTTTGTGATTTTCTCCA 180
DB 118 AAAAGCAGATGTATTTGAAAATGAAAGCTATTTTGTGATTTTCTCCA 177
QY 181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCTTGAAACCTAAAGACATGA 240
DB 178 AGTTCAAGGAACCTAAAGATATCTCCATTAACATATACCTTGAAACCTAAAGACATGA 237
QY 241 CAATCCCCCAAGAAATGAACAACTGAAGTACTGAAAAATGTACAAATGCAACTAT 300
DB 238 CAATCCCCCAAGAAATGAACAACTGAAGTACTGAAAAATGTACAAATGCAACTAT 297
QY 301 GAGACGAATATTGATTTGGCAAAAGCATGAAACAAAAGATCCGATTTTCCCAACGGG 360
DB 298 GAGACGAATATTGATTTGGCAAAAGCATGAAACAAAAGATCCGATTTTCCCAACGGG 357
QY 361 GGTTAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGCTTCAAGCTTATTA 420
DB 358 GGTTAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGCTTCAAGCTTATTA 417
QY 421 TAGATTGAGAGTGTCTCAGGAAGCAGTATGGGAAGCATATCGGATCTTCTGGATGGCAT 480
DB 418 TAGATTGAGAGTGTCTCAGGAAGCAGTATGGGAAGCATATCGGATCTTCTGGATGGCAT 477
QY 481 CCCTGACACAGGGGAATATCAGGACTGGGTCAAGCATCTGCACAGAGACCTTCTGCT 540
DB 478 CCCTGACACAGGGGAATATCAGGACTGGGTCAAGCATCTGCACAGAGACCTTCTGCT 537
QY 541 CTTTGAATTGAAAAAATTCCAGCAATTTCCAGAGACCTGGATCTTCTCCAGAGAG 600
DB 538 CTTTGAATTGAAAAAATTCCAGCAATTTCCAGAGACCTGGATCTTCTCCAGAGAG 597

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QY 601 AATAAACAAGAGATTTCCCTGACAGAAAAGATGAATATCTGCAGAGAGACATTGGG 660
DB 598 AATAAACAAGAGATTTCCCTGACAGAAAAGATGAATATCTGCAGAGAGACATTGGG 657
QY 661 AGAGCTGTGAAAACCATTTGATTTCAACAGCAATCTACATTTCAAAAGACTGGGCACT 720
DB 658 AGAGCTGTGAAAACCATTTGATTTCAAC----- 687
QY 721 ATTCTAAGAAAACCTCAGAAAGACCAATTCAGATGTTGGCAACGTCTCACTTGGGCT 780
DB 688 -----AGATGTTGCCAACGTCTCACTTGGGCT 715
QY 781 TTCCCTCTCACTCTGATGACACCCCTCTCATATGAATTTCTGATTAATACATCAAGAC 840
DB 716 TTCCCTCTCACTCTGATGACACCCCTCTCATATGAATTTCTGATTAATACATCAAGAC 775
QY 841 ACCAAGATGCTTACACAGAAAAGAAAACAGAAATTCGTGTGTGGAGAGACAGAGGTG 900
DB 776 ACCAAGATGCTTACACAGAAAAGAAAACAGAAATTCGTGTGTGGAGAGACAGAGGTG 835
QY 901 GAGCTCAGCGTCTCTGTGTAAACCAAGATTTCAAGGACAGAGCTGCTACCTCCAGTCC 960
DB 836 GAGCTCAGCGTCTCTGTGTAAACCAAGATTTCAAGGACAGAGCTGCTACCTCCAGTCC 895
QY 961 CCATATTACAGAGACTAGCAGAAAAGTCCCAACTTCAGATGACAAAAGATATTTAAGAA 1020
DB 896 CCATATTACAGAGACTAGCAGAAAAGTCCCAACTTCAGATGACAAAAGATATTTAAGAA 955
QY 1021 CTTCCAGGATTTCAAAAAATTCATGTGTAGGATTTAGACCAAAAGAAAAGATGGC 1080
DB 956 CTTCCAGGATTTCAAAAAATTCATGTGTAGGATTTAGACCAAAAGAAAAGATGGC 1015
QY 1081 TCAAGCTTCACAGAGATGCACTTACCGGCATCTTTAAGAAACAGAGTGAAGCAAAA 1140
DB 1016 TCAAGCTTCACAGAGATGCACTTACCGGCATCTTTAAGAAACAGAGTGAAGCAAAA 1075
QY 1141 AGCCCTGCAAGTGAACCTCTGTCTTTGATTTCAACAAAATTTGAAAGTGAAGTCTAT 1200
DB 1076 AGCCCTGCAAGTGAACCTCTGTCTTTGATTTCAACAAAATTTGAAAGTGAAGTCTAT 1135
QY 1201 CATGGAACCATGAGAGAGAGACCAAGCAACCAAAATCTATCTCACAGTACAGACCTCAA 1260
DB 1136 CATGGAACCATGAGAGAGAGACCAAGCAACCAAAATCTATCTCACAGTACAGACCTCAA 1195
QY 1261 AGGCTGATCAGCAAAAGCACTAGAGAAAGAACTTTGATGTGGGGAACAATTCAGTTC 1320
DB 1196 AGGCTGATCAGCAAAAGCACTAGAGAAAGAACTTTGATGTGGGGAACAATTCAGTTC 1255
QY 1321 ACTGATGAATTTGCTGATCACTGCACAGCTTTGGTCTGACACCCATTCAGAGCTGCC 1380
DB 1256 ACTGATGAATTTGCTGATCACTGCACAGCTTTGGTCTGACACCCATTCAGAGCTGCC 1315
QY 1381 ACATCTTTTGTCTGTATTAACAGAGATGCTATCTTTAGTGCAGAACTTCTCTGTGAA 1440
DB 1316 ACATCTTTTGTCTGTATTAACAGAGATGCTATCTTTAGTGCAGAACTTCTCTGTGAA 1375
QY 1441 CCCGAGCTTGAACAGTGAAGAGAGACAGAGATGTCTACTGACACTTCTTGGTCTCA 1500
DB 1376 CCCGAGCTTGAACAGTGAAGAGAGACAGAGATGTCTACTGACACTTCTTGGTCTCA 1435
QY 1501 CCTGCTATGAGCTCTCACTCCCTGTCAAGAACTCCACTTCTTTATGGCATCAAGCATC 1560
DB 1436 CCTGCTATGAGCTCTCACTCCCTGTCAAGAACTCCACTTCTTTATGGCATCAAGCATC 1495
QY 1561 TTTCTCTGACTGATCAAGGACCAACAGATCAATATGCACTGACACAGAACTGCTAGTA 1620
DB 1496 TTTCTCTGACTGATCAAGGACCAACAGATCAATATGCACTGACACAGAACTGCTAGTA 1555
QY 1621 CCAAGGCTCAACATCCCAACCAAGATATTTCTGAAATCAGACCAACTGGCTCTGGGAAT 1680
DB 1556 CCAAGGCTCAACATCCCAACCAAGATATTTCTGAAATCAGACCAACTGGCTCTGGGAAT 1615
QY 1681 TCACATTCACCTGATCTTTCAGATGACAGCGCATCAATGACAGGTGGGAAGATATGCTC 1740

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Db      1616 TCACATCCACCTGCATCTTCAATGACAGCCGATCAAGTGGAGTGGCAAGATATGTC 1675
Qy      1741 AGACACTTGAATGAATGATCTGTCTGACACTCTGCCCCATCTGAGTTACAGAGCTC 1800
Db      1676 AGACACTTGAATGAATGATCTGTCTGACACTCTGCCCCATCTGAGTTACAGAGCTC 1735
Qy      1801 AGGAATATGTTCTGCTCCAGATCATTTCTTGGAGATACCATCTCTGCTCAAGCTTTA 1860
Db      1736 AGGAATATGTTCTGCTCCAGATCATTTCTTGGAGATACCATCTCTGCTCAAGCTTTA 1795
Qy      1861 CAGTATATCACCACTAGTCTATGACCATTTGCCCCAGAGGCGAGAGCTGTAAGTTC 1920
Db      1796 CAGTATATCACCACTAGTCTATGACCATTTGCCCCAGAGGCGAGAGCTGTAAGTTC 1855
Qy      1921 TTCACTCTGCTGTTGCTCAATGAGCTTCTCCAGAGCTGTTCAAGAGCTCTGT 1980
Db      1856 TTCACTCTGCTGTTGCTCAATGAGCTTCTCCAGAGCTGTTCAAGAGCTCTGT 1915
Qy      1981 GAGTACCGAGCTCTGGAGCAAACTTCAACAGAGCTGCTGCTCATATCTAGATCCAT 2040
Db      1916 GAGTACCGAGCTCTGGAGCAAACTTCAACAGAGCTGCTGCTCATATCTAGATCCAT 1975
Qy      2041 CTTACAGATTTAAGCACTTGAATATCTTAACCTTCAAGAAAGGAGTGTGTAAT 2100
Db      1976 CTTACAGATTTAAGCACTTGAATATCTTAACCTTCAAGAAAGGAGTGTGTAAT 2035
Qy      2101 AGCAAAATGAATTTGCTAAGTCTGTGCGGTATTAACCTTCAAGAGCTGTGACGGGATC 2160
Db      2036 AGCAAAATGAATTTGCTAAGTCTGTGCGGTATTAACCTTCAAGAGCTGTGACGGGATC 2095
Qy      2161 TTGGAGATTTTCTGCTCTGCTGACGCCAACTTCACTGGAATATGACGCTACTT 2220
Db      2096 TTGGAGATTTTCTGCTCTGCTGACGCCAACTTCACTGGAATATGACGCTACTT 2155
Qy      2221 CTCAACATTTGAACAGCTGATCAAGAGATCCCTGCAAGTCTTGGCGTGGCGGAATTT 2280
Db      2156 CTCAACATTTGAACAGCTGATCAAGAGATCCCTGCAAGTCTTGGCGTGGCGGAATTT 2215
Qy      2281 GCCCAATGTGTAAAGAACGAAACGAACTGAGAAAGCGAGTGTGCTGCAAAACAGGATAT 2340
Db      2216 GCCCAATGTGTAAAGAACGAAACGAACTGAGAAAGCGAGTGTGCTGCAAAACAGGATAT 2275
Qy      2341 GACACCCAGAGGAGCTGTGACGGTCTGGAACCAAGGCTTGTGCGCTTGGCAAAAGAA 2400
Db      2276 GACACCCAGAGGAGCTGTGACGGTCTGGAACCAAGGCTTGTGCG--CTTGGCAAAAGAA 2334
Qy      2401 TSCGAGTCTCTCAGGGAAGGAGGCTCATGCAAGTTGCGAGTCACTCTGAATATCA 2460
Db      2335 TSCGAGTCTCTCAGGGAAGGAGGCTCATGCG--GTTCCAGATCACTCTGAATATCA 2392
Qy      2461 GCATACAAATAGTGTATAAAAGTTCCAAAATCAACAAATATACAGGTAATCAATAA 2520
Db      2393 GCATACAAATAGTGTATAAAAGTTCCAAAATCAACAAATATACAGGTAATCAATAA 2452
Qy      2521 AGAATTTCTGAATTA-CTGACCGTAGAATATGAAATTTAACATCAAGATTGGAGAG 2579
Db      2453 AGAATTTCTGAATTA-CTGACCGTAGAATATGAAATTTAACATCAAGATTGGAGAG 2512
Qy      2580 AAAATTTAAAACTGAAAATGATATGAAATTAATGAGCTATCTCAAGAGAGATTTTGGC 2639
Db      2513 AAAATTTAAAACTGAAAATGATATGAAATTAATGAGCTATCTCAAGAGAGATTTTGGC 2572
Qy      2640 TTCTCAAGGAAAATGAGACAGGCAATTCATGAGTCAATCAAAATCTCAACATACAGTCA 2699
Db      2573 TTCTCAAGGAAAATGAGACAGGCAATTCATGAGTCAATCAAAATCTCAACATACAGTCA 2632
Qy      2700 AACCTGAGAACTGACACACACATATTTCAATATGAAAGATCATGTACTTGGCAACA 2759
Db      2633 AACCTGAGAACTGACACACACATATTTCAATATGAAAGATCATGTACTTGGCAACA 2692
Qy      2760 GTAATTTCTGAAAAAAGACCTTACTATTAATTAACCCCAATGCAATCAGGAAA 2819

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Db      2693 GTAATTTCTGAAAAAAGACCTTACTATTTATAAACCCCAATGCAATCAGGAAA 2752
Qy      2820 CATATTTTACTATTTCTTGGATGATGATCAAAATGATCAATACAGAGTTGCTTCACC 2879
Db      2753 CATATTTTACTATTTCTTGGATGATGATCAAAATGATCAATACAGAGTTGCTTCACC 2812
Qy      2880 TTCCCTGAAAAATTTTACTACAGATCATTTTGAACAAGATGCTTACTATTTGTTAAG 2939
Db      2813 TTCCCTGAAAAATTTTACTACAGATCATTTTGAACAAGATGCTTACTATTTGTTAAG 2872
Qy      2940 GACTGAACAAATTTATTTGGGAAGCAACTCTTATATGCTAGAGAAGTACATTTAAAGATG 2999
Db      2873 GACTGAACAAATTTATTTGGGAAGCAACTCTTATATGCTAGAGAAGTACATTTAAAGATG 2932
Qy      3000 ACTACTTACGACAGGAGATGACAGGTCTCTTAAACGATGAATGTATGATGTAGGAC 3059
Db      2993 ACTACTTACGACAGGAGATGACAGGTCTCTTAAACGATGAATGTATGATGTAGGAC 2992
Qy      3060 ACTGATGAGTGTATATATGCTCCACACTAGTCTGATTAACACAAACCTCAGATTTCA 3119
Db      2993 ACTGATGAGTGTATATATGCTCCACACTAGTCTGATTAACACAAACCTCAGATTTCA 3052
Qy      3120 GTTATTTAGGACACTAGTTTATTTAGCAACTAGCTGCTTACATATGATGACTGTTTGTGC 3179
Db      3053 GTTATTTAGGACACTAGTTTATTTAGCAACTAGCTGCTTACATATGATGACTGTTTGTGC 3112
Qy      3180 CATATATCTTTGAAATTTGTTCTTTAAAGAACTGAGGTTCAATACATACATGAAA 3239
Db      3113 CATATATCTTTGAAATTTGTTCTTTAAAGAACTGAGGTTCAATACATACATGAAA 3172
Qy      3240 AATCTTACTTTTCTTGTGTACTACACAAAGCTATTTTAAAGAAAGCTATGTTGGAGAA 3299
Db      3173 AATCTTACTTTTCTTGTGTGTACTACACAAAGCTATTTTAAAGAAAGCTATGTTGGAGAA 3232
Qy      3300 GGGCGAAGTGTACTATATGACATATCAAT 3330
Db      3233 GGGCGAAGTGTACTATATGACATATCAAT 3263

RESULT 4
ACCS7960
ID      ACCS7960 standard; cDNA; 3261 BP.
XX
AC      ACCS7960;
XX
DT      11-AUG-2003 (first entry)
XX
DE      Human Interphotoreceptor matrix IPM 150, isoform A variant, cDNA.
XX
KW      Human; Interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW      receptor; ophthalmological; gene therapy; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      128..2443
FT      FT      /*tag= a
FT      FT      /product= "IPM 150"
XX
XX      MO2003039346-A2.
XX      PD      15-MAY-2003.
XX      PF      08-NOV-2002; 2002WO-US036090.
XX      PR      08-NOV-2001; 2001US-0007270.
XX      XX      (IOWA ) UNIV IOWA RES FOUND.
XX      PA      Hageman GS, Kuehn MH;
XX      PI      Hageman GS, Kuehn MH;
XX      DR      MPI, 2003-441440/41.
XX      DR      P-PSDB; ABR42354.

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QY 1741 AGACACCTAGATGAATGGATCTGTCTGACACTCCCGCCCATCTGAGGTACAGAGCTC 1800  
 Db 1676 AGACACCTAGATGAATGGATCTGTCTGACACTCCCGCCCATCTGAGGTACAGAGCTC 1735  
 QY 1801 AGCGAATATGTTCTGTCTCCAGATCATTTCTTGAGAGATACCACTCTGTCTCAGCTTTA 1860  
 Db 1726 AGCGAATATGTTCTGTCTCCAGATCATTTCTTGAGAGATACCACTCTGTCTCAGCTTTA 1795  
 QY 1861 CAGTATATCAACCACTAGATTCTATGACCATTTGCCCAAGGGGCGAGAGCTGTAGTGTTC 1920  
 Db 1796 CAGTATATCAACCACTAGATTCTATGACCATTTGCCCAAGGGGCGAGAGCTGTAGTGTTC 1855  
 QY 1921 TTCACTGCGCGTGTCTTAACATGAGCTTCTGCAACGACCTGTGTAACAGAGCTCTCG 1980  
 Db 1856 TTCACTGCGCGTGTCTTAACATGAGCTTCTGCAACGACCTGTGTAACAGAGCTCTCG 1915  
 QY 1981 GAGTACCGAGCTCTGAGAGCAAACTTCAACAGCTGTGTTCATATCTACATCCAACT 2040  
 Db 1916 GAGTACCGAGCTCTGAGAGCAAACTTCAACAGCTGTGTTCATATCTACATCCAACT 1975  
 QY 2041 CTTACAGATTTTAAAGCACTGAAATCTTAACTTCAAGAAAGGAGGTGTATGTGAAT 2100  
 Db 1976 CTTACAGATTTTAAAGCACTGAAATCTTAACTTCAAGAAAGGAGGTGTATGTGAAT 2035  
 QY 2101 AGCAAAATGAATTTGCTTAAGTCTGTGCGGTATTAACCTCAACAGGCTGTGACGGGGTC 2160  
 Db 2036 AGCAAAATGAATTTGCTTAAGTCTGTGCGGTATTAACCTCAACAGGCTGTGACGGGGTC 2095  
 QY 2161 TTGAGAGATTTTGTCTGTCTGCTGACGCCCAACAACTCTGGAATATGACAGACTACTCT 2220  
 Db 2096 TTGAGAGATTTTGTCTGTCTGCTGACGCCCAACAACTCTGGAATATGACAGACTACTCT 2155  
 QY 2221 CTCAACATTTGAACAGCTGATCAAGCAAGATCCCTCAAGTTCTGTGCGTGTGCGCAATTT 2280  
 Db 2156 CTCAACATTTGAACAGCTGATCAAGCAAGATCCCTCAAGTTCTGTGCGTGTGCGCAATTT 2215  
 QY 2281 GCCCAATGTCTTAAGAAAGAAAGGAGCTGAGAGAGGGAGTGTCTGTGCAAAACAGAGATAT 2340  
 Db 2216 GCCCAATGTCTTAAGAAAGAAAGGAGCTGAGAGAGGGAGTGTCTGTGCAAAACAGAGATAT 2275  
 QY 2341 GACAGCCAGGGAGGCTGTGAGCGGTCTGGAACCAAGGCTCTGTGCGCTGTGCAAAAGGA 2400  
 Db 2276 GACAGCCAGGGAGGCTGTGAGCGGTCTGGAACCAAGGCTCTGTGCGCTGTGCAAAAGGA 2334  
 QY 2401 TGGAGGTCTCTCAGAGAAAGGAGCTCCATGACAGTTGCGAGTCACTCTGAAATCA 2460  
 Db 2335 TGGAGGTCTCTCAGAGAAAGGAGCTCCATGCG--GGTTCCAGATCACTCTGAAATCA 2392  
 QY 2461 GCATTCAAAATCTAGCTTTAAAGTTCCAAAATCAACAAAATTAACAGGTAATCTGTTAA 2520  
 Db 2393 GCATTCAAAATCTAGGTTT-AAAAGTTCCAAAATCAACAAAATTAACAGGTAATCTGTTAA 2451  
 QY 2521 AGAATTTCTGAATCTAGCCGTAGATATGAAGAAATTTAACTACCAAGATTGGGAAGA 2580  
 Db 2452 AGAATTTCTGAATCTAGCCGTAGATATGAAGAAATTTAACTACCAAGATTGGGAAGA 2511  
 QY 2581 AATTTAAAACTGAAATGTACATTAATCACTTAGGCTATCTTCAGAGAGATGATTGGCT 2640  
 Db 2512 AATTTAAAACTGAAATGTACATTAATCACTTAGGCTATCTTCAGAGAGATGATTGGCT 2571  
 QY 2641 TCTCAAGGAAATGAGACAGGATATTCATGTGGTCAATCAAAATCAACATACAGTCA 2700  
 Db 2572 TCTCAAGGAAATGAGACAGGATATTCATGTGGTCAATCAAAATCAACATACAGTCA 2631  
 QY 2701 CACTAGATACGACACACCATATTTCAAAATATGAAGAGTCAATCTTGGAACAG 2760  
 Db 2632 CACTAGATACGACACACCATATTTCAAAATATGAAGAGTCAATCTTGGAACAG 2691  
 QY 2761 TAAATTTGAAAAAAAAGCACTTAATTATTTAAAAACCCCAATGCAATCAGGAAC 2820  
 Db 2692 TAAATTTGAAAAAAAAGCACTTAATTATTTAAAAACCCCAATGCAATCAGGAAC 2751

QY 2821 ATATTTTACTATTCTGGATGATATGCAAAATGATCATAAAGCCAGGTTTGCTCACCT 2880  
 Db 2752 ATATTTTACTATTCTGGATGATATGCAAAATGATCATAAAGCCAGGTTTGCTCACCT 2811  
 QY 2881 TCCCTGAAAAATTTTACTCACAGATCATTTGCAACAAGCATATGCTTACTTATTTGTTAGG 2940  
 Db 2812 TCCCTGAAAAATTTTACTCACAGATCATTTGCAACAAGCATATGCTTACTTATTTGTTAGG 2871  
 QY 2941 ACTGAACAATTTATTTGGAGCAAACTTTATATGCTAGAAAGTACATTTAAAGATGA 3000  
 Db 2872 ACTGAACAATTTATTTGGAGCAAACTTTATATGCTAGAAAGTACATTTAAAGATGA 2931  
 QY 3001 CTACTTACGAGGGAGATGACAGTCTCTTAAAGCATGAATGTATGTAGTGTAGGCA 3060  
 Db 2932 CTACTTACGAGGGAGATGACAGTCTCTTAAAGCATGAATGTATGTAGTGTAGGCA 2991  
 QY 3061 CTGTAGTAGTATATATGTCTCCACACTAGCTGTATAAACAAACCTCAGTATTCAG 3120  
 Db 2992 CTGTAGTAGTATATATGTCTCCACACTAGCTGTATAAACAAACCTCAGTATTCAG 3051  
 QY 3121 TTATTTAGCACACTAGTTTATATAGCAACTATCTGTATCATAGTACTGTTTGTGCC 3180  
 Db 3052 TTATTTAGCACACTAGTTTATATAGCAACTATCTGTATCATAGTACTGTTTGTGCC 3111  
 QY 3181 AATAATCTTTGAATTTGTTCTTTAAAGAACTGAGGTTCAATACATACATGGAATA 3240  
 Db 3112 AATAATCTTTGAATTTGTTCTTTAAAGAACTGAGGTTCAATACATACATGGAATA 3171  
 QY 3241 ATCTTACTTTCTTGTACTACACAAAGCTATTTTAAAGAAAGTCTATGTTGGAGAAG 3300  
 Db 3172 ATCTTACTTTCTTGTACTACACAAAGCTATTTTAAAGAAAGTCTATGTTGGAGAAG 3231  
 QY 3301 GGCGAAGTTGTACTATATGACATATCAAT 3330  
 Db 3232 GGCGAAGTTGTACTATATGACATATCAAT 3261

RESULT 5  
 ADA14866  
 ID ADA14866 standard; cDNA; 3261 BP.  
 XX  
 AC ADA14866;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Human cDNA encoding variant IPWC 150 isoform A.  
 XX  
 KW ss: gene; human; IPWC 150 isoform A; gene therapy;  
 KW interphotoreceptor matrix component; IPWC; ocular disorder;  
 KW macular degeneration; photoreceptor death; retinal detachment.  
 OS  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 128..2443  
 FT /\*tag= a  
 FT /product= "Variant IPWC 150 isoform A"  
 PD US2002160954-A1.  
 PD 31-OCT-2002.  
 PF 08-NOV-2001; 2001US-00007270.  
 PR 29-OCT-1998; 98US-00183972.  
 PR 29-OCT-1999; 99US-00430195.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX PA  
 XX Hageman GS, Kuehn MH;  
 XX PI  
 XX WPI; 2003-238235/23.  
 DR P-PsDB; ADA14867.



XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.

XX Claim 3, Page 63-66; 76pp; English.

XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding  
CC variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
XX  
SQ

Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;

Query Match 93.8%; Score 3124.6; DB 10; Length 3261;

Beat Local Similarity 97.8%; Pred. No. 0;

Matches 3256; Conservative 0; Mismatches 5; Indels 69; Gaps 6;

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QY 1 TAAACCAAGAGGTTATCCTCAATCATCTGTATCATATATATATTTTCACTTC 60
DB 1 TAAACCAAGAGGTTATCCTCAATCATCTGTATCATATATATATTTT--CCTT 58
QY 61 TGTATCTTTTATGAGATTGAGGTTGTTCTGTATGTTATTCAGAAATTCAGATGAC 120
DB 59 TGTATCTTTTATGAGATTGAGGTTGTTCTGTATGTTATTCAGAAATTCAGATGAC 117
QY 121 AAAACCCAGAAATGTTATTTGAAAACCTAGAAAGCTATTTTGTGTTTGTGTTTCTCA 180
DB 118 AAAACCCAGAAATGTTATTTGAAAACCTAGAAAGCTATTTTGTGTTTGTGTTTCTCA 177
QY 181 AGTTCAAGAAACCAAGATATCTCCATTATACATATACATTTCTGAAACCTAAAGACATGA 240
DB 178 AGTTCAAGAAACCAAGATATCTCCATTATACATATACATTTCTGAAACCTAAAGACATGA 237
QY 241 CAATCCCCCAAGAAATGAAAACAATGAAAGTACTGAAATAATGTACAAATGTCAACTAT 300
DB 238 CAATCCCCCAAGAAATGAAAACAATGAAAGTACTGAAATAATGTACAAATGTCAACTAT 297
QY 301 GAGAGGAATATTCGATTTGGCAAGCATCGAACAAAGATCCGATTTTCCCAACGGG 360
DB 298 GAGAGGAATATTCGATTTGGCAAGCATCGAACAAAGATCCGATTTTCCCAACGGG 357
QY 361 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGTCTTCAAGCTTATTA 420
DB 358 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGTCTTCAAGCTTATTA 417
QY 421 TAGATTGAGAGTGTCTCAGGAAGCAGTATGGAGACATATCGATCTTTCTGGATCGAT 480
DB 418 TAGATTGAGAGTGTCTCAGGAAGCAGTATGGAGACATATCGATCTTTCTGGATCGAT 477
QY 481 CCCTGACACAGAGGGAATATCAGGACTGGGTCTGCACTTGCACGACGAGACCTTCTGCT 540
DB 478 CCCTGACACAGAGGGAATATCAGGACTGGGTCTGCACTTGCACGAGGAGACCTTCTGCT 537
QY 541 CTTTGACATTGGAAAAAATTGAGCAATCCGAGAGACCTGGAATCTTCTCCAGACAG 600
DB 538 CTTTGACATTGGAAAAAATTGAGCAATCCGAGAGACCTGGAATCTTCTCCAGACAG 597
QY 601 AATAAAACAGAGAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTGGG 660
DB 598 AATAAAACAGAGAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTGGG 657
QY 661 AGAGCTGTGTGAACCATTTGATTTCAACAGCAATCTACATTTCAAAAGACTTGGGCACT 720
DB 658 AGAGCTGTGTGAACCATTTGATTTCAAC----- 687
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QY 721 ATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTGGCAAGTCTCACTTGGGCT 780
DB 688 -----AATGTGGCAAGTCTCACTTGGGCT 715
QY 781 TTCCCTCTCACTCTGTATGACACCTCTCTCAATGAAATTTCTGATATATACATCAACGAC 840
DB 716 TTCCCTCTCACTCTGTATGACACCTCTCTCAATGAAATTTCTGATATATACATCAACGAC 775
QY 841 ACCAAGATGCTTAAACAGAAAGAAAGAAATTCGCTGTGTGGAGACACAGAGGTG 900
DB 776 ACCAAGATGCTTAAACAGAAAGAAAGAAATTCGCTGTGTGGAGACACAGAGGTG 835
QY 901 GAGCTCAGCGTCTCTGTGTAAACAGAAAGTTCAGAGCAGAGTCTGCTGATCCAGTCC 960
DB 836 GAGCTCAGCGTCTCTGTGTAAACAGAAAGTTCAGAGCAGAGTCTGCTGATCCAGTCC 895
QY 961 CCATATTACACAGAGCTAGCAGAAAGTCCCACTTCAGATGACAAAGATATTTAAGAA 1020
DB 896 CCATATTACACAGAGCTAGCAGAAAGTCCCACTTCAGATGACAAAGATATTTAAGAA 955
QY 1021 CTTCCAGATTTCAAAAAATTCATGTGTGTAGATTTAGACCAAGAAAGAAAGATGCG 1080
DB 956 CTTCCAGATTTCAAAAAATTCATGTGTGTAGATTTAGACCAAGAAAGAAAGATGCG 1015
QY 1081 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAACAAA 1140
DB 1016 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAACAAA 1075
QY 1141 AGCCCTGCAAGTGAACCTCTGTCTTTTGTATTCACAAATAATTTGAAGAAAGTCTAT 1200
DB 1076 AGCCCTGCAAGTGAACCTCTGTCTTTTGTATTCACAAATAATTTGAAGAAAGTCTAT 1135
QY 1201 CATGGAACCATGAGAGAGAGAAACAAACCAAAATCTATCTCACAGCTACAGACCTGAA 1260
DB 1136 CATGGAACCATGAGAGAGAGAAACAAACCAAAATCTATCTCACAGCTACAGACCTGAA 1195
QY 1261 AGGCTGATCAGCAAGCACTAGAGAAAGAAACAATCTTTGATGTGGGACAAATTCAGTTC 1320
DB 1196 AGGCTGATCAGCAAGCACTAGAGAAAGAAACAATCTTTGATGTGGGACAAATTCAGTTC 1255
QY 1321 ACTGATGAATGTCTGTATCATCTGCCAGCCTTTGTCTGTACACCCCAATCAGAGCTGCC 1380
DB 1256 ACTGATGAATGTCTGTATCATCTGCCAGCCTTTGTCTGTGTACACCCCAATCAGAGCTGCC 1315
QY 1381 ACATCTTTTGTGTATTAACAGAGAGTCTACTTTGATCCAGAACTTCTCTGTGTAA 1440
DB 1316 ACATCTTTTGTGTATTAACAGAGAGTCTACTTTGATCCAGAACTTCTCTGTGTAA 1375
QY 1441 CCCCACTTGTGAGACAGTGAACGAGACAGAGCATGGTCTACCTGACACTTTCTTGGTCTCA 1500
DB 1376 CCCCACTTGTGAGACAGTGAACGAGACAGAGCATGGTCTACCTGACACTTTCTTGGTCTCA 1435
QY 1501 CTTGCTATGGCTCTTACCTCTCTGTCCAGAAAGCTCCACTTTCTTTATGACATCAAGATC 1560
DB 1436 CTTGCTATGGCTCTTACCTCTCTGTCCAGAAAGCTCCACTTTCTTTATGACATCAAGATC 1495
QY 1561 TTTCTCTGATGATCAAGGACACACAGATCAATGTGCACTGACACAGACATGTAGTA 1620
DB 1496 TTTCTCTGATGATCAAGGACACACAGATCAATGTGCACTGACACAGACATGTAGTA 1555
QY 1621 CCAGGAGTCAACATCCCAACAGATGATTAATCTGCAATCAGCCAACTGGCTCTGGGAAT 1680
DB 1556 CCAGGAGTCAACATCCCAACAGATGATTAATCTGCAATCAGCCAACTGGCTCTGGGAAT 1615
QY 1681 TCAATTCACCTGTGATCTTCAGATGACAGCCGATCAAGTGAAGTGGGAAAGATATGCTC 1740
DB 1616 TCAATTCACCTGTGATCTTCAGATGACAGCCGATCAAGTGAAGTGGGAAAGATATGCTC 1675
QY 1741 AGACACTGATGAATGATATCTGTCTGACACTCTGCCCCATCTGAGATACCAAGCTC 1800
DB 1676 AGACACTGATGAATGATATCTGTCTGACACTCTGCCCCATCTGAGATACCAAGCTC 1735
QY 1801 AGCGAATATGTTGTGTCTCCAGATCATTTCTTGAGAGATACCACTCTGTCTCAGCTTTA 1860
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Db 1726 AGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGATACACCTCTGTCTCAGCTTTA 1795
Qy 1861 CAGTATATCACCACTAGTTCTATGACATGCCCCCAAGGCGGAGCTGTAGTGTTC 1920
Db 1796 CAGTATATCACCACTAGTTCTATGACATGCCCCCAAGGCGGAGCTGTAGTGTTC 1855
Qy 1921 TTCACTGTCCGCTGTGTAACTGAGCTTCTCCAAAGACCTGTTCACAAAGAGCTCTGTG 1980
Db 1856 TTCACTGTCCGCTGTGTAACTGAGCTTCTCCAAAGACCTGTTCACAAAGAGCTCTGTG 1915
Qy 1981 GAGTACCGAGCTCTGTGAGCAACATTTCAACAGCTGTGTCTTCATATCTAGATCCAT 2040
Db 1916 GAGTACCGAGCTCTGTGAGCAACATTTCAACAGCTGTGTCTTCATATCTAGATCCAT 1975
Qy 2041 CTATACAGATTTTAAAGCACTTGAATACTTAACTTCAAGAACGGAGTGTATGTGAT 2100
Db 1976 CTATACAGATTTTAAAGCACTTGAATACTTAACTTCAAGAACGGAGTGTATGTGAT 2035
Qy 2101 AGCAAAATGAAGTTGTCTAAAGCTGTGCGCTTAACTTCAACAGGCTGTGACGGGGTC 2160
Db 2036 AGCAAAATGAAGTTGTCTAAAGCTGTGCGCTTAACTTCAACAGGCTGTGACGGGGTC 2095
Qy 2161 TTGAGAGATTTTCTGTCTGTGACAGCCCAACAATCTCCATCTGAAATAGACAGTACTCT 2220
Db 2096 TTGAGAGATTTTCTGTCTGTGACAGCCCAACAATCTCCATCTGAAATAGACAGTACTCT 2155
Qy 2221 CTCAACATTGAAACAGCTGATCAGACAGATCCCTGCAAGTTCTGTGCGCTGTGCGCAATTT 2280
Db 2156 CTCAACATTGAAACAGCTGATCAGACAGATCCCTGCAAGTTCTGTGCGCTGTGCGCAATTT 2215
Qy 2281 GCCCAATGTCTAAAGCAACGAACTGAGAAAGGGAGTGTCTGTGCAACACAGATAT 2340
Db 2216 GCCCAATGTCTAAAGCAACGAACTGAGAAAGGGAGTGTCTGTGCAACACAGATAT 2275
Qy 2341 GACAGCCAGGGAGGCTGTGAGCGGTCTGGAACCAAGGCTCTGTGAGCCCTGTGCAAAAGAA 2400
Db 2276 GACAGCCAGGGAGGCTGTGAGCGGTCTGGAACCAAGGCTCTGTGAGCCCTGTGCAAAAGAA 2334
Qy 2401 TGGCAGGCTCTTCCAGGAAAGGAGCTCCATGCAAGTGTGCAAGTCACTCTGAAATCA 2460
Db 2335 TGGCAGGCTCTTCCAGGAAAGGAGCTCCATGCG--GGTTCCAGATCACTCTGAAATCA 2392
Qy 2461 GCATTCAAAACCTAGTGTAAAAAGTTCCAAAATCACAAAATTAACAAGTATCTGTAA 2520
Db 2393 GCATTCAAAACCTAGTGT--AAAAGTTCCAAAATCACAAAATTAACAAGTATCTGTAA 2451
Qy 2521 AGAAATTCGAATTACTGACCGTAGAATATGAAGAAATTTAACCATCAAGATTGGAGGA 2580
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Qy 2581 AATTAAAACTGAAATGTACATATTATGACTTGGCTATCTCAAGAGATGATTTGGCT 2640
Db 2512 AATTAAAACTGAAATGTACATATTATGACTTGGCTATCTCAAGAGATGATTTGGCT 2571
Qy 2641 TCTCAAGGAAATGAGACAGGCAATTCATGGTCAATCAAAATCAAGATCACTCA 2700
Db 2572 TCTCAAGGAAATGAGACAGGCAATTCATGGTCAATCAAAATCAAGATCACTCA 2631
Qy 2701 CACTGAGATGAGACACACCAATTTTCAAAATATGAAGAGTCAATGTTGGCAACAG 2760
Db 2632 CACTGAGATGAGACACCAATTTTCAAAATATGAAGAGTCAATGTTGGCAACAG 2691
Qy 2761 TAAATTCGAAAAAAGACACTTATTTATTTAAACCCCAATGCAATCAGGAAAC 2820
Db 2692 TAAATTCGAAAAAAGACACTTATTTATTTAAACCCCAATGCAATCAGGAAAC 2751
Qy 2821 ATATTTTACTATTTCTTGGATATATGTCAAAATGATCATAGCCAGGTTTGTTCACCT 2880
Db 2752 ATATTTTACTATTTCTTGGATATATGTCAAAATGATCATAGCCAGGTTTGTTCACCT 2811
Qy 2881 TCCCTGAATAATTTTACTGACAGATGATTTGCAACAGGATGCTACTTATTTGTTAGG 2940

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Db 2812 TCCGTAATAATTTTACTGACAGATCATTTGCAACAAGATAGCTACTTATGTTAGGG 2871
Qy 2941 ACTGAACAATTTTATTTGGGAACCAACTTTTATATGCTAGAAAGTACATTTTAAAGATGA 3000
Db 2872 ACTGAACAATTTTATTTGGGAACCAACTTTTATATGCTAGAAAGTACATTTTAAAGATGA 2931
Qy 3001 CTACTTACGAGGGAGATGAGTGTCTCTTAAAGCATGAATGTATGTATGTGTAGGCA 3060
Db 2932 CTACTTACGAGGGAGATGAGTGTCTCTTAAAGCATGAATGTATGTATGTGTAGGCA 2991
Qy 3061 CTGTAGTAGTATATATATGCTCCACACTAGCTGTATTAACAAACCACTAGATTGAG 3120
Db 2992 CTGTAGTAGTATATATATGCTCCACACTAGCTGTATTAACAAACCACTAGATTGAG 3051
Qy 3121 TTATTTAGCACACTAGTTTATTAACGCACTACTGCTTACATAGTACTGTTTGTGCC 3180
Db 3052 TTATTTAGCACACTAGTTTATTAACGCACTACTGCTTACATAGTACTGTTTGTGCC 3111
Qy 3181 AATAATCTTGAATTTGTTCTTTAAAGAACGAGGTTCAATACATACATGGAATA 3240
Db 3112 AATAATCTTGAATTTGTTCTTTAAAGAACGAGGTTCAATACATACATGGAATA 3171
Qy 3241 ATCTTACTTTCTTGTACTACACAAAGCTATTTTAAAGAAATGCTATGTTGGAGAG 3300
Db 3172 ATCTTACTTTCTTGTACTACACAAAGCTATTTTAAAGAAATGCTATGTTGGAGAG 3231
Qy 3301 GCGGAAGTTGACTATATGACATATCAAT 3330
Db 3232 GCGGAAGTTGACTATATGACATATCAAT 3261

RESULT 6
ACCS7947
ID ACCS7947 standard; cDNA; 2887 BP.
XX
AC CCS7947;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human interphotoreceptor matrix IPM 150, isoform B, cDNA.
XX
KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX receptor; ophthalmological; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..2143
FT /tag= a
FT /product= "IPM 150"
FT /partial
FT /note= "No start codon"
XX
PW MO2003039346-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036090.
XX
PR 08-NOV-2001; 2001US-0007270.
XX
PA (IOWA ) UNIV IOWA RES POUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI, 2003-441440/41.
XX
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX
PS Claim 1; Page 78-79; 105pp; English.
XX

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CC The present sequence is that of cDNA encoding isoform B of novel human  
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polypeptides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression  
XX  
SQ Sequence 2887 BP, 899 A, 659 C, 606 G, 723 T, 0 U, 0 Other;

Query Match 83.1%; Score 2765.8; DB 9; Length 2887;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 2851; Conservative 0; Mismatches 22; Indels 62; Gaps 1;

QY 396 TTTTGAAGAGCTTCAAGCTTATTAATTAAGAGTGTGTCAGAGAGCAAGTATGGAG 455  
DB 15 TTTTGGATTTTCTCCAAAGTTCAAGAACCAAGTGTGTCAGAGAGCAAGTATGGAG 74  
QY 456 CATATCGATCTTTCTGATGTCATCCCTGACACAGGGGAAATATGAGATCGGGTCACA 515  
DB 75 CATATCGATCTTTCTGATGTCATCCCTGACACAGGGGAAATATGAGATCGGGTCACA 134  
QY 516 TCTGCGACAGAGAGACCTTCTGCTCTTGTGACATTTGAAAAAATCTTCAGCAATTC 575  
DB 135 TCTGCGACAGAGAGACCTTCTGCTCTTGTGACATTTGAAAAAATCTTCAGCAATTC 194  
QY 576 AGCAGCTGATCTTCTCCAGACAGAGAAATTAACAGAGAAATTTCCCTGACAGAAAAATG 635  
DB 195 AGCAGCTGATCTTCTCCAGACAGAGAAATTAACAGAGAAATTTCCCTGACAGAAAAATG 254  
QY 636 AAATTCGCGAGAGAGACATTTGGAGAGAGCTGTGAAAAACCTTGTCAATTTCAACGAA 695  
DB 255 AAATTCGCGAGAGAGACATTTGGAGAGAGCTGTGAAAAACCTTGTCAATTTCAACGAA 309  
QY 696 TCTACATTTCAAGAAGCTTGGGAGATTTCTAAGAAAAACCTCAGAGAGCAATTCAGAA 755  
DB 310 -----AGA 312  
QY 756 TGTTCGCAAGCTCTCACTTGGGCTTTTCCCTCTCACTCTGTATGACACCTTCCTCAATGA 815  
DB 313 TGTTCGCAAGCTCTCACTTGGGCTTTTCCCTCTCACTCTGTATGACACCTTCCTCAATGA 372  
QY 816 AATTCGCAATATATACATCAACGACCAAGATGCTCTACACAGAAAAAGAAACAGAAAT 875  
DB 373 AATTCGCAATATATACATCAACGACCAAGATGCTCTACACAGAAAAAGAAACAGAAAT 432  
QY 876 CGCTGTGTTGAGAGAGAGAGGTGAGCTGAGCTCTCTGTGTAACACAGAAATTTCAA 935  
DB 433 CGCTGTGTTGAGAGAGAGAGGTGAGCTGAGCTCTCTGTGTAACACAGAAATTTCAA 492  
QY 936 GCGAGAGCTCGCTGACTCCCAAGTCCCATATTTACAGAGAGCTAGACAGAGAAATGCCAACT 995  
DB 493 GCGAGAGCTCGCTGACTCCCAAGTCCCATATTTACAGAGAGCTAGACAGAGAAATGCCAACT 552  
QY 996 TCAGATGCAAAAGATATTTAAGAACTTCAGAGATTTCAAAAAAATTCATGTGTATGAGATT 1055  
DB 553 TCAGATGCAAAAGATATTTAAGAACTTCAGAGATTTCAAAAAAATTCATGTGTATGAGATT 612  
QY 1056 TAGACCAAGAGAGAGAGAGATGGCTCAAGCTCCACAGAGATGCAACTAGCGCATGTT 1115  
DB 613 TAGACCAAGAGAGAGAGAGATGGCTCAAGCTCCACAGAGATGCAACTAGCGCATGTT 672  
QY 1116 TAAGAGACACAGTGAAG 1175  
DB 1175

DB 673 TAAGAGACACAGTGCAG 732  
QY 1176 CAAATTTGAAGTGAAGAGAGAGTCTATCATGAAACCATGAGAGAGAGAGAGAGAGAGAGAT 1235  
DB 733 CAAATTTGAAGTGAAGAGAGAGTCTATCATGAAACCATGAGAGAGAGAGAGAGAGAGAGAT 792  
QY 1236 CTATCTCAGAGCTACAGAGCTCAAAAAGCTGATGACAGCAAGCACTAGAGAGAGAGAGAGATC 1295  
DB 793 CTATCTCAGAGCTACAGAGCTCAAAAAGCTGATGACAGCAAGCACTAGAGAGAGAGAGATC 852  
QY 1296 TTTGATGTGGAGCAATTTCACTGATGAAATTTGCTGATCATCTGCCACCTTTGG 1355  
DB 853 TTTGATGTGGAGCAATTTCACTGATGAAATTTGCTGATCATCTGCCACCTTTGG 912  
QY 1356 TCTGACACCCCAATCAGAGCTGCCCACTTTTGTGTTTAAACAGAGAGATGCTACTTT 1415  
DB 913 TCTGACACCCCAATCAGAGCTGCCCACTTTTGTGTTTAAACAGAGAGATGCTACTTT 972  
QY 1416 GAGTCCAGAACTTCTCTGTTGAAACCCAGAGCTTGAACAGTGAACGAGAGAGAGATG 1475  
DB 973 GAGTCCAGAACTTCTCTGTTGAAACCCAGAGCTTGAACAGTGAACGAGAGAGAGATG 1032  
QY 1476 TCTACCTGACACTTCTGTTGTTCACTGCTATGAGCTCTACCTCTGTCAGAAAGCTCC 1535  
DB 1033 TCTACCTGACACTTCTGTTGTTCACTGCTATGAGCTCTACCTCTGTCAGAAAGCTCC 1092  
QY 1536 ACCTTTCTTTATGACATGTAACATCTCTCTGATGATGATGATGATGATGATGATGATGAT 1595  
DB 1093 ACCTTTCTTTATGACATGTAACATCTCTCTGATGATGATGATGATGATGATGATGATGAT 1152  
QY 1596 GGCACATGACCAAGCAATGTAGTACAGAGGCTGACATCCCAAGATTTATTTCTGC 1655  
DB 1153 GGCACATGACCAAGCAATGTAGTACAGAGGCTGACATCCCAAGATTTATTTCTGC 1212  
QY 1656 AATGACCAACTGCTCTGGAATTTTCACTCACTGATCTTCAAGTGAACAGCGATC 1715  
DB 1213 AATGACCAACTGCTCTGGAATTTTCACTCACTGATCTTCAAGTGAACAGCGATC 1272  
QY 1716 AAGTGCAGTGGCGAAGATAGTTCAGACACTGATGAAATGAAATGAAATGAAATGAAATG 1775  
DB 1273 AAGTGCAGTGGCGAAGATAGTTCAGACACTGATGAAATGAAATGAAATGAAATGAAATG 1332  
QY 1776 TGCCCCATCTGAGTACAGAGCTCAGAGATATGTTCTGTCCAGATCAATTTCTTGA 1835  
DB 1333 TGCCCCATCTGAGTACAGAGCTCAGAGATATGTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GATATCACTCTGCTCACTTTTACATATATACCACTAGTTCTATGACCATTTGCC 1895  
DB 1393 GATATCACTCTGCTCACTTTTACATATATACCACTAGTTCTATGACCATTTGCC 1452  
QY 1896 CAAGGCGGAGAGAGCTGATGATGTTCTTCAAGTCTGCTGATGATGATGATGATGATGATGAT 1955  
DB 1453 CAAGGCGGAGAGAGCTGATGATGTTCTTCAAGTCTGCTGATGATGATGATGATGATGATGAT 1512  
QY 1956 CGACTGTTCAACAAGAGCTCTGAGATACAGAGCTCTGAGCAACAATTCACAGAGCT 2015  
DB 1513 CGACTGTTCAACAAGAGCTCTGAGATACAGAGCTCTGAGCAACAATTCACAGAGCT 1572  
QY 2016 GCTGGTTCATATCTAGATCAATCTTACAGATTTAAGCACTTGAATTAATTAATTAATTA 2075  
DB 1573 GCTGGTTCATATCTAGATCAATCTTACAGATTTAAGCACTTGAATTAATTAATTAATTA 1632  
QY 2076 CAGAAAGGAGAGTGAATGGAATAGCAAAATGAAGTTGCTAAAGTCTGAGCGGTATTA 2135  
DB 1633 CAGAAAGGAGAGTGAATGGAATAGCAAAATGAAGTTGCTAAAGTCTGAGCGGTATTA 1692  
QY 2136 CCTCACAAGAGCTGACAGGGGCTTGTGAGAGATTTTGTCTGTGACGCCCAACAAT 2195  
DB 1693 CCTCACAAGAGCTGACAGGGGCTTGTGAGAGATTTTGTCTGTGACGCCCAACAAT 1752  
QY 2196 CCAATCTGAAATTAAGACAGCTACTCTGCAATTTGAACCAAGCTGATCAAGAGATCCCTG 2255  
DB 1753 CCAATCTGAAATTAAGACAGCTACTCTGCAATTTGAACCAAGCTGATCAAGAGATCCCTG 1812

OY	2256	CAAGTTCCTGGGCCTGGCGCGAAATTTGCCCATATGTGTAAAGAACAAACGCACTGAGCAAGC	2315
Db	1813	CAAGTTCCTGGGCCTGGCGCGAAATTTGCCCATATGTGTAAAGAACAAACGCACTGAGCAAGC	1872
OY	2316	GGAGTGTGCTGCGCAAAACCGAGATATGACAGCGAGGGAGCCTGGAACGCTCTGGAAACGAG	2375
Db	1873	GGAGTGTGCTGCGCAAAACCGAGATATGACAGCGAGGGAGCCTGGAACGCTCTGGAAACGAG	1932
OY	2376	CCTCTGTGGCCCTGGCAAAAGAAATGGGAGGTCTCCAGGGAAAGGAGCTCCATGCGAG	2435
Db	1933	CCTCTGTGGCCCTGGCAAAAGAAATGGGAGGTCTCCAGGGAAAGGAGCTCCATGCGAG	1992
OY	2436	GTTGCGACAGATCACTCTGAAAATCTCAAGCACTAACAAAACCTGTGTAAAAAGTCCAAAATCA	2495
Db	1993	GTTGCGACAGATCACTCTGAAAATCTCAAGCACTAACAAAACCTGTGTAAAAAGTCCAAAATCA	2052
OY	2496	ACAAAATTAACAAGGTAATCAGTAAAGAAATTCGAAATTAACCTGACCCGTGAATATGAAGA	2555
Db	2053	ACAAAATTAACAAGGTAATCAGTAAAGAAATTCGAAATTAACCTGACCCGTGAATATGAAGA	2112
OY	2556	ATTTAACCATGAAGTTTGGGAAGGAAATTAATACTGAAATATGACAAATTAATCACTTAGG	2615
Db	2113	ATTTAACCATGAAGTTTGGGAAGGAAATTAATACTGAAATATGACAAATTAATCACTTAGG	2172
OY	2616	CTATCTCAAGAGAGATGATTTGGCTTCCCTCAAGAAAATGAGAGACAGGCATATTCATGGGT	2675
Db	2173	CTATCTCAAGAGAGATGATTTGGCTTCCCTCAAGAAAATGAGAGACAGGCATATTCATGGGT	2232
OY	2676	CATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGACACACCATATTTCAAATATA	2735
Db	2233	CATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGACACACCATATTTCAAATATA	2292
OY	2736	GAAAGTCATGTATCTGGGCAACGAGTAATCTGAAAAAAAAGACACTTACTTATTTATA	2795
Db	2293	GAAAGTCATGTATCTGGGCAACGAGTAATCTGAAAAAAAAGACACTTACTTATTTATA	2352
OY	2796	AAACCCCAATGCAATCAGCGAAAACATATTTTATCTATCTTGGATGATGTCAAAATGA	2855
Db	2353	AAACCCCAATGCAATCAGCGAAAACATATTTTATCTATCTTGGATGATGTCAAAATGA	2412
OY	2856	TCATTAAGCAGAGTTTGGCTTCCACTCCCTCGTAAAAATTTTACTCAAGATCAATTTGGCAACA	2915
Db	2413	TCATTAAGCAGAGTTTGGCTTCCACTCCCTCGTAAAAATTTTACTCAAGATCAATTTGGCAACA	2472
OY	2916	AGCATAGCTTACTTATTTGTTTGGGACTGAACAAATTTTGGGAAGCAAACTCTTTATAT	2975
Db	2473	AGCATAGCTTACTTATTTGTTTGGGACTGAACAAATTTTGGGAAGCAAACTCTTTATAT	2532
OY	2976	GCTAGAAAGTACATTTAAAGATGACCTTACCGAGGAGATGCAAGGTCTCTTAAACG	3035
Db	2533	GCTAGAAAGTACATTTAAAGATGACCTTACCGAGGAGATGCAAGGTCTCTTAAACG	2592
OY	3036	CATGATATGTATGTGTGTGGTGGGCACTGTATGTATGTATATATATGCTCCACATACGCT	3095
Db	2593	CATGATATGTATGTGTGTGGTGGGCACTGTATGTATGTATATATATGCTCCACATACGCT	2652
OY	3096	GATAAACCAAAACCTCAGTATTTCAATTATTAAGGACACTAGTTTATACGCACTACTGC	3155
Db	2653	GATAAACCAAAACCTCAGTATTTCAATTATTAAGGACACTAGTTTATACGCACTACTGC	2712
OY	3156	TTACCTAGTAACTGTTTTTTTGGCCAAATATCTTTGAATTTGTTCTTTTAAAGAACTGAG	3215
Db	2713	TTACCTAGTAACTGTTTTTTTGGCCAAATATCTTTGAATTTGTTCTTTTAAAGAACTGAG	2772
OY	3216	GTTCCAGATACATACCAATGGAATAATCTTACTTTTCTGTACTACCAAGCATATTTT	3275
Db	2773	GTTCCAGATACATACCAATGGAATAATCTTACTTTTCTGTACTACCAAGCATATTTT	2832
OY	3276	AAAGAAATGCTATGTGTGGAGAGAGGCGAAAGTTGTACTATATATGACATATCAAT	3330
Db	2833	AAAGAAATGCTATGTGTGGAGAGAGGCGAAAGTTGTACTATATATGACATATCAAT	2887

XX	RESUTF 7
ID	ADA14842
AD	ADA14842 standard; cDNA, 2887 BP.
AC	ADA14842;
XX	
DT	06-NOV-2003 (first entry)
XX	
DE	Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.
XX	
KM	ss; gene; human; IPMC 150 isoform B; gene therapy;
KW	interphotoreceptor matrix component; IPMC; ocular disorder;
KX	macular degeneration; photoreceptor death; retinal detachment.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	CDS 5..2143
FT	/tag= a
FT	/partial
FT	/product= "IPMC 150 isoform B"
FT	/note= "No start codon given. Encodes residues 8-719 of {seqid:4}"
PN	US2002160954-A1.
PD	31-OCT-2002.
PF	08-NOV-2001; 2001US-00007270.
PR	29-OCT-1998; 98US-00183972.
PR	29-OCT-1999; 99US-00430195.
PA	(IOMA ) UNIV IOWA RES FOUND.
PI	Hageman GS, Kuehn MH;
DR	WPI; 2003-238235/23.
DR	P-Psdb; ADA14843.
PT	New isolated or recombinant interphotoreceptor matrix component
PT	polynucleotide and polypeptide, useful for diagnosing, preventing,
PT	treating or prognosticating ocular disorders, e.g. macular degeneration
PT	or retinal detachment.
PS	Claim 3; Page 33-34; 76pp; English.
CC	The invention relates to an isolated or recombinant interphotoreceptor
CC	matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC	comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC	gene operatively linked to the IPMC polynucleotide. The IPMC
CC	polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC	preventing, treating or prognosticating ocular disorders, e.g. macular
CC	degeneration, photoreceptor death or retinal detachment. They are also
CC	useful for identifying a compound capable of modulating IPMC gene
CC	expression in a cell. The present sequence represents cDNA encoding human
CC	interphotoreceptor matrix component, IPMC, 150 isoform B.
SQ	Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;
Query Match	83.1%; Score 2765.8; DB 10; Length 2887;
Best Local Similarity	97.1%; Fred. No. 0;
Matches 2851; Conservative	0; Mismatches 22; Indels 62; Gaps 1
DG	396 TTTTGAAGCTTCCTCAAGCTTATTATTAAGTAGAGTGTCAGAGAAGATGGAGAAG 455
15 TTTTGGATTTTTCTCCAAGTTCAAGAACCAAAAGTGTGCAGGAACAAGATGGAGAAG 74	
DG	456 CATATCGATCTTTCTGGATGCGATCCTTGACACAGGGGAATATAGACTGGGTCAGCA 515
75 CATATCGATCTTTCTGGATGCGATCCTTGACACAGGGGAATATAGACTGGGTCAGCA 134	

QY 516 TCTGCCAGCAGGAGACTTCTGCTCTTGTGACATTTGAGAAAACTTCAGCAATTCAGG 575  
Db 135 TCTGCCAGCAGGAGACTTCTGCTCTTGTGACATTTGAGAAAACTTCAGCAATTCAGG 194  
QY 576 AGCAGCTGGATCTTCTCCAGCAGAGAAATPAAAACAGAGAGTTTCCCTGACGAAAAAGTG 635  
Db 195 AGCAGCTGGATCTTCTCCAGCAGAGAAATPAAAACAGAGAGTTTCCCTGACGAAAAAGTG 254  
QY 636 AAATATCTGCAGAGAGACATTTGGGAGAGCTGTGAAACCATTTGCAATTTCAACAGAA 695  
Db 255 AAATATCTGCAGAGAGACATTTGGGAGAGCTGTGAAACCATTTGCAATTTCAAC----- 309  
QY 696 TCTACATTTCAAAAGACTTGGGAGATTTTAAAGAAAACTTCAGAGAGCAATTTCAAGA 755  
Db 310 -----AGA 312  
QY 756 TGTTCGCAACGTCTCACTTTGGGCTTTTCCCTCTCACTCTGTGATGACACCTTCATATGA 815  
Db 313 TGTTCGCAACGTCTCACTTTGGGCTTTTCCCTCTCACTCTGTGATGACACCTTCATATGA 372  
QY 816 AATTCTGATATATACCTCAACGAGACCAAGATGCTCAACAGAGAAAGAGAAACAGAAATT 875  
Db 373 AATTCTGATATATACCTCAACGAGACCAAGATGCTCAACAGAGAAAGAGAAACAGAAATT 432  
QY 876 CGCTGTGTTGAGAGCAGAGAGGTGAGCTCAGCGTCTCTGTGTAAACAGAGAGTTCAA 935  
Db 433 CGCTGTGTTGAGAGCAGAGAGGTGAGCTCAGCGTCTCTGTGTAAACAGAGAGTTCAA 492  
QY 936 GGCAGAGCTCGCTGACTCCCAAGTCCCATATTAACAAGAGCTAGCAGAGAAAGTCCCAACT 995  
Db 493 GGCAGAGCTCGCTGACTCCCAAGTCCCATATTAACAAGAGCTAGCAGAGAAAGTCCCAACT 552  
QY 996 TCAGATGCAAAAGATATTTAAGAACTTCAGAGATTTCAAAAAATCCATGTGTAGATT 1055  
Db 553 TCAGATGCAAAAGATATTTAAGAACTTCAGAGATTTCAAAAAATCCATGTGTAGATT 612  
QY 1056 TAGACCAAGAGAGAGAGATGCTCAAGCTCCAAGAGATGCACTTACCGGCATCTT 1115  
Db 613 TAGACCAAGAGAGAGAGATGCTCAAGCTCCAAGAGATGCACTTACCGGCATCTT 672  
QY 1116 TAAAGAGACAGATGCAAG 1175  
Db 673 TAAAGAGACAGATGCAAG 732  
QY 1176 CAAAATTGAG 1235  
Db 733 CAAAATTGAG 792  
QY 1236 CTATCTCAGAGCTACAGACCTCAAAAGGCTGATCAGCAAGAGAGAGAGAGAGAGAGAGAG 1295  
Db 793 CTATCTCAGAGCTACAGACCTCAAAAGGCTGATCAGCAAGAGAGAGAGAGAGAGAGAGAG 852  
QY 1296 TTTGAGATGAGGAGACATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCTTTGG 1355  
Db 853 TTTGAGATGAGGAGACATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCTTTGG 912  
QY 1356 TCCCTGACACCAATCAG 1415  
Db 913 TCCCTGACACCAATCAG 972  
QY 1416 GAGTCAGAGAACTTCTCTGTTGAAACCCAGAGTTGAGAGAGAGAGAGAGAGAGAGAGAG 1475  
Db 973 GAGTCAGAGAACTTCTCTGTTGAAACCCAGAGTTGAGAGAGAGAGAGAGAGAGAGAGAG 1032  
QY 1476 TTTACCTGACATTTCTTGGTCTTCACCTGCTATGAGCTTCTTACCTCTCTGCAAGAGCTC 1535  
Db 1033 TTTACCTGACATTTCTTGGTCTTCACCTGCTATGAGCTTCTTACCTCTCTGCAAGAGCTC 1092  
QY 1536 ACCCTTCTTATGAGATCAAGAGATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1595  
Db 1093 ACCCTTCTTATGAGATCAAGAGATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1152  
QY 1596 GGCACATGACAGACATGCTAGTACAGAGAGCTCAACATCCACAGTGAATTAATTCAGC 1655

Db 1153 GGCACATGACAGACATGCTAGTACAGAGAGCTCAACATCCCAACAGTGAATTAATTCAGC 1212  
QY 1656 AATGAGCCAACTGGCTCTGGGAAATTTCAATCCACCTGCACTTCAAGTGAACAGCCGATC 1715  
Db 1213 AATGAGCCAACTGGCTCTGGGAAATTTCAATCCACCTGCACTTCAAGTGAACAGCCGATC 1272  
QY 1716 AAGTGAAGTGGCAAGATATGATCAGACACTAGATGAATGGAATCTGTCTGACACTCC 1775  
Db 1273 AAGTGAAGTGGCAAGATATGATCAGACACTAGATGAATGGAATCTGTCTGACACTCC 1332  
QY 1776 TGCCCATCTGAGGTACAGAGCTCAAGGAAATATGTTTCTGTCCAGATCAATTTCTTGA 1835  
Db 1333 TGCCCATCTGAGGTACAGAGCTCAAGGAAATATGTTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GGAATACCACTCTGTCTCAGCTTTTACAGTATATACCACTAGTTCTATGACATTTGCCCC 1895  
Db 1393 GGAATACCACTCTGTCTCAGCTTTTACAGTATATACCACTAGTTCTATGACATTTGCCCC 1452  
QY 1896 CAAGGAGCCGAGAGCTGGTATGTTCTTCAAGCTGAGGTTGCTAAATAGGCTTCTCCAA 1955  
Db 1453 CAAGGAGCCGAGAGCTGGTATGTTCTTCAAGCTGAGGTTGCTAAATAGGCTTCTCCAA 1512  
QY 1956 CGACTGTTCAACAGAGCTCTGAGATACAGAGCTCTGAGCAACAAATTCACAGACT 2015  
Db 1513 CGACTGTTCAACAGAGCTCTGAGATACAGAGCTCTGAGCAACAAATTCACAGACT 1572  
QY 2016 GCTGTTTCAATATCTAGATCCAACTTTACAGAGATTTAAGCACTTGAAATATCTTAATT 2075  
Db 1573 GCTGTTTCAATATCTAGATCCAACTTTACAGAGATTTAAGCACTTGAAATATCTTAATT 1632  
QY 2076 CAGAAACGGAGAGTGAATTTGATGATAGCAAAATGAATTTGCTAAGTGTGCGCTATAA 2135  
Db 1633 CAGAAACGGAGAGTGAATTTGATGATAGCAAAATGAATTTGCTAAGTGTGCGCTATAA 1692  
QY 2136 CCTGACCAAGGCTGTGACAGGAGTCTTGAGAGATTTTCTGTCTGTGACCCCAACACT 2195  
Db 1693 CCTGACCAAGGCTGTGACAGGAGTCTTGAGAGATTTTCTGTCTGTGACCCCAACACT 1752  
QY 2196 CCATCTGGAATATACAGACTACTCTCTCAATTTGAACACCACTGATCAAGAGATCCCTG 2255  
Db 1753 CCATCTGGAATATACAGACTACTCTCTCAATTTGAACACCACTGATCAAGAGATCCCTG 1812  
QY 2256 CAAGTCTCTGAGCTGCGGAGAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2315  
Db 1813 CAAGTCTCTGAGCTGCGGAGAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1872  
QY 2316 GAGAGTGTGCTGCAACCAAGATATGACAGCCAGGAGAGCTGGAACGATCGAAG 2375  
Db 1873 GAGAGTGTGCTGCAACCAAGATATGACAGCCAGGAGAGCTGGAACGATCGAAG 1932  
QY 2376 CCTCTGTGGCCCTGAGCAAAAGAGATGAGAGTCTCCAGAGAGAGAGAGAGAGAGAGAG 2435  
Db 1933 CCTCTGTGGCCCTGAGCAAAAGAGATGAGAGTCTCCAGAGAGAGAGAGAGAGAGAGAG 1992  
QY 2436 GTTGACAGATCACTCTGAAATCAAGCATACAAAATCTAGTGTAAAGAGTTCCAAATATCA 2495  
Db 1993 GTTGACAGATCACTCTGAAATCAAGCATACAAAATCTAGTGTAAAGAGTTCCAAATATCA 2052  
QY 2496 ACAAAATPACAAAGTATCAGTAAAGAAATTTGAAATTAAGTACCGTGAATATGAAAG 2555  
Db 2053 ACAAAATPACAAAGTATCAGTAAAGAAATTTGAAATTAAGTACCGTGAATATGAAAG 2112  
QY 2556 ATTTAACATCAAGATTTGGAGAGAAATTTAAATTTGAAATTTGATCAATTAATCACTT 2615  
Db 2113 ATTTAACATCAAGATTTGGAGAGAAATTTAAATTTGAAATTTGATCAATTAATCACTT 2172  
QY 2616 CTATCTCAAGAGAGATGTTGCTTCTCAAGAGAAATGAGAGACAGGATATTCATGAGGT 2675  
Db 2173 CTATCTCAAGAGAGATGTTGCTTCTCAAGAGAAATGAGAGACAGGATATTCATGAGGT 2232  
QY 2676 CATCAAAATCCAGATATCAGTCAACACTGGAATCAGACACACATATTTCAATATA 2735

Db 2233 CATCAAAATCCAGACATATAGTCACACTGAGATCAGACACACCATATATTTCAATATATA 2292  
 QY 2736 GAAGAGTCATGTACTTGGACACCGATTAATTCGAAAAAAGACCTTACTATATATTA 2795  
 Db 2293 GAAGAGTCATGTACTTGGACACCGATTAATTCGAAAAAAGACCTTACTATATATTA 2352  
 QY 2796 AAACCCCAATGCAATCAGCGAAGAAATTTTACTATTCTTGGAGATAGTCAAAATGA 2855  
 Db 2353 AAACCCCAATGCAATCAGCGAAGAAATTTTACTATTCTTGGAGATAGTCAAAATGA 2412  
 QY 2856 TCATTAAGCAGAGTTTCTTCCACTTCCCTGAAAATTTTACTCAGACATATTTGGACAGA 2915  
 Db 2413 TCATTAAGCAGAGTTTCTTCCACTTCCCTGAAAATTTTACTCAGACATATTTGGACAGA 2472  
 QY 2916 AGCATAGCTTACTTATTTGTTTAGGAGCTGAAACAATTTATTTGGAGCAAACTCTTATAT 2975  
 Db 2473 AGCATAGCTTACTTATTTGTTTAGGAGCTGAAACAATTTATTTGGAGCAAACTCTTATAT 2532  
 QY 2976 GCTAGAAAGTACATTTAAAAAGATGACTACTTACGCGAGAGATGCGAGTCTCTTAAAG 3035  
 Db 2533 GCTAGAAAGTACATTTAAAAAGATGACTACTTACGCGAGAGATGCGAGTCTCTTAAAG 2592  
 QY 3036 CATGAATGATAGTATGATGAGCACTGATGAGTATATATGCTCCACACTAGCTCT 3095  
 Db 2593 CATGAATGATAGTATGATGAGCACTGATGAGTATATATGCTCCACACTAGCTCT 2652  
 QY 3096 GATTAACACAAACCTCAGTATTCAGTTATTTAGGACACATGATTTATACGCACTAGTGC 3155  
 Db 2653 GATTAACACAAACCTCAGTATTCAGTTATTTAGGACACATGATTTATACGCACTAGTGC 2712  
 QY 3156 TTACATAGTAGACTGTTTGTGGCCAAATATCTTGAATGTTCTTTAAAAAGAACTGAG 3215  
 Db 2713 TTACATAGTAGACTGTTTGTGGCCAAATATCTTGAATGTTCTTTAAAAAGAACTGAG 2772  
 QY 3216 GTTCAGATACACATACCATGAGAAATCTTACTTTCTTGTACTACACAAAGCTATTT 3275  
 Db 2773 GTTCAGATACACATACCATGAGAAATCTTACTTTCTTGTACTACACAAAGCTATTT 2832  
 QY 3276 AAAAGAAATGCTATGTTGGAGAGAGGCGAAGTTGATCTATATGACATATCAAT 3330  
 Db 2833 AAAAGAAATGCTATGTTGGAGAGAGGCGAAGTTGATCTATATGACATATCAAT 2887

## RESULT 8

ID AAA46328 standard; DNA; 2966 BP.  
 AC AAA46328;

DT 04-SEP-2000 (first entry)

DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.

XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 XX choroidretinal degeneration; retinal disease; retinal detachment;  
 KW choroidretinal degeneration; retinal degeneration; cone degeneration;  
 KW age related macular degeneration; photoreceptor degeneration;  
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KW rod-cone dystrophy; cone-rod dystrophy; ss.

OS Homo sapiens.

PN WO200026367-A2.

PD 11-MAY-2000.

PF 29-OCT-1999; 99MO-US025440.

PR 29-OCT-1998; 98US-00183972.

PA (IOWA ) UNIV IOWA RES FOUND.

PI Hageman GS, Kuehn MH;

XX MPI: 2000-365616/31.  
 DR Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 XX preventing, diagnosing and treating ocular disorders such as retinal  
 PT detachment and chorioretinal degeneration.  
 PS Claim 3; Fig 18; 183pp; English.  
 CC The present sequence represents a splice variant of an interphotoreceptor  
 CC matrix (IPM) proteoglycan, designated IPM150. The sequence is missing  
 CC exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs,  
 CC IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome  
 CC 6q13-q15, between markers CHL1, GAT11F10 and D6S284. The IPM proteins may  
 CC be used to supplement a patient's own production of the protein or to  
 CC rectify alterations in their nucleic acids that result in expression of  
 CC an inactive protein. The IPM nucleic acids may be used in this way to  
 CC treat ocular diseases such as retinal detachment, chorioretinal  
 CC degeneration, retinal degeneration, age related macular degeneration,  
 CC photoreceptor degeneration, RPS (retinal pigment epithelium)  
 CC dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also  
 CC be used to assay for other modulators of IPM proteoglycan expression and  
 CC activity that may be used as diagnostic reagents to detect the presence  
 CC of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies  
 SQ Sequence 2966 BP; 918 A; 687 C; 624 G; 737 T; 0 U; 0 Other;  
 Query Match 81.8%; Score 2724.6; DB 3; Length 2966;  
 Best Local Similarity 96.9%; Pred. No. 0;  
 Matches 2845; Conservative 0; Mismatches 24; Indels 66; Gaps 4;  
 QY 336 TTTTGAAGAGTCTTCAAGCTTATTTATGATGAGAGTGTCTCAGAGACGATGAGAG 455  
 Db 15 TTTTGAAGATTTTCTCCAGATTCAGAGAACCAAGTGTCTCAGAGACGATGAGAG 74  
 QY 456 CATATCGAATCTTTCTGAGATCGATCCCTGACACAGGGGAAATATACAGACTGGTACGCA 515  
 Db 75 CATATCGAATCTTTCTGAGATCGATCCCTGACACAGGGGAAATATACAGACTGGTACGCA 134  
 QY 516 TCTGCCACAGAGACCTTTGCCCTTGTGACATTTGAGAAAAAATTCCAGCAATTTCCAGG 575  
 Db 135 TCTGCCACAGAGACCTTTGCCCTTGTGACATTTGAGAAAAAATTCCAGCAATTTCCAGG 194  
 QY 576 AGCAGCTGAGATCTTCTCCAGAGAGATTAACAGAGAGTTTCCCTGACAGAAAGATG 635  
 Db 195 AGCAGCTGAGATCTTCTCCAGAGAGATTAACAGAGAGTTTCCCTGACAGAAAGATG 254  
 QY 636 AAATATCTGACAGAGAAACATTTGGAGAGCCTGTGAAACCAATTTGCAATTTCAACAGCA 695  
 Db 255 AAATATCTGACAGAGAAACATTTGGAGAGCCTGTGAAACCAATTTGCAATTTCAAC----- 309  
 QY 696 TCTACATTTCAAGACTTTGGGACATTTCTAAGAAAAACCTTCAGAAAGCAAAATTCAGGA 755  
 Db 310 -----AGG 312  
 QY 756 TGTTCGCAAGCTCTCACTTGGGCTTTTCCCTCTCACTCTGATGACACCTCTCTCAATGA 815  
 Db 313 TGTTCGCAAGCTCTCACTTGGGCTTTTCCCTCTCACTCTGATGACACCTCTCTCAATGA 372  
 QY 816 AATTCTGATATATACACTCAACGACCAAGATGCTTCAACAGAAAGAAAGAAAGCAATTT 875  
 Db 373 AATTCTGATATATACACTCAACGACCAAGATGCTTCAACAGAAAGAAAGAAAGCAATTT 432  
 QY 876 CGCTGTGTTGAGAGAGAGAGGTGAGCTCAGGCTCTCTCTGTTAAACCAAGATTTCA 935  
 Db 433 CGCTGTGTTGAGAGAGAGAGGTGAGCTCAGGCTCTCTCTGTTAAACCAAGATTTCA 492  
 QY 936 GGCAGAGCTCGCTGACTCCCAAGTCCCATATTTACAGAGAGCTAGCAGAGAAAGTCCCACT 995  
 Db 493 GGCAGAGCTCGCTGACTCCCAAGTCCCATATTTACAGAGAGCTAGCAGAGAAAGTCCCACT 552

QY	996	TCAGATGCAAAAGATATTTTAAGAACTTCACAGATTCAAAAAATCCATGTTGATG	1055
Db	553	TCAGATGCAAAAGATATTTTAAGAACTTCACAGATTCAAAAAATCCATGTTGATG	612
QY	1056	TAGACCAAGAAGAAAGAAAGATGAGCTCAAGCTCCACAGAGATGACCACTTAACGCGCATCTT	1115
Db	613	TAGACCAAGAAGAAAGAAAGATGAGCTCAAGCTCCACAGAGATGACCACTTAACGCGCATCTT	672
QY	1116	TAAAGACACAGTGCAGAAAGCAAAAAGCCCTGCAAGTGAACCTCTGTCCTTTGATTCGAA	1175
Db	673	TAAAGACACAGTGCAGAAAGCAAAAAGCCCTGCAAGTGAACCTCTGTCCTTTGATTCGAA	732
QY	1176	CAAAATTGAAGTGAAGAGATCTATCATGAGAACATGAGAGAGAGACAAGCAACAGAAAT	1235
Db	733	CAAAATTGAAGTGAAGAGATCTATCATGAGAACATGAGAGAGAGACAAGCAACAGAAAT	792
QY	1236	CTATCTCACAGCTACAGACTCTCAAAAGGCTGATCAGCAAAAGCACTAGAGAGAAATC	1295
Db	793	CTATCTCACAGCTACAGACTCTCAAAAGGCTGATCAGCAAAAGCACTAGAGAGAAATC	852
QY	1296	TTTGAGATGAGGAGCAATTCAAGTTCACATGAGAAATTGCTGAGATCACTGCGCAGCTTGG	1355
Db	853	TTTGAGATGAGGAGCAATTCAAGTTCACATGAGAAATTGCTGAGATCACTGCGCAGCTTGG	912
QY	1356	TCTTGACACCCAAATCAGAGCTGCCACATCTTTTGCTGTTATTAACAGAGATGCTACTTT	1415
Db	913	TCTTGACACCCAAATCAGAGCTGCCACATCTTTTGCTGTTATTAACAGAGATGCTACTTT	972
QY	1416	GAGTCCAGAACTTCTCTCTGTTTGAACCCCACTTGAGACAGTGAACGAGACAGACATGG	1475
Db	973	GAGTCCAGAACTTCTCTCTGTTTGAACCCCACTTGAGACAGTGAACGAGACAGACATGG	1032
QY	1476	TCTACCTGACACTTCTTGATCTCCACCTGCTATGAGGCTCTACCTCCCTGTCAGAAAGCTCC	1535
Db	1033	TCTACCTGACACTTCTTGATCTCCACCTGCTATGAGGCTCTACCTCCCTGTCAGAAAGCTCC	1092
QY	1536	ACCTTTCTTTATGCGATCAAGCATCTTCTCTGATCTGATCAAGGACACACAGATTAACAT	1595
Db	1093	ACCTTTCTTTATGCGATCAAGCATCTTCTCTGATCTGATCAAGGACACACAGATTAACAT	1152
QY	1596	GAGCAGTACACAGACAATGCTAGTACAGAGGCTCACATGCCCAACAGATATTATTTGTC	1655
Db	1153	GAGCAGTACACAGACAATGCTAGTACAGAGGCTCACATGCCCAACAGATATTATTTGTC	1212
QY	1656	AATCAGCCAACTGAGCTCTGGGAATTTCCATCACTGCATCTTCAGATGACAGCCGATC	1715
Db	1213	AATCAGCCAACTGAGCTCTGGGAATTTCCATCACTGCATCTTCAGATGACAGCCGATC	1272
QY	1716	AAGTGCAGATGCGGCAAGATATGCTGCAGACACTTAAATGGAATCTGTCTGACATCC	1775
Db	1273	AAGTGCAGATGCGGCAAGATATGCTGCAGACACTTAAATGGAATCTGTCTGACATCC	1332
QY	1776	TGCCCATCTGAGTACACAGAGCTCAGGAATATGTTCTGTCCAGATCATTTCTTGGA	1835
Db	1333	TGCCCATCTGAGTACACAGAGCTCAGGAATATGTTCTGTCCAGATCATTTCTTGGA	1392
QY	1836	GATATCCACTCTGTCTCAAGCTTTACAGTATATCACTAAGTTCTATAGCAATTCGCC	1895
Db	1393	GATATCCACTCTGTCTCAAGCTTTACAGTATATCACTAAGTTCTATAGCAATTCGCC	1452
QY	1896	CAAGGAGCCGAGAGCTGATAGTATTTCAAGCTGAGGTGATCAATAGGCTTCTCGAA	1955
Db	1453	CAAGGAGCCGAGAGCTGATAGTATTTCAAGCTGAGGTGATCAATAGGCTTCTCGAA	1512
QY	1956	GCACTGTGTTCAACAAGAGCTCTCTGAGATACCGAGCTCTGAGACCAATTCACAGAGCT	2015
Db	1513	GCACTGTGTTCAACAAGAGCTCTCTGAGATACCGAGCTCTGAGACCAATTCACAGAGCT	1572
QY	2016	GCTGGTTCCATATCTACGATCCAACTCTTACAGATTTAAGCACTTGAAATCTTAACCTT	2075
Db	1573	GCTGGTTCCATATCTACGATCCAACTCTTACAGATTTAAGCACTTGAAATCTTAACCTT	1632

QY	2076	CAGAAACGGGAGTGTGATTTGGAAATAGCAAAATGAATTTGCTAAAGTCTGTGCGGTATTA	2135
Db	1633	CAGAAACGGGAGTGTGATTTGGAAATAGCAAAATGAATTTGCTAAAGTCTGTGCGGTATTA	1692
QY	2136	CCTCAACCAAGGCTGTGCACGGGGGTCTTGGAGGATTTTTCGTTCTGTCTGACGCCAACAAT	2195
Db	1693	CCTCAACCAAGGCTGTGCACGGGGGTCTTGGAGGATTTTTCGTTCTGTCTGACGCCAACAAT	1752
QY	2196	CCATCTGGAAATAGACAGCTACTCTCTCAACATTTGAACCAAGCTATCAAGCAGATCCCTG	2255
Db	1753	CCATCTGGAAATAGACAGCTACTCTCTCAACATTTGAACCAAGCTATCAAGCAGATCCCTG	1812
QY	2256	CAAGTTCCTGGGCTCGCGCGGAATTTGGCCAAATGTGTAAAGAACGAACGAACGACGAGAAC	2315
Db	1813	CAAGTTCCTGGGCTCGCGCGGAATTTGGCCAAATGTGTAAAGAACGAACGAACGACGAGAAC	1872
QY	2316	GGAAGTGTGCTGTGCAACCAAGATATGACAGCCAGGGAGCCTGGACGGTCTGGAAACAG	2375
Db	1873	GGAAGTGTGCTGTGCAACCAAGATATGACAGCCAGGGAGCCTGGACGGTCTGGAAACAG	1932
QY	2376	CCTCTGTGGCCCTTGGCAACAAAGAAATGCAAGTCTCTCCAGGGAAAGGAGCTCATGCA	2435
Db	1933	CCTCTGTGG - CCTGGCAAAAGAAATGCAAGTCTCTCCAGGGAAAGGAGCTCATGC - -	1989
QY	2436	GTTCGCAGATCACTCTGAAAATCAAGCATACAAAATTAAGTTTAAAGTTCCAAAATCA	2495
Db	1990	GGTTCAGATCACTCTGAAAATCAAGCATACAAAATTAAGTTT - AAAAGTTCCAAAATCA	2048
QY	2496	ACAAAATTAACAAGGTATCAGTAAAGAAATTCGAAATTAAGTCTGACCGTAGAATATGAGA	2555
Db	2049	ACAAAATTAACAAGGTATCAGTAAAGAAATTCGAAATTAAGTCTGACCGTAGAATATGAGA	2108
QY	2556	ATTTAACCATCAAGATTGGGAAAGAAATTAAAACTGAAAATGTACATTAATCACTTAG	2615
Db	2109	ATTTAACCATCAAGATTGGGAAAGAAATTAAAACTGAAAATGTACATTAATCACTTAG	2168
QY	2616	CTATCTCAAGAGATGATTTTGCCTTCTCAAGGAAATGAGACAGGCATTTCAATGGGT	2675
Db	2169	CTATCTCAAGAGATGATTTTGCCTTCTCAAGGAAATGAGACAGGCATTTCAATGGGT	2228
QY	2676	CATCAAAATCCAGACATACAGTCTCAACACTGAAATCAGACACACCAATATTCCAATATA	2735
Db	2229	CATCAAAATCCAGACATACAGTCTCAACACTGAAATCAGACACACCAATATTCCAATATA	2288
QY	2736	GAAAGTCATGTACTTTGGCAACAGATAATTTCTGAAAAAAAAGACATTAATTATTA	2795
Db	2289	GAAAGTCATGTACTTTGGCAACAGATAATTTCTGAAAAAAAAGACATTAATTATTA	2348
QY	2796	AAACCCCAATGCATCAGCGAAACATATTTTACTATTTCTTGGATGATGTCAAAATGA	2855
Db	2349	AAACCCCAATGCATCAGCGAAACATATTTTACTATTTCTTGGATGATGTCAAAATGA	2408
QY	2856	TCATTAAGCAGGTTTGCTTCCACCTCCGTAATAATTTTACTCAACATCTATTGGCAACA	2915
Db	2409	TCATTAAGCAGGTTTGCTTCCACCTCCGTAATAATTTTACTCAACATCTATTGGCAACA	2468
QY	2916	AGCATAGCTTACTTATTTGTTTGAAGGACTGAAACAATTTATTTGGGAAGCAACCTCTTATAT	2975
Db	2469	AGCATAGCTTACTTATTTGTTTGAAGGACTGAAACAATTTATTTGGGAAGCAACCTCTTATAT	2528
QY	2976	GCTAGAAAGTACATTTAAAGATGACTATACGACGGAGATGACAGGTCTCTCTAAACG	3035
Db	2529	GCTAGAAAGTACATTTAAAGATGACTATACGACGGAGATGACAGGTCTCTCTAAACG	2588
QY	3036	CATGAATGTAATGTATGTGTAGGACCTGTATGAGTGTATATATAGTCCCAACATACGCT	3095
Db	2589	CATGAATGTAATGTATGTGTAGGACCTGTATGAGTGTATATATATAGTCCCAACATACGCT	2648
QY	3096	GATTAACCAACAACCTCAGATATTCAGTATTTAGGACACACTAGTTTATACGACATACG	3155
Db	2649	GATTAACCAACAACCTCAGATATTCAGTATTTAGGACACACTAGTTTATACGACATACG	2708
QY	3156	TTACATAGTAGACTGTTTGTGGCCAAATCTTTGAATGTGTTCTTTAAAAAACAATG	3215

Db 2709 TTACATAGAGACTGTTTGTGTCACATATCTTGAAATGTTCTTTAAAGAACTGAG 2768  
 Qy 3216 GTTCAGATACACATACCATGAGAAAACTTACTTTCTGTACTACACAAAGCTATTTT 3275  
 Db 2769 GTTCAGATACACATACCATGAGAAAACTTACTTTCTGTACTACACAAAGCTATTTT 2828  
 Qy 3276 AAAAGAAAGCTATGTTGGAGAGAGGCGAAGTTGACTATATGACATATCAAT 3330  
 Db 2829 AAAAGAAAGCTATGTTGGAGAGAGGCGAAGTTGACTATATGACATATCAAT 2883  
 RESULT 9  
 AAA46329  
 ID AAA46329 standard, DNA; 2244 BP.  
 XX AAA46329;  
 AC  
 XX  
 DT 04-SBP-2000 (first entry)  
 XX  
 DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.  
 XX  
 KM Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 KM chromosome 6q13-q15; ocular disease; retinal detachment;  
 KM choriorretinal degeneration; retinal degeneration; cone degeneration;  
 KM age related macular degeneration; photoreceptor degeneration;  
 KM retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KM rod-cone dystrophy; cone-rod dystrophy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200026367-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 29-OCT-1999; 99WO-US025440.  
 XX  
 PR 29-OCT-1998; 98US-00183972.  
 XX  
 PA (IOWA) UNIV IOWA RES FOUND.  
 XX  
 PI Hageman GS, Kuehn MJ;  
 XX  
 DR WPI; 2000-365616/31.  
 XX  
 PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 PT preventing, diagnosing and treating ocular disorders such as retinal  
 PT detachment and choriorretinal degeneration.  
 XX  
 PS Claim 3, Fig 19; 183pp; English.  
 XX  
 CC The present sequence represents a splice variant of an interphotoreceptor  
 CC matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an  
 CC additional intron after exon 5. The protein is an IPM component (IPMC).  
 CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
 CC is located on chromosome 6q13-q15, between markers CHC.GAT11F10 and  
 CC D6S284. The IPM proteins may be used to supplement a patient's own  
 CC production of the protein or to rectify alterations in their nucleic  
 CC acids that result in expression of an inactive protein. The IPM nucleic  
 CC acids may be used in this way to treat ocular diseases such as retinal  
 CC detachment, choriorretinal degeneration, retinal degeneration, age related  
 CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment  
 CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
 CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
 CC also be used to assay for other modulators of IPM proteoglycan expression  
 CC and activity that may be used to treat ocular diseases. The nucleic acids  
 CC and proteins may also be used as diagnostic reagents to detect the  
 CC presence of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies  
 CC  
 SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;  
 Query Match 65.6%; Score 2184.2; DB 3; Length 2244;

Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
 Qy 1 TAAACCAAGAGGTTATCTCATATCATCTGTATCATATATATATATTTTTCACATTTTC 60  
 Db 22 TAAACCAAGAGGTTATCTCATATCATCTGTATCATATATATATATATTTTTCACATTTTC 81  
 Qy 61 TGTATCTTTTAAATGAGATTGAGGTTGTTCTGTATTTGTTATTCGAATTACCAATGCAC 120  
 Db 82 TGTATCTTTTAAATGAGATTGAGGTTG-TCTGTATTTGTTATTCGAATTACCAATGCAC 140  
 Qy 121 AAAAGCAGAAATGATTTTGGAAAATGAAAGAGCTATTTTGTGTTTGGATTTTCTCCA 180  
 Db 141 AAAAGCAGAAATGATTTTGGAAAATGAAAGAGCTATTTTGTGTTTGGATTTTCTCCA 200  
 Qy 181 AGTTCAAGAAACCAAGATATCTCCATTATACATATATACATTTCTGAAGCTAAAGACATAGA 240  
 Db 201 AGTTCAAGAAACCAAGATATCTCCATTATACATATATACATTTCTGAAGCTAAAGACATAGA 260  
 Qy 241 CAATCCCCCAAGAAATGAAACATGAAAGTATCTGAATAAATATGTAACAAATGTCACTAT 300  
 Db 261 CAATNCCCCCAAGAAATGAAACATGAAAGTATCTGAATAAATATGTAACAAATGTCACTAT 320  
 Qy 301 GAGAGCAATATTCGATTTTGGCAAGCATCGAACAAAAGATCCGATTTTTCGAACGGG 360  
 Db 321 GAGAGCAATATTCGATTTTGGCAAGCATCGAACAAAAGATCCGATTTTTCGAACGGG 380  
 Qy 361 GGTAAAGTCTGTCCACAGAAATCCATGAAACAGATTTTGAACAGTCTTCAAGCTTAATTA 420  
 Db 381 GGTAAAGTCTGTCCACAGAAATCCATGAAACAGATTTTGAACAGTCTTCAAGCTTAATTA 440  
 Qy 421 TAGATTGAGTGTCTCAGAAACGATATGGAAGCATATGGAATCTTTCTGGAATGCAT 480  
 Db 441 TAGATTGAGTGTCTCAGAAACGATATGGAAGCATATGGAATCTTTCTGGAATGCAT 500  
 Qy 481 CCTGACACAGGGGAATATCAGAACTGGGTGACATCTGCCACAGAGACCTTCTGCT 540  
 Db 501 CCTGACACAGGGGAATATCAGAACTGGGTGACATCTGCCACAGAGACCTTCTGCT 560  
 Qy 541 CTTTGACATTTGAAAAAACTTCAGCAATTTCCAGAGACCTGTGATCTTCTCCAGCAGAG 600  
 Db 561 CTTTGACATTTGAAAAAACTTCAGCAATTTCCAGAGACCTGTGATCTTCTCCAGCAGAG 620  
 Qy 601 AATTAACAGAAAGTTTCCCTGACAGAAAGATGAATATCTGACAGAAAGACATTTGGG 660  
 Db 621 AATTAACAGAAAGTTTCCCTGACAGAAAGATGAATATCTGACAGAAAGACATTTGGG 680  
 Qy 661 AGAGCTGTGAAACCATTTGCAATTTGCAACAGCAATCTACATTTCAAAGACTTGGGCACT 720  
 Db 681 AGAGCTGTGAAACCATTTGCAATTTGCAACAGCAATCTACATTTCAAAGACTTGGGCACT 740  
 Qy 721 ATTCTAAGAAAACCTCAGAAAGCAATTAAGATGTTGGCAAGCTCTCACTTGGGCT 780  
 Db 741 ATTCTAAGAAAACCTCAGAAAGCAATTAAGATGTTGGCAAGCTCTCACTTGGGCT 800  
 Qy 781 TTCCTCTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATATACCTCAAGCAGC 840  
 Db 801 TTCCTCTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATATACCTCAAGCAGC 860  
 Qy 841 ACCAAGATGCTTACAAAGAAAGAAAGAAACAAATTCGTGTGTGAGAGAGAGGGGTG 900  
 Db 861 ACCAAGATGCTTACAAAGAAAGAAAGAAACAAATTCGTGTGTGAGAGAGAGGGGTG 920  
 Qy 901 GAGCTCAGCGTCTCTGTGTAACCAAGAGTTCAGAGAGCTGCTGACTCCAGTCC 960  
 Db 921 GAGCTCAGCGTCTCTGTGTAACCAAGAGTTCAGAGAGCTGCTGACTCCAGTCC 980  
 Qy 961 CCAATTTACCAAGAGCTGACAGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAA 1020  
 Db 981 CCAATTTACCAAGAGCTGACAGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAA 1040  
 Qy 1021 CTTCCAGATTCAAAATAATCCATGTGTTAGATTTTACCAAGAAAGAAAGATGTC 1080



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Db 1041 CTTCCAGATTCAAAAAATCCATGTTAGATTAGACCAAGAAAAAAGATGAC 1100
Qy 1081 TCAAGCTCCAGAGATGCAACTTAACGGCATCTTAAAGAGACAGAGTGCAGAACAAA 1140
Db 1101 TCAAGCTCCAGAGATGCAACTTAACGGCATCTTAAAGAGACAGAGTGCAGAACAAA 1160
Qy 1141 AGCCCTGCAAGTGAAGCTCTGTCTTTTGAATTCACAAATTAAGAAAGTGAAGTCTAT 1200
Db 1161 AGCCCTGCAAGTGAAGCTCTGTCTTTTGAATTCACAAATTAAGAAAGTGAAGTCTAT 1220
Qy 1201 CATGGAACCATGAGAGAGAGACAGAACCAAAATCTATCTCAGCTACAGACTCAAA 1260
Db 1221 CATGGAACCATGAGAGAGAGACAGAACCAAAATCTATCTCAGCTACAGACTCAAA 1280
Qy 1261 AGGCTGATCAGAAAGCCTTAGAGAGAAACAATCTTGAATGTGGGAGCAATTCAGTTC 1320
Db 1281 AGGCTGATCAGAAAGCCTTAGAGAGAAACAATCTTGAATGTGGGAGCAATTCAGTTC 1340
Qy 1321 ACTGATGAAAATTGCTGATCACTGCACGCTTTGGTCTTGAACCCCAATCAGAGCTGCC 1380
Db 1341 ACTGATGAAAATTGCTGATCACTGCACGCTTTGGTCTTGAACCCCAATCAGAGCTGCC 1400
Qy 1381 ACATCTTTTGTCTTTATAACAGAGAGATGCTTGAAGTCCAGAACTTCTCTGTGAA 1440
Db 1401 ACATCTTTTGTCTTTATAACAGAGAGATGCTTGAAGTCCAGAACTTCTCTGTGAA 1460
Qy 1441 CCCGAGCTTGAAGAGTGAACGGAGACAGAGATGTCTTACCTGACACATCTTGTGCTCA 1500
Db 1461 CCCGAGCTTGAAGAGTGAACGGAGACAGAGATGTCTTACCTGACACATCTTGTGCTCA 1520
Qy 1501 CCTGCTATGGCCTTACCTCCCTGTCAGAAAGTCCACCTTTTATGAGCATCAAGATC 1560
Db 1521 CCTGCTATGGCCTTACCTCCCTGTCAGAAAGTCCACCTTTTATGAGCATCAAGATC 1579
Qy 1561 TTCTCTCTGACTGATCAGAGAGACACAGATCAATGAGCCACTGACCAAGTCTAGTA 1620
Db 1580 TTCTCTCTGACTGATCAGAGAGACACAGATCAATGAGCCACTGACCAAGTCTAGTA 1639
Qy 1621 CGAGGGCTCAGCATCCCAACGAGTATTAATCTGCAATCAGCAATCTGCTTGGAAAT 1680
Db 1640 CGAGGGCTCAGCATCCCAACGAGTATTAATCTGCAATCAGCAATCTGCTTGGAAAT 1699
Qy 1681 TCACATCCACCTGATCTTTCAGATGACAGCCGATCAAGTGAAGTGGCAAGATATGTC 1740
Db 1700 TCACATCCACCTGATCTTTCAGATGACAGCCGATCAAGTGAAGTGGCAAGATATGAC 1759
Qy 1741 AGACACTTATGATGAATGATGATCTGTCTGACACTCTGCCCATCTGAGGTACCAAGCTC 1800
Db 1760 AGAGACTTATGATGAATGATGATCTGTCTGACACTCTGCCCATCTGAGGTACCAAGCTC 1819
Qy 1801 AGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGATACCACTCTGTCTCACTTTA 1860
Db 1820 AGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGATACCACTCTGTCTCACTTTA 1879
Qy 1861 CAGTATATCACCAGTATGTTCTATGACATTTGCCCAAGGGCCGAGAGTGTAGTGTTC 1920
Db 1880 CAGTATATCACCAGTATGTTCTATGACATTTGCCCAAGGGCCGAGAGTGTAGTGTTC 1939
Qy 1921 TTCAGTCTGCGTGTGTTCTAACAATGAGCTTTCTCCAAAGACCTGTTCACAAAGAGCTCTCTG 1980
Db 1940 TTCAGTCTGCGTGTGTTCTAACAATGAGCTTTCTCCAAAGACCTGTTCACAAAGAGCTATTG 1999
Qy 1981 GAGTACCGAGCTCTGAGAGAGAAATTCACACAGCTGTGTTCATATTTAAGATTCAT 2040
Db 2000 GAGTACCGAGCTCTGAGAGAGAAATTCACACAGCTGTGTTCATATTTAAGATTCAT 2059
Qy 2041 CTTACAGATTTAAGCACTTGAATACTTAATCTCAGAAAGGGAGTGTGATTTGGAAT 2100
Db 2060 CTTACAGATTTAAGCACTTGAATACTTAATCTCAGAAAGGGAGTGTGATTTGGAAT 2119
Qy 2101 AGCAAAATGAAGTTGTCTAAGTCTGTGCGGTATTAACCTCAGCAAGGCTGTGACGGGGTC 2160
Db 2120 AGCAAAATGAAGTTGTCTAAGTCTGTGCGGTATTAACCTCAGCAAGGCTGTGACGGGGTC 2179

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Qy 2161 TTGAGAGATTTTGTCTGCTGACAGCCCAACAACCTCCATCTGAAATAGACAGCTACTCT 2220
Db 2180 TTGAGAGATTTTGTCTGCTGACAGCCCAACAACCTCCATCTGAAATAGACAGCTACTCT 2239
Qy 2221 CTC 2223
Db 2240 CTC 2242

RESULT 10
ACC57948
ID ACC57948 standard; cDNA; 2244 BP.
XX
AC ACC57948;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human Interphotoreceptor matrix IPM 150, isoform C, cDNA.
XX
KM Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KM receptor; ophthalmological; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key
FH CDS 151..747
FT /*tag= a
FT /product= "IPM 150"
FT sig_peptide 151..210
FT /*tag= b
FT unsure 265..267
FT /*tag= c
FT /note= "encodes Pro"
FT unsure 346..348
FT /*tag= d
FT /note= "encodes His"
XX
PN WO2003039346-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036090.
XX
PR 08-NOV-2001; 2001US-00077270.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI, 2003-441440/41.
DR P-PSDB; ABR42344.
XX
PT New interphotoreceptor matrix proteins and polynucleotides, useful for
PT treating or preventing photoreceptor death or retinal detachment, or for
PT treating ocular disorders.
XX
PS Claim 1; Page 79-80; 105pp; English.
XX
CC The present sequence is that of cDNA encoding isoform C of novel human
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
CC is located on chromosome 6q13-q15, a region that also contains loci for
CC progressive bifocal choroidretinal atrophy, autosomal dominant Stargardt's
CC -like macular dystrophy, North Carolina macular dystrophy and Salla
CC disease. Members of the IPMC gene family have been identified in humans,
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
CC Subfamilies are designated IPM 150 (or IMPG1) and IPM 200 (or IMPG2). The
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
CC antibodies that specifically bind the polypeptides, and vectors
CC comprising the polynucleotides. A claimed method of treating or
CC preventing photoreceptor death or retinal detachment involves
CC administering an IPMC polynucleotide, polypeptide or antibody. Also

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Db      2060 CTTACAGATTAAACCACTTGAATTAATTACCTCAGAAACGAGAGTGTGATTTGAAAT 2119
Qy      2101 AGCAAAATGAAGTTGCTAGCTGTGCGGTATACCTCACCAGGCTGTGACGGGGTTC 2160
Db      2120 AGCAAAATGAAGTTGCTAGCTGTGCGGTATACCTCACCAGGCTGTGACGGGGTTC 2179
Qy      2161 TTGAGAGATTTTCTGCTGTGCTGACGCCCAACAACCTCCTGGAATAGACAGTACTCT 2220
Db      2160 TTGAGAGATTTTCTGCTGTGCTGACGCCCAACAACCTCCTGGAATAGACAGTACTCT 2239
Qy      2221 CTC 2223
Db      2240 CTC 2242

RESULT 11
ADA14844
ID      ADA14844 standard; cDNA; 2244 BP.
XX
AC      ADA14844;
XX
DT      06-NOV-2003 (first entry)
XX
DE      Human interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.
XX
KW      ss; gene; human; IPMC 150 isoform C; gene therapy;
KW      interphotoreceptor matrix component; IPMC; ocular disorder;
KW      macular degeneration; photoreceptor death; retinal detachment.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      151..747
FT      /tag= b
FT      /product= "IPMC 150 isoform C"
FT      sig_peptide 151..200
FT      /tag= a
FT      /note= "Signal sequence"
FT      mat_peptide 201..744
FT      /tag= C
FT      /note= "Mature IPMC 150 isoform C"
FT      unsure    265..267
FT      /tag= d
FT      /note= "Encodes Pro"
FT      unsure    346..348
FT      /tag= e
FT      /note= "Encodes His"
XX
PN      US2002160954-A1.
PD      31-OCT-2002.
PF      08-NOV-2001; 2001US-00007270.
PR      29-OCT-1998; 98US-00183972.
PR      29-OCT-1999; 99US-00430195.
XX
PA      (IOWA ) UNTIV IOWA RES FOUND.
XX
PI      Hageman GS, Kuehn MH;
XX
DR      WPI; 2003-238235/23.
XX
DR      P-PsDB; ADA14845.
XX
PT      New isolated or recombinant interphotoreceptor matrix component
PT      polynucleotide and polypeptide, useful for diagnosing, preventing,
PT      treating or prognosticating ocular disorders, e.g. macular degeneration
PT      or retinal detachment.
XX
PS      Claim 3; Page 36-37; 76pp; English.
XX
CC      The invention relates to an isolated or recombinant interphotoreceptor

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CC      matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC      comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC      gene operatively linked to the IPMC polynucleotide. The IPMC
CC      polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC      preventing, treating or prognosticating ocular disorders, e.g. macular
CC      degeneration, photoreceptor death or retinal detachment. They are also
CC      useful for identifying a present capable of modulating IPMC gene
CC      expression in a cell. The present sequence represents cDNA encoding human
CC      interphotoreceptor matrix component, IPMC, 150 isoform C.
SQ      Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
Query Match      65.6%; Score 2184.2; DB 10; Length 2244;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
Qy      1 TAAACCAAGAAAGTTATCTCAATCATCTGGTATCAATATATATTTTTCACATTTTC 60
Db      22 TAAACCAAGAAAGTTATCTCAATCATCTGGTATCAATATATATTTTTCACATTTTC 81
Qy      61 TGTACTTTTATAGATTGAGTTGAGTTGTTCTGTGATTTGATTCAGAAATTAACAATGAC 120
Db      82 TGTACTTTTATAGATTGAGTTGAGTTG-TCTGTGATTTGTTATCAGAAATTAACAATGAC 140
Qy      121 AAAAGCCGAATGTATTTGGAAGCTAAGAAAGCTATTTTGTGATTTTCTGCA 180
Db      141 AAAAGCCGAATGTATTTGGAAGCTAAGAAAGCTATTTTGTGATTTTCTGCA 200
Qy      181 AGTTCAAGAAACCAAGATATCTGCATTAACATATACATTTCTGAAACTTAAAGACATGA 240
Db      201 AGTTCAAGAAACCAAGATATCTGCATTAACATATACATTTCTGAAACTTAAAGACATGA 260
Qy      241 CAATCCCCCAAGAAATGAAACAACTGAAGATGTAAGAAATATGTAATATGTCACATAT 300
Db      261 CAATCCCCCAAGAAATGAAACAACTGAAGATGTAAGAAATATGTAATATGTCACATAT 320
Qy      301 GAGACGAATATTCGATTTGGCAAGATCGAACCAAAAAGATCCGATTTTTCACACGGG 360
Db      321 GAGACGAATATTCGATTTGGCAAGATCGAACCAAAAAGATCCGATTTTTCACACGGG 380
Qy      361 GGTAAAGTCTGTGCACAGGAATCGATTAACAAAGATTTTAAACAGTCTTCAAGCTTATTA 420
Db      381 GGTAAAGTCTGTGCACAGGAATCGATTAACAAAGATTTTAAACAGTCTTCAAGCTTATTA 440
Qy      421 TAGATTGAGAGTGTGTCAGAAAGCTATGGAAGCATATGGAATCTTCTGATCGCAT 480
Db      441 TAGATTGAGAGTGTGTCAGAAAGCATATGGAAGCATATGGAATCTTCTGATCGCAT 500
Qy      481 CCTGACACAGGGGAATATCAGAACTGGGTGAGCATCTGCACAGAGAACCTTCTGCT 540
Db      501 CCTGACACAGGGGAATATCAGAACTGGGTGAGCATCTGCACAGAGAACCTTCTGCT 560
Qy      541 CTTGACATTGGAAAAAACTTCAGCAATTTCCAGAGACCTTGATCTTCTCCAGACAG 600
Db      561 CTTGACATTGGAAAAAACTTCAGCAATTTCCAGAGACCTTGATCTTCTCCAGACAG 620
Qy      601 AATAAACAAGAAAGTTTCCCTGACAGAAAAAGATGAATATCTGACAGAAAGACATTGGG 660
Db      621 AATAAACAAGAAAGTTTCCCTGACAGAAAAAGATGAATATCTGACAGAAAGACATTGGG 680
Qy      661 AGAGCTGTGTAACCATTTGTCAATTTCAACAGCAATCTACATTTCAAGACCTTGGGAGT 720
Db      681 AGAGCTGTGTAACCATTTGTCAATTTCAACAGCAATCTACATTTCAAGACCTTGGGAGT 740
Qy      721 ATTCTAAGAAAAACCTCAGAAAGAGCAATTTCAAGATGTTGGCAAGTCTCACTTGGGCT 780
Db      741 ATTCTAAGAAAAACCTCAGAAAGAGCAATTTCAAGATGTTGGCAAGTCTCACTTGGGCT 800
Qy      781 TTCCCTCTCAGCTCGATGAGACACCTCTCATATGAATTTCTGATTAATACCTCAAGAGC 840
Db      801 TTCCCTCTCAGCTCGATGAGACACCTCTCATATGAATTTCTGATTAATACCTCAAGAGC 860
Qy      841 ACCAAGATGCTACAAAGAAAGAAAGAAAGAAATTCGCTGTGTTGAGAGCAGAGGTTG 900

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Db      861 ACCAAGATGCTACAAGAGAAAGAGAAAGAAATTCGTGTGTGGAGAGCAGAGGGTGG 920
Qy      901 GAGCTCAGGCTCTCTGTGTAAACCAAGATTCAAGGCGAGCTGGCTGCCAGTCC 960
Db      921 GAGCTCAGGCTCTCTGTGTAAACCAAGATTCAAGGCGAGCTGGCTGCCAGTCC 980
Qy      961 CCATTTACAGAGAGTACAGAGAAAGTCCAACTTCAGATGCAAAAGATATTTAAGAA 1020
Db      981 CCATTTACAGAGAGTACAGAGAAAGTCCAACTTCAGATGCAAAAGATATTTAAGAA 1040
Qy      1021 CTTCCAGAGATCAAAAAATCCATGTGTAGATTAGACCAAGAAAGAAAAAGTGC 1080
Db      1041 CTTCCAGAGATCAAAAAATCCATGTGTAGATTAGACCAAGAAAGAAAAAGTGC 1100
Qy      1081 TCAGCTCAAGAGATGCACTTACGGCCATCTTTAAGAGACAGTGCAGAGCAAA 1140
Db      1101 TCAGCTCAAGAGATGCACTTACGGCCATCTTTAAGAGACAGTGCAGAGCAAA 1160
Qy      1141 AGCCCTGCAAGTACCTCTGTCTTTGATTCACAAATTTGAAGTGAAGGATCTAT 1200
Db      1161 AGCCCTGCAAGTACCTCTGTCTTTGATTCACAAATTTGAAGTGAAGGATCTAT 1220
Qy      1201 CATGGAACCATGAGAGAGAGCAAGCAACCAAAATCTATCTCAGCTACAGACTCAAA 1260
Db      1221 CATGGAACCATGAGAGAGAGCAAGCAACCAAAATCTATCTCAGCTACAGACTCAAA 1280
Qy      1261 AGGCTGATCAGAAAGCACTAGAGAGAAACAATCTTTGATGTGGGACAAATTCAGTTC 1320
Db      1281 AGGCTGATCAGAAAGCACTAGAGAGAAACAATCTTTGATGTGGGACAAATTCAGTTC 1340
Qy      1321 ACTGATGAATTTGCTGATCATCTGCCAGGCTTTGGTCCCTGACACCCCAATCAGAGCTGCC 1380
Db      1341 ACTGATGAATTTGCTGATCATCTGCCAGGCTTTGGTCCCTGACACCCCAATCAGAGCTGCC 1400
Qy      1381 ACATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCCGAACTTCTCTGTGAA 1440
Db      1401 ACATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCCGAACTTCTCTGTGAA 1460
Qy      1441 CCCCACTTTGAGACAGTGCAGGAGCAAGACATGCTTACTGACACTTCTGTCTCCA 1500
Db      1461 CCCCACTTTGAGACAGTGCAGGAGCAAGACATGCTTACTGACACTTCTGTCTCCA 1520
Qy      1501 CCTGCTAATGGCTCTTACTCTCTCTGTCAAGAGCTCCACTTTTATATGCGATCAAGCATC 1560
Db      1521 CCTGCTAATGGCTCTTACTCTCTCTGTCAAGAGCTCCACTTTTATATGCGATCAAGCATC 1579
Qy      1561 TTCTCTGATGATCAAGGACCAAGATACATGAGCCACTGACCAAGCAATGTAGTA 1620
Db      1580 TTCTCTGATGATCAAGGACCAAGATACATGAGCCACTGACCAAGCAATGTAGTA 1639
Qy      1621 CCAAGGCTCACCATCCCAACAGATATTCTGCAATCAGCCAACTGGCTCTGGAAAT 1680
Db      1640 CCAAGGCTCACCATCCCAACAGATATTCTGCAATCAGCCAACTGGCTCTGGAAAT 1699
Qy      1681 TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGGAGATATGTGC 1740
Db      1700 TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGGAGATATGTGC 1759
Qy      1741 AGACACCTAGATGAATGATCTGTCTGCACTCTGCCCCCATGAGGATACAGAGCTC 1800
Db      1760 AGACACCTAGATGAATGATCTGTCTGCACTCTGCCCCCATGAGGATACAGAGCTC 1819
Qy      1801 AGCGAATATGTTCTGTCCAGATCATTTCTTGAGATACCACTCTGTCTCAGCTTTA 1860
Db      1820 AGCGAATATGTTCTGTCCAGATCATTTCTTGAGATACCACTCTGTCTCAGCTTTA 1879
Qy      1861 CAGTATATCAACCACTAGTTCTATGACATTTGCCCAAGGCGCGAGCTGTAGTTC 1920
Db      1880 CAGTATATCAACCACTAGTTCTATGACATTTGCCCAAGGCGCGAGCTGTAGTTC 1939
Qy      1921 TTCAGTGTGCGTGTGCTAACATGAGCTTCTTCAACGACCTTTCAACAGAGCTCTCG 1980

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Db      1940 TTCAGTGTGCGTGTGCTAACATGAGCTTCTTCCAAAGACCTGTTCACAGAGCTATTGG 1999
Qy      1981 GAGTACCAAGCTCTGAGCAACATTTCAACAGCTGTGTGTTCCATATCTACGATCCAAT 2040
Db      2000 GAGTACCAAGCTCTGAGCAACATTTCAACAGCTGTGTGTTCCATATCTACGATCCAAT 2059
Qy      2041 CTTACAGATTTTAACCACTTGAATTAATCTTAACCTTCAAGAAAGGAGTGTATTTGAAAT 2100
Db      2060 CTTACAGATTTTAACCACTTGAATTAATCTTAACCTTCAAGAAAGGAGTGTATTTGAAAT 2119
Qy      2101 AGCAAAATGAAGTTGTCTAAGTCTGTGCCGTATACCTCAACCAAGGCTGTGACGGGGTTC 2160
Db      2120 AGCAAAATGAAGTTGTCTAAGTCTGTGCCGTATACCTCAACCAAGGCTGTGACGGGGTTC 2179
Qy      2161 TTGGAGATTTTGTGCTGTGCTGACGCCCAACCACTTCATCTTGAATATGACAGCTACTCT 2220
Db      2180 TTGGAGATTTTGTGCTGTGCTGACGCCCAACCACTTCATCTTGAATATGACAGCTACTCT 2239
Qy      2221 CTC 2223
Db      2240 CTC 2242

RESULT 12
ACCS7950
ID ACC57950 standard; cDNA, 3668 BP.
XX
XX ACC57950;
AC AC
XX
XX 11-AUG-2003 (first entry)
DT
XX
DE Mouse Interphotoreceptor matrix IPM 150, isoform A, cDNA.
XX
XX Mouse Interphotoreceptor matrix; IPM 150; chromosome 9; IPMC; receptor;
KW ophthalmological; gene therapy; gene; ss.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH 196..2592
FT /*tag= a
FT /product= "IPM 150"
FT
XX
XX WO2003039346-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002MO-US036090.
XX
XX 08-NOV-2001; 2001US-00077270.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-441440/41.
XX
XX P-P8DB; ABR42345.
XX
XX
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX
XX Claim 1; Page 81-82; 105pp; English.
XX
XX The present sequence is that of cDNA encoding isoform A of novel mouse
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 9. Members of the IPMC gene family have been
XX identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and
XX rat IPM. 2 Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or
XX IPMG2). The invention provides IPM 150 and IPM 200 polynucleotides and
XX polypeptides, antibodies that specifically bind the polypeptides, and
XX vectors comprising the polynucleotides. A claimed method of treating or
XX

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CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression

XX Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;

Query Match 41.3%; Score 1375.6; DB 9; Length 3668;  
Best Local Similarity 70.7%; Pred. No. 0;  
Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19;

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Oy 1 TAAACCAAGAGGTTATCTCAATCATCTGTATCAATATATATATATTTTTCACATTTTC 60
Db 62 TAAACCAAGAGGTCGTCTGTACTCAGCCGACCTGATTTGATTTATTTTCATATTTTC 121
Oy 61 TGTATCTTTT-----AATGAGATTGAGGTTGTTCTGTGATTTGATTCAGATTACC 113
Db 122 AGTCACTTATTTCTTTAAGTGTGACTGTGATTTGTTCTGTGATTTT--TCGAAATTTACC 179
Oy 114 AATGCACAAAGCCAGAAATGTATTTGGAAACTAGAAAGCTATTTTGTGTTTGGATTTT 173
Db 180 AGTATACAGAA-CCGAATGAAATTTTCAATTTAAACATGCTATCTTTGTTTGGATTTT 238
Oy 174 TTCTCAAGTTCAAGAAACCAAGATATCTCCATTACATATACATTTCTGAACTAAG 233
Db 239 TTCTCAAGTTCAAGAAATCAAAAGATACCTCTATTTAAATATTCAGTTCTGAAATTTAAA 298
Oy 234 ACATGACATATCCCAAGAAATGAAACAACTGAAAGTCTGAAATTTGTCAAATATGT 293
Db 299 ACATGACAAACCCCAAGAAATGAAACAAATGAAAGTACTTCAACAGTGCACAAAGTGT 358
Oy 294 CAATATGAGACGAATATTCGATTTGGCAAGATTCGAAACAAATAAGATCCGATTTTTC 353
Db 359 CAACCATGAAAGGATTTTCGATTTGGCCAAAGCTTCGAAACAAAGATCAGACTTTTTC 418
Oy 354 CAACGGGGGTTAAAGTCTGTCTGACAGAAATCCATGAAACAGATTTTGAACAGTCTTCAAG 413
Db 419 CA---GCTGCTAACTGTGTCCACAGAAATCTTGAGACAGATTTTGAACAGTCTTCAAG 475
Oy 414 CTATTTATGATTTGAGAGTGTCTGAGAAAGCATGATGGAAGCATATGGAATCTTTCTGG 473
Db 476 AATATTTATGACTGAGAGATATGTCAAGAGTGTGTGGAAACATATGATATCTTTCTGG 535
Oy 474 ATCGATCCCTGACACAGAGGAATATCAGGACTGGGTGAGATCTGCGCAGCAGAGACCT 533
Db 536 ACCGAATTCCTACACAGAGGAATATCAGAGACTGGGTGAGCTCTGCGCAGAAAGAAACCT 595
Oy 534 TCTGCTCTTTGACATTTGGAAAAAACTTCAGCAATTTCCAGAGACCTGATCTTCTTC 593
Db 596 TCTGCTCTTTGACATTTGGAAAAAACTTCAGCAATCTCCAGAGACCTGATCTTCTTC 655
Oy 594 AGCAGAGAAATTAACAGAGAAATTTCCCTGACAGAAAAAGATGAATATTTGACAGAAAGA 653
Db 656 AGCAGAGAAATTAACAGAGAAATTTCCCTGAGAGAAAGATGAGACAGCTTCATGAGAGA 715
Oy 654 CATTTGGAGAGCTGGTGAACCATTTGTCAATTTCAACAGCAATCTAATTTCAAGAGACT 713
Db 716 CACTGAAAGCACTTACTGAGGCCCTGTGTGTACCCAC----- 752
Oy 714 GGGGAGTATTTTAAGAAAACTCTCAGAAAGCAAAATTCAGAGTGTGGCAACGTCTCACT 773
Db 753 -----AGATGTTTCCAGAGATGTCCCT 773
Oy 774 TGGGCTTTCTCTCTCACTCTGATGACACCTCTCTCAATGAATTTCTGATTAATACACT 833
Db 774 GGGGCTCTCTCTCTCTCTCTGATGACACAGACCTCAAGAGATTTCTCAGTGTACCTCT 833
Oy 834 CAACGACACCAAGATGCTTACAAAGAAAGAGAAACAGAA-----TTGGCTGT 881
Db 834 CAAGGACATTTCAAAAGCCACACAGAAAGTAAACAGAACTTATTCAGTGTCTGAAAT 893
Oy 882 GTTGGAGAGCAGAGGTGAGCTCAGCTCTCTCTGTAAACAGAAAGTTCAAGGACAGA 941
Db 882 GTTCTCTATGACCTGTTCACCAAGAGTCTCTGTGAGATATCAAGCCCTGAAACAGATT 2021
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Db 894 CTCATCAGAGAGAGAGGTGATTCAGAGCTCTCTGCGCAAAACACAGGTTCAAGGACAGA 953
Oy 942 GCTGCTGATCTCCAGTCCCATATTAACAGAGCTAGCAGAAAGTCCCACTTCAAT 1001
Db 954 GCTCAACAACTCTGGGTACACTACACAGAACTGTGGAGACAGTCCCACTGCAAT 1013
Oy 1002 GCAAAAGATATTTAAGAACTTCCAGAGATTCAAAAAATCCATGTGTTAGATTAGACC 1061
Db 1014 GCAAAAGATATTTAAGAACTTCCAGAGATTGAGAAATCCGTGTATTAAGATTTAGACC 1073
Oy 1062 AAAGAAAGAAAGATGAGCTCAAGCTCCACAGAGATGCACTTACGAGCATTTTAAGAG 1121
Db 1074 AAAGAAAGAAAGATGAGTTCAAGCTCCACAGAAATACAGCTTATGAGCATTTTAAGAG 1133
Oy 1122 ACACAGTCAAGAACCAAAAGCCCTGCAAGTACCTCTGTCTTTTGAATTTCCAAATAAT 1181
Db 1134 GACACATGCAAGAACCAAAAGCCCTGATGATCTACTGTCTCTTGAATTTCCAAATAAT 1193
Oy 1182 TGAAGTGAAGAGGCTATCATGGAACCATGAGAGAGCAAGCAACCAAGAAATCTATCT 1241
Db 1194 TGAAGTGAAGAAATCCATCATGAGATCATAGAA--GACAAACACAGAAACCTACT 1250
Oy 1242 CACAGCTACAGACTCAAAAGGCTGATGAGCAAAAGCACTAAGAGAAACAATCTTTGGA 1301
Db 1251 CACAGCTACAGACTCAAAAGGCTGATGATCACTAATCAATGATGAGACCTGTCTTGGT 1310
Oy 1302 TGTGGGCAATTTCAAGTTCACTGATGAAATGCTGTGATCACTGCGCAGCTTTGTCTGGA 1361
Db 1311 AGAAGGAGAAATTCATTCAGTGTGATGAAATTAAGTCTGAGACCT-----CTTCAAGCTGT 1364
Oy 1362 CACCAATCAGAGCTGCCCCACATCTTTTGTGTTAATACAGAGATGCTACTTTGAGTCC 1421
Db 1365 CACTGAAACAGATCTGCCCAAGCCCTTGTGATGTCAAGAGATGCACTTTGAGTCC 1424
Oy 1422 AGAATCTCTCTGTTGAACCCCAAGCTTGAACAGTGAACGAGACAGATGTCTTACC 1481
Db 1425 AGAATCTCTCTGTTGAACCCCAAGCTTGAACAGTGAACAGAGATGATGAGTCTCC 1484
Oy 1482 T-----GACATCTCTGTGTCACCTGCTATGAGCTTACTCCCTGTC 1526
Db 1485 TGAATGTCTCCAAAGCAGTCTTGTGTCTCCACCTGATCAAGCTCAATTTCCGATTC 1544
Oy 1527 AGAAGCTCACCTTTCTTTATGACATCAAGCATCTTCTCTGACTGATCAAGGACACAC 1586
Db 1545 AGAAATATCTACTCTGTTT---CACCTAGCATCTTCTCTAGATGCTCAAAAGCCCCC 1601
Oy 1587 AGATACAAATGACCTGACAGACATGCTAGTACAGAGGCTCACCATTCACCAAGTGA 1646
Db 1602 TCCCTTATGACCACTGGCCCAACAGACATCTCCCAAGCCACTCTCCCACTATGGA 1661
Oy 1647 TTATTTGCAATTCAGCCCACTGTGCTGTGGAAATTTCAATCCACTGTGATCTTCAGATGA 1706
Db 1662 TTATTTGCAATTCAGCCCACTGTGCTGTGGAAATTCGTCATTTGGCTGTGATCTTCAGTGA 1721
Oy 1707 CAGCCGATCAAGTCAAGTGTGCGAAGATATGCTCAGACCACTAGATGAATGATCTGTC 1766
Db 1722 CAGAGAGCTGATCAAGAGACCATGACACATTCGAAACCTAAGATGCAATGATGTGTC 1781
Oy 1767 TGAACCTCTGCCCCATCTGAGTACAGAGCTCAGCAATATGTTTCTGTCCAGATCA 1826
Db 1782 TGAACCTCTGCCCCATCTGAGTACAGAGCTCAGCAATATGTTTCTGTCCAGATCA 1841
Oy 1827 TTTCTTGAAGATATCACTCTCTGTCTCAGCTTTACAGTATATCACTAATGTTCTATGAC 1886
Db 1842 GTTCTTGAAGATATCACTCTCTGTCTCAGCTTTACAGTATATCACTAATGTTCTATGAC 1901
Oy 1887 CATTTGCCCCCAAGGCGCAGAGCTGTGTGTGTTCTTCAAGTCTGAGTGTGCTTAAATGAC 1946
Db 1902 CATTTGCCCCCAAGGCGCAGAGCTGTGTGTGTTCTTCAAGTCTGAGTGTGCTTAAATGAC 1961
Oy 1947 CTTCCTCAAGCACTGTTTCAACAGAGCTCTCTGAGTACGAGCTCTGAGCAACAAAT 2006
Db 1962 GTTCTCTATGACCTGTTCACCAAGAGTCTCTGTGAGATATCAAGCCCTGAAACAGATT 2021
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QY	2007	CACACAGCTGCTGGTTCATATCTACACGATCCAACTTACAGATTTAAAGCACTTGAAT	2066
Db	2022	CACAGACTGCTGGTCCCTATCTACAGATCAATCTTACGGATTTAAAGCAACTGGAAT	2081
QY	2067	ACTTAACTTCGAAAACGGAGTGTGATTTGTGAATAGCAAAATGAAAGTTTGTATAGTCTGT	2126
Db	2082	ACTCAGCTTCGAAAACGGAGTGTGATTCGTGAACAGCAAACTGGCGTTTGCAAAGCGCT	2141
QY	2127	GCCGTATTACTCACCAAGCTGTGACAGGGCTCTTGAGGATTTTCGTTCTGCTCAAC	2186
Db	2142	ACCCATCAACCTCACCCAGCGCGGGGCTCTTGAGGATCTTGGTCCACCGAGC	2201
QY	2187	CCAAACAATCTCATCTGGAATATGACAGTACTCTCTCAAACTTGAACGAGTATCAAC	2246
Db	2202	TCMAAGGCTCAATCTGGAATCGAAGCTTCTCCCTGACATTAACAGCTGATCAAGC	2261
QY	2247	AGATCCCTGCAAGTTCCTGGCTCGCGCGAAATTTGCCCATGTGTAAAGAACGACGAC	2306
Db	2262	GGATCCCTGCAAACTCTAGACTGTGGCAATTTTGCCCAAGTGTAAAGATGAGTGAC	2321
QY	2307	TGAGAAAGCGGAGTGTGCTGTCCAAACAGGATATGACAGCCAGGGAGCTTGACGGCT	2366
Db	2322	AGAGGAAGCAAGTGTGCTGTCAACAGGACATGAGGCCACGGGACCTCGACCTACA	2381
QY	2367	GGAACCAAGGCTCTGTGGCCTGTGGCACAAAGAAATGCAAGGTCTCCAGGAAAGGAGC	2426
Db	2382	GACCTGAACCTCTGTCCCCCTGG---AAACACTTGTGTGGCCGGCCGAGAACAGACAC	2438
QY	2427	TCCATGCAAGTTGGCCAGATCACTCTGAAATTCAGATCAAAACTAGTGTAAAGAT	2486
Db	2439	TCCATGCAAGGCGACACAGATCACTTACAAACCAAGCTCAGAGACCTGTGTTAAAGCT	2498
QY	2487	CCAAATCAACAAATATACAGGTATATAGTAAAGAAATCTGAATTACTGACCGTAGA	2546
Db	2499	ACGTCAAGCA-----ATTAAGTAGTGTAAAGAAAGAAATCTTAACTATAGCTTAGG	2552
QY	2547	ATATGAAGATTTTAACCATCAAGATTGGGAAGAAATTTAAACTGAAA-----	2595
Db	2553	ATTGAAGATTTGAAGACAGGACTGGGAAGAAATTTAAAGCTGGAATCATATGACTT	2612
QY	2596	-----ATGTAAATTTATCACTTAGGCTATCTCAGAGAGATGATTTGCC	2640
Db	2613	ATGTTGCAAACTCTGTGAAGAAAGAACTTTATTTCTTAAAGAAAGGTGTATGTGTTCT	2672
QY	2641	TCTCAAGGAATGAGACAGGCACTATTATCATGGGTATCAAAATCCAGACATACAGTCAA	2700
Db	2673	TAACTTCTGAAAAACAGAGGAGATTCAGTGTCTATTGGAAATACAGGATGTATCA	2732
QY	2701	CACTGAGATCAGACACACATATTTCAAAATATGAAAGACTCATGTACTTGGCAACAG	2760
Db	2733	CTTTGAGACTGAG-----CATCTTGAAACAAAGACACAGGCGTGTATTTGATGA-CA	2784
QY	2761	TAAATTCGAAAAAAAAGACACTTACTTATTAATA--AAACCCAAATGCAATGAGGAA	2818
Db	2785	TTAAAGCCTGTGGGGCGGGGGGACATATTTTATGTCAAAATCTCAAAACATATTTGA	2844
QY	2819	ACATATTTTAACTATCTTGAGATATGTCAAAATGATCATTAACCGAGTTTGGCTTCAAC	2878
Db	2845	ACACA-ATTGACTATTTTGTGACAGTACTC--AAGTAGCAAAAGATTAAGTTAGCTTTTT	2901
QY	2879	CTTCCCTGAAAATTTTACTCACAATCATTTTGCACAAGCATAGCTTACTTATTTGTTAG	2938
Db	2902	CTTCTTTTAAATTTATCATTAACCTTAATTTCAATTAATTAAC-----TTGTTTAA	2954
QY	2939	GGACTGAAATTTTATTTGGGAAGCAACTTTTATATGCTGAAGATCAATTTAAAGAT	2998
Db	2995	TGGGTGTACATATTTAGAGATTCGATTCCTTTTATATGTTAGATATACGTTAAAGAT	3014
QY	2999	GACTACTTACGC 3010	
Db	3015	TATCATTTGGGC 3026	

XX	RESULT 13
XX	ADAI14847
ID	ADAI14847 standard; cDNA, 3668 BP.
XX	
AC	ADAI14847;
XX	
XX	06-NOV-2003 (first entry)
DT	
XX	
DE	Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX	
KW	ss; gene; mouse; IPMC 150 isoform A; gene therapy;
KW	interphotoreceptor matrix component; IPMC; ocular disorder;
KW	macular degeneration; photoreceptor death; retinal detachment.
XX	
OS	Mus sp.
XX	
FH	Key Location/Qualifiers
FT	196..2592
FT	/*tag= a
FT	/product= "IPMC 150 isoform A"
XX	
PN	US2002160954-A1.
XX	
PD	31-OCT-2002.
XX	
PF	08-NOV-2001; 2001US-00007270.
XX	
PR	29-OCT-1998; 98US-00183972.
PR	29-OCT-1999; 99US-00430195.
XX	
PA	(IOWA ) UNIV IOWA RES FOUND.
XX	
PI	Hageman GS, Kuehn MH;
DR	WPI; 2003-238235/23.
XX	
DR	P-PSDB; ADAI14848.
XX	
PT	New isolated or recombinant interphotoreceptor matrix component
PT	polynucleotide and polypeptide, useful for diagnosing, preventing,
PT	treating or prognosticating ocular disorders, e.g. macular degeneration
PT	or retinal detachment.
XX	
PS	Claim 3; Page 39-41; 76pp; English.
XX	
CC	The invention relates to an isolated or recombinant interphotoreceptor
CC	matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC	comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC	gene operatively linked to the IPMC polynucleotide. The IPMC
CC	polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC	preventing, treating or prognosticating ocular disorders, e.g. macular
CC	degeneration, photoreceptor death or retinal detachment. They are also
CC	useful for identifying a compound capable of modulating IPMC gene
CC	expression in a cell. The present sequence represents cDNA encoding mouse
XX	interphotoreceptor matrix component, IPMC, 150 isoform A.
XX	
SO	Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;
	Query Match 41.3%; Score 1375.6; DB 10; Length 3668;
	Best Local Similarity 70.7%; Pred. No. 0;
	Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19
OY	
DB	1 TAAACCAAGAGGTATCTCTCAATCATCTGTTATCAATATATATTTTTCACATTTC 60
	62 TAAACCAAGGAGGTCTCTGATCTACGCGGACCTGATTTGATATTTTTCATATTTTC 121
OY	61 TGTACTTTT-----AATGAGATTGAGGTTGTTCTGATTTGTTATCAGATTACC 113
DB	122 AGTACCTTATTTCTTTAAAGTGTACCTTGATTTGTTCTGTGATTT--TCGAAATTACC 179
OY	114 AATGACAAAGCCAGAAATGATTTTGGAACTAGAAAGCTATTTTGTTTTGGATT 173
DB	180 AGTATACGAA--CCAGATGAAATTTTCAAAATTAAACATGATATCTTGTTTGGATT 238

174 TTCTCAAGTTCAAGGAACCAAGATATCTCAATTACATATACCATTTCTGAAGCTTAAG 233  
239 TTCTCAAGTTCAAGGAATCAAGATACCTCTATTTAAATATTCAGTTCTGAATTTAAA 298  
234 ACATAGACATCTCCCAAGAAATGAAACCACTGAAGATCTGAAAAAATGTACAAATGT 293  
239 ACATAGACAAAACCCCAAGATTCGAAACAAATTGAAGTACTTCAACAGTGCAAAAGTGT 358  
294 CAACATAGAGAGATATTCGATTTGGGCAAGCATTCGAAACAAAGATCCGATTTTTC 353  
339 CAACATAGAAAGAAATTCGATTTGGGCAAGCATTCGAAACAAAGATTCGATTTTTC 418  
334 CAACGGGGGTTAAAGTCTGTCCACAGAAATCCATGAACAGATTTTGAACAGCTTTCAAG 413  
419 CA---GCTGTAACTCTGTCCACAGGAATCTTGTAGACAGATTTTGAAGATCTTCAAG 475  
414 CTATTTATGATTTGAGAGTGTGTCAAGAAAGCATATGGGAAGCATATCGATCTTTCTGG 473  
476 AATATTTATGACTGAGAGATATGTCAAGAAAGTGTGTGGGAAGCATATCGATCTTTCTGG 535  
474 ATGGAATCCCTGACACAGGGGAATATCAGAGATTTGGGTGAGCATCTGTCCAGCAGAGACT 533  
536 ACCGAATTCCTGACACAGAGAAATATCAGAGCTGGGTGAGCTCTGTCCAGAAAGAACT 595  
534 TCTGCTCTTTGACATTTGGAAAAAATTCAGCAATTTCCAGAGGACCTGTGATCTTCTCC 593  
536 TCTGCTCTTTGACATTTGGAAAAAATTCAGCAATTTCCAGAGGACCTGTGATCTTCTCC 655  
534 AGCAGAGAAATTAACAGAGAAAGTTCCTCTGACAGAAAGATGAATATCTGACAGAAAG 653  
656 AGCAGAGAAATTAACAGAGAAAGTTCCTCTGAGAGAAAGATGAAGACGCTCATGAGAA 715  
654 CATTTGGAGAGCTGTGTGAAGCATTTGTCAATTTCAACAGCATCTACATTTCAAGACTT 713  
716 CACTGAAGACCTACTGAAGCCCTGTGTGATCCAC----- 752  
714 GGGCAGTATTTCAAGAAAACTCAGAAAGCAAAATTCAGATGTTGCGCAAGCTCTCACT 773  
753 -----AGATGTTTCCAGAGATGCTCT 773  
774 TGGGCTTTTCCCTCACTCTGATGACACCTCTCTCAATGAATTTCTGATTAATACCT 833  
774 GGGGCTTTTCCCTCACTCTGATGACACACCTCTCAAGAGATTTCTGATGATCACTCT 833  
834 CAACGACCAAGATGCTTACACAGAAAGAAACAGAA-----TTGGCTGT 881  
834 CAAGGACATTTCAAAAGCCCAACAGAAAGTAAACAGAACTTATTCAGTGTCTGAAT 893  
882 GTTGGAGAGCAGAGGGTGAAGCTCAGCGTCTCTGTGTAAACAGAAATTCAGAGCAGA 941  
884 CTCATCAGAGGAGAGGTGGAATTCAGCATCTCTGTCCAAACACAGGTTCAAGGACAGA 953  
942 GCTCGCTGATCTCCAGTCCCATATTTACAGAGAGCTAGCAGAAAGTCCCACTTCAGAT 1001  
954 GCTTCACCAACTCTGGGTCACTACATCTACACAGAACTGTGTGAGCAGTCCCACTCGAAT 1013  
1002 GCAAAAGATTTTAAGAACTTCAGAGATTTCAAAAAATTCATGTGTGAATTTAGAC 1061  
1014 GCAAAAGATTTTAAGAACTTCAGAGATTTGGAAGAAATTCGTGAATTTAGAGC 1073  
1062 AAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCACTTACGGCATCTTTAAGAG 1121  
1074 AAAGAAAGAAAGATGCTCAAGCTCCACAGAAATTCAGCTTTAAGGACCTTTAAGAG 1133  
1122 ACACAGTGCAGAGCAAAAGCCCTGCAAGTGAAGCTCTGTCTTTGATTTCCAAACAAAT 1181  
1134 GCAACCATGCGAAGCAAAAGCCCTGATGATCTACGTCTCTGATTTCCAAACAAAT 1193  
1182 TGAAGTGAAGAGTCTATCATGGAACATGAGAGAGGACAGCAACCGAAATCTATCT 1241  
1194 TGAAGTGAAGAGATTCATCATGAGTCTATGAA---GACAAACAAACGAAACCTTACCT 1250

1242 CACAGCTACAGACCTCAAAAGGCTGATCAGCAAGACATGAGAGAAAGCAATCTTTGGA 1301  
1251 CACAGCTACAGACCTCAAAAGGCTGATCAGCAAGACATGAGAGAAAGCAATCTTTGGA 1310  
1302 TGTGGGACAAATTCAGTTCACTGATGAATTTGTGATGATCTGTCCAGCTTTGTCTGA 1361  
1311 AGAAGGGAATTTCCATTCGGTGAATGAAGTTACTGGGACACT-----CTTCAGACCTGT 1364  
1362 CACCCAAACAGAGCTGCCACATCTTTGTCTGTTATTAACAAGATGCTACTCTTGAATCC 1421  
1365 CACTGAACCAATCTGCCCCAAGCCCTGTGTGATGTCACAGAGATGTCACATTTGAAGTCC 1424  
1422 AGAATCTCTCTGTGTAACCCAGCTTGACACAGTGAACGAGAGAGACATGTCTACC 1481  
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1602 TCCCTGATGACACTGAGCCCAACAGACATCTACCCCAAGCCACTCTCCCACTATGGA 1661  
1647 TTATTTGCAATCAGCCAACTGGCTCTGGAAATTTACATCCACCTGATCTTCAGATGA 1706  
1662 TTATTTCTACATCGCCCAATTTGCTGGAATTCGTCATTTGGCTGTGATCCTCAAGTGA 1721  
1707 CAGCGGATCAATGAGGTGAGCAAGATATGTCAGACACCTTAAGTGAATGATCTGTCT 1766  
1722 CAGAGAGTGAATCAACAGACCCATGACACAAATCCGAACCTTAAGTGAATGATGTGTC 1781  
1767 TGAACATCTCTGCCCATCTGAGATACAGAGCTCAGCAATATGTTTCTGTCCAGATCA 1826  
1782 TGAACGCGACCTTTGTGAGAAATTCAGAACTGATGATGATGATTTCTGCTCGGATCA 1841  
1827 TTTCTTGAAGATACCACTCTGTCTGATCACTTTACAGTATATCACCACTAGTTCTATGAC 1886  
1842 GTTCTTGAAGATGACACACCAATCCCAAGTACGATTCATCACCAAGCTCCGAGAC 1901  
1887 CATTTGCCCCCAAGGCGCAGAGCTGTGTGATTTCTTCAAGTCTGTGTGTGCTTAACATGC 1946  
1902 CATTTGCCCCCAAGGCGCAGAGCTGTGTGATTTCTTCAAGCTGTGTGTGTGCTTAACATGC 1961  
1947 TTTCTCAAGACCTGTTCACAAAGAGCTCTGTGAGTACGAGCTCTGAGCAACAAT 2006  
1962 GTTCTCTTGAAGCTGTTCACAAAGAGTTCGTGAGTATCAAGGCTCTGAGCAACAAT 2021  
2007 CACACAGCTGTGTGTCATATCTAGATCCAATCTTACAGATTTTAAGCAACTTGAAT 2066  
2022 CACAGACCTGTGTGTCATATCTTACAGATCCAATCTTACAGATTTTAAGCAACTTGAAT 2081  
2067 ACTTAATCTTCAAGAAACGGAAGTGTATGTGAACAGCAAAAGTGTGTGCAAAAGCGGT 2141  
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2187 CCAACAACTCATCTGAAATTAAGACGCTACTCTCTCAACATTTGAACCAAGCTGATCAAG 2246  
2202 TCAAGGCTCATCTGAAATTCGAAAGCTACTCCCTCAGCAATTTGAACCAAGCTGATCAAG 2261  
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2262 GGAATCCCTGCAAGTTCCTGCAAGTGTGCGGGAATTTGCCCCAAGTGTGTAAAGATGATGAG 2321  
2307 TGAAGAACGGAAGTGTGCTGCAAAACAGATATGACAGCGGAGCTGTGACGATCT 2366

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Db      2322 AGAGGAGAGAGTCTCGCTGACAGACAGGAGCATGAGACCGGACCTTGATACCA 2381
Qy      2367 GGAACCAAGCCCTCTGTGGCCCTTGCGCAAAAGAAATGCGAGGTCTTCCAGGAGAGGAGC 2426
Db      2382 GACCCCTGAACCTCTGTCCCTCG---AAAGACTGTGTGGCCGGCCGAGAACAGCAAC 2438
Qy      2427 TCCAGGAGGTTGCCAGATCACTCTGAAATCAAGCATCAAAACTAGTGTAAAAAGTT 2486
Db      2439 TCCATGACGGCCACAGATCACTCAAAACCAAGCTCGAAACCTGGGTAAAAAGCT 2498
Qy      2487 CCAAAATCACAAAATTAACAAGGTATCATGTAAGAAATTCGATTATCGACCGTGA 2546
Db      2499 AGCTGACGA-----AATAGGTAGTCAAGAAAAGAAATTTAAACTATGACTATAG 2552
Qy      2547 ATATGAGAAATTTAAACATCAAGATTGGAGAGAAATTTAAAACTGAAA----- 2595
Db      2553 ATTTGAGAAATTTGAAGACCAAGACTGGAGGAAATTTAAAGCTGAAATCATATGCAAT 2612
Qy      2596 -----ATGTACAATTAATCATCTTAGCTATCTCAAGAGATGATTTGGCT 2640
Db      2613 ATGTGCAAACTCTGTGAAGAAAATTATTTCTTAAAGAAAGGTATCTGTCTGT 2672
Qy      2641 TCTCAAGGAAATGAGACAGGCAATATTCATGGGTCAATCAAAATCCAGACATACAGTCA 2700
Db      2673 TAACTTCAAAAACAGAGGAGAGATTCAGTGTCAATGGAATCAGGCATGTATATCA 2732
Qy      2701 CACTGAAATCGACACACCATATTTTCAATATAGAAAGTCATGTACTTGGAACCG 2760
Db      2723 CTTTGAGACTGAG-----CATGCTGAACAGACAGCGGTATTTGATGA-CA 2784
Qy      2761 TAAATTCGAAAAAAGACACTTACTTATTTA--AAACCCCAATGCAATCGCGAA 2818
Db      2785 TTAAACCTGTGTGGCGCGGGGACATATTTTGTCAAACTCAAAACATCATTTGGA 2844
Qy      2819 ACATATTTTACTATTTCTGATGATGATCAAAATGATCATTAAGCAGTTGCTTCAC 2878
Db      2845 ACAC- TTTGACTATTTTGGACAGTACTC--AAGTAGCAAAAGATTAAGGTATGCTTTT 2901
Qy      2879 CTTCCTGAAATTTTACTCAGATCATTTGCCAACAGATAGCTTACTTATTTAG 2938
Db      2902 CTTCCTTAAATATTAACATAARCTTATTTCAAAATAATACAC-----TTGTTAG 2954
Qy      2939 GGACTGAACATTTATTTGGGAACAACTCTTATATGCTAGAAAGTACATTTAAAGAT 2998
Db      2955 TGGGTGACATATTTGAGATCTGATCTTTATATGTATAGAAATATACATTAAGAT 3014
Qy      2999 GACTACTTAACG 3010
Db      3015 TATCATTTGGGC 3026

RESULT 14
AAA46309
ID      AAA46309 standard; cDNA; 3206 BP.
XX      AAA46309;
AC      04-SEP-2000 (first entry)
DT      XX
DE      cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).
XX      XX
XX      Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
XX      chromosome 6q13-q15; ocular disease; retinal detachment;
XX      choroidretinal degeneration; retinal degeneration; cone degeneration;
XX      age related macular degeneration; photoreceptor degeneration;
XX      retinal pigment epithelium degeneration; mucopolysaccharidosis;
XX      rod-cone dystrophy; cone-rod dystrophy; ss.
XX      XX
OS      Mus sp.
XX      Key
XX      Location/Qualifiers
XX      CDS
XX      1..2130

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FT      /tag= a
FT      /transl_except= (pos: 16..18, aa: Val)
FT      /transl_except= (pos: 55..57, aa: Ala)
FT      /transl_except= (pos: 58..60, aa: Tyr)
FT      /transl_except= (pos: 73, aa: Asp)
FT      /transl_except= (pos: 234..236, aa: Xaa)
FT      /transl_except= (pos: 271..272, aa: Xaa)
FT      /transl_except= (pos: 403..405, aa: Xaa)
FT      /transl_except= (pos: 2107..2109, aa: Xaa)
FT      /product= "interphotoreceptor matrix proteoglycan IPM150"
FT      /note= "Xaa is an unspecified amino acid"

PN      WO200026367-A2.
PD      11-MAY-2000.
PF      29-OCT-1999; 99WO-US025440.
PR      29-OCT-1998; 98US-00183972.
PA      (IOWA ) UNIV IOWA RES FOUND.
PI      Hageman GS, Kuehn MH;
DR      WPI: 2000-355616/31.
DR      P-PSDB; AAY93338.
PT      Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT      preventing, diagnosing and treating ocular disorders such as retinal
PT      detachment and choroidretinal degeneration.
XX      Claim 2, Fig 6A; 183pp; English.
XX      XX
XX      The present sequence encodes an interphotoreceptor matrix (IPM)
XX      proteoglycan, designated IPM150. The protein is an IPM component (IPMC).
XX      Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
XX      is located on chromosome 6q13-q15, between markers CHIC.CAT11P10 and
XX      D6S284. The IPM proteins may be used to supplement a patient's own
XX      production of the protein or to rectify alterations in their nucleic
XX      acids that result in expression of an inactive protein. The IPM nucleic
XX      acids may be used in this way to treat ocular diseases such as retinal
XX      detachment, choroidretinal degeneration, retinal degeneration, age related
XX      macular degeneration, photoreceptor degeneration, RPE (retinal pigment
XX      epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
XX      cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
XX      also be used to assay for other modulators of IPM proteoglycan expression
XX      and activity that may be used to treat ocular diseases. The nucleic
XX      acids and proteins may also be used as diagnostic reagents to detect the
XX      presence of IPM nucleic acids and their products in samples from patients
XX      according to standard methodologies
XX      SQ      Sequence 3206 BP; 937 A; 778 C; 686 G; 793 T; 0 U; 12 Other;

Query Match      33.8%; Score 1127.2; DB 3; Length 3206;
Best Local Similarity 68.9%; Pred. No. 1.6e-290;
Matches 1824; Conservative 5; Mismatches 665; Indels 152; Gaps 15;

Qy      418 TTATGATTGAGTGTGTGAGAAAGCATATGGAACATATGATCTTTCTGGATCG 477
Db      18 TCAAGGAATCAAAATATCTCAAGAAAGTGTGTGGAGAAATGATCTTATCTTTGGNAG 77
Qy      478 CATCTTGACACAGGGGAATATCAGACTGGGTGATCTGTCAGACAGAGAACCTTCTG 537
Db      78 AATTCCTGACACAGAGAAATATCAAGGCTGGGTGAGCTTGCCAGAAAGAAACCTTCTG 137
Qy      538 CCTCTTTGACATTTGGAATAAATTTCCAGAGACACTTGGATCTTTTCCAGCA 597
Db      138 CTTCTTTGACATTTGGAAAAAATCTGAGCAACTCCAGAGACCACTTGAATCTTTTCAGCA 197
Qy      598 GAGATATAAACAAGAAATTTCCCTGACAGAAAGATGAATATCTGACAGAGACATTT 657
Db      198 GAGATATAAACAAGAACTTCCCTGGAGAGAAAGATGACACACCTTCATGAGACACT 257

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QY	658	GGAGAGAGCTGGTGAACCATTTGTCATTTCAACAGCAATCTACATTTCAAAAGACTTGGGC	717
Db	258	GGAAACACCTTACTGAGGCCCTGTGTATCCAC-----	290
QY	718	AGTATTTAAGAAAACCTCAGAAAGCAAAATTCAAGATGTTGGCAAGCTCACTTGGG	777
Db	291	-----AGATGTTTCCAGATGTCTCTGGGG	315
QY	778	CCTTTCCTCTGACTCTGTATGACACCTCTCTCAATGAAATTTCTGATTAATACCTCAAC	837
Db	316	CCMTTCCCACTTCTTGTGATGACACAGACTCAAGAGATTCTCAGTGCACCTCAAG	375
QY	838	GACACCAAGATGCCCTACAAAGAAAAGAAAAGAA-----TTGCTGTGTG	885
Db	376	GACATTTCAAAAGCCCAACAAGAAAAGTMAAGAAAGAACTTATTCAGTGTCTGAATTTCTCA	435
QY	886	GAGAGACAGAGGGTGAAGCTCAGCGCTCTCTGTGTAAACAGAAAGTTCAAGGACAGCTC	945
Db	436	TCAGAGAGAAAGTGBARTTCAGCATCTCTCTGCCAAACACAGGTTCAAGGACAGCTC	495
QY	946	GCTGACTCCAGTCCCATATTATACAGAGACTGACAGAAAGTCCCAATTCCAGATGCA	1005
Db	496	ACCAACTCTGGGTCAACATACACAGAGAACTGTGGGACAGTCCCACTGCAAGTTGCA	555
QY	1006	AAGATATTTTAAAGAACTTCCAGGATTTCAAAAAATTCATGTGTATGATTTAGACCAAG	1065
Db	556	AAGATATTTTAAAGAACTTCCAGGATTTCCGAGAAATCCGTGTATTTAGCAATTTAGACCAAG	615
QY	1066	AAAGAAAAAGATGGCTCAAGCTCCAAGAGATGCAACTTACGGCCATCTTTAAGAGACAC	1122
Db	616	AAAGAAAGAAAGATGTTTCAAGCTCCACAGAAATACAGCTTTATGGCAATCTTTAAGAGGAC	675
QY	1126	AGTGCAGAAAGCAAAAAGCCCTGCAAGTGAACCTCTGTCTTTTGTATTCACAAATAATGA	1185
Db	676	CATGCAGAAAGCAAAAAGCCCTGATGTGTCATCTACTGTCTTGTATTCACAAATAATGA	735
QY	1186	AGTGAAGAAAGTATATCATATGAAACCATGAGAGAGACAAAGCAACCGAAATCTATTCACA	1245
Db	736	AGTGAAGAAAGTATATCATATGAGAGTCT--AGAAAGCAAAACCAAGAAACCTCACTTCACA	792
QY	1246	GCTACAGAGCTCAAAAAGGCTGATCAAGAAAGCATAGAGAAAGCAATCTTTGATGATGG	1305
Db	793	GCTACAGAGCTCAAAAAGGCTGATCAATCATATACATCTAGATGAGACCTGTCTTTGATGAA	852
QY	1306	GGGACAAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCCCTTGTGTCTGACAC	1365
Db	853	GGGAAATTTCAATTCGGTGTATGAATTTACTGGGACCT-----CTTGACACTGTCTACT	906
QY	1366	CAATCAGAGCTGCCACATCTTTTGTCTGTTATTAACAGAGAGTCTACTTTGATGCCAGA	1425
Db	907	GAAACAGATCTGCCAGAGCCCTTGTCTATATGACAGAGAGTCCACTTTGTGATCCAGAA	966
QY	1426	CTTCTCCCTGTGAAACCCAGCTTGAACAGATGAGACGAGAGACAGACATGATCTACT---	1482
Db	967	CTTCTCTTGTGAGCTTAGGCTTTGAGGCAATGAGACAGAAAGATCTGAGCTGCTTGA	1022
QY	1483	-----GACACTTCTTGATCTCCACCTGTATGGCTCTTACTCTCTCTCAGAA	1533
Db	1027	ATGTCTCTCAAAAGACAGTTCTTGTGTCTCACTGTATACAGCTCAATTTCCCGATACAGA	1086
QY	1531	GCTCCACCTTTCTTTATGAGCATACAGATCTTCTCTGTACTGTATACAGACACACAGAT	1596
Db	1087	AATCTACCTTCCGTTTA--CACCTTAGCATCTTCTCTGATGTCTCAAGCCCTCTCC	1144
QY	1591	ACAAATGGCCACTGAGCCAGACAGATGCTAGTACCAAGGGCTCACATCCCAACAGTATAT	1653
Db	1144	TTGATGACCACTGGCCCAACACACTCATCCCAAGCCACTCTCCCACTATGCAATAT	1203
QY	1651	TCTGCAATCAGCAACTGAGCTCTGGGAATTTTACATCCACTGCATCTTCAATGACAC	1711
Db	1204	TCTTACATCCGCAATTTGCTCTGGAATGTCTACATTTGGCTCTCTCCAGTACAGAA	1263
QY	1711	CGATCAAGTCAAGTGGCGAAGATATGTCAAGACCTTAGATGAATGATCTGTCTGAC	1770

Db	1264	GAGCTGATCA	CAAGACG	CATGAC	CAATCCGAA	CCTAGTGG	CAATGATG	CTGAC	13333	
OY	1771	ACTCCG	CCCCAT	CTGAG	GTACG	AGCTC	AGAGCA	AAATGTTTCG	CCAGATCAT	1830
Db	1324	ACGCCAG	CTTGT	CAGAA	ATATCA	GAACTAG	TGATG	ATGATCTT	CGCTCGGGTCA	1383
OY	1831	TTGGAG	ATAC	CACTCCT	GTCTCA	GCTTTAC	AGTAT	TACCACT	AGTTCTAT	1890
Db	1384	TTGGAG	ATGAC	CAAC	CCATCC	CAAC	AGTAC	GGTTCT	CACCA	1443
OY	1891	GGCCCC	AAAGGG	CCGAG	AGCTGT	GTGTCTT	CAGCTCG	GGTGTG	CTTAAC	1956
Db	1444	GCAC	CCAAAGGG	CCAGAG	CTAG	GTGTATTT	CTTCA	AGCTCG	GTGTGCTT	1503
OY	1951	TC	CAACG	ACCTGT	CAACA	AGAGCT	CTCTG	AGTAC	CGAGCTTG	2010
Db	1504	TC	CTATG	ACCTGT	TCAC	MAAGTT	CTCTG	AGTAT	CAAGCCCT	1563
OY	2011	CAG	CTGTGT	TCATAT	CTAC	AGATCC	AACTTTA	CAAGATTTA	AGCACTT	2070
Db	1564	GAC	CTGTGT	GTCC	CTATCT	ACATCG	AACTT	ACGGGATTTA	AGCAACTG	1623
OY	2071	AAC	TTCA	GAAG	ACGGG	ATGTAT	TTGTGA	ATAGCAAA	TGAAGTTT	2130
Db	1624	AG	CTTCA	AAAA	CGGA	AGTGTAT	GTGTGA	ACGAAG	CGGTTTG	1683
OY	2131	TATA	ACCTCA	CAAG	CTGTG	CA	CGGGGTCT	TGAGAG	ATTTTCGTT	2190
Db	1684	TC	AACTCT	CA	CCCA	AGCCGT	GTG	AGATCTT	CGGTCC	1743
OY	2191	CA	ACTCT	CACTG	GAAT	TAG	CAGCTACT	CTCTCA	ACATTTGA	2256
Db	1744	GG	GTCAAT	CTG	AAATAT	GAAAG	CTACTCC	CTGACA	ATTGAAC	1803
OY	2251	CC	CTGCA	AGTTCC	CTG	CGCTG	GGGGAATTT	TGCC	CAATGTGT	2310
Db	1804	CC	CTGCA	AACTCT	CTG	AGATTT	TGGCAAA	TTTGG	CCAGTGTGT	1863
OY	2311	GAA	GGAG	GTGTCC	GTG	CAAC	ACAG	ATATG	ACACG	2370
Db	1864	GAA	GCAG	GTGTCC	GTG	CAAC	ACAG	ATATG	ACACG	1923
OY	2371	CA	AGG	CTCT	GTG	CCCTG	GCA	AAAGG	ATG	2430
Db	1924	CT	GAACTCT	GTG	CCCC	CTG	---AAAG	CTGTGTG	GGCCG	1968
OY	2431	TG	CAG	GTG	CCAG	ATCA	CTTGA	AAAT	TACAT	2490
Db	1981	TG	CAG	GTG	CCAG	ATCA	CTTGA	AAAT	TACAT	2040
OY	2491	AAT	CA	AAATTA	CAAG	GTAT	CAGT	TA	AAAGAA	2550
Db	2041	CAG	CA	-----AAT	AG	GTAT	CAG	AAAGAA	TTTAA	2094
OY	2551	GAA	GAATTT	AA	CAAT	CAAG	ATTG	GGAG	AAATTT	2609
Db	2095	GAA	GAATTT	AA	CAAT	CAAG	ATTG	GGAG	AAATTT	2154
OY	2610	CT	TAG	GCAT	CTCA	AGAG	ATG	ATTTG	CCCTT	2648
Db	2155	TG	CAAA	CTGT	TGA	AGAA	CTTTAT	CTTTAA	AGAA	2214
OY	2650	-----AA	TG	AG	CA	AG	CAAT	TTCAT	GGGAT	2704
Db	2215	TT	CTG	AAAA	CA	AG	GGG	ATTC	AGT	2274
OY	2705	GAG	AT	CA	GA	CA	CACTAT	TTTCA	ATAT	2764
Db	2275	GAG	AT	CA	GA	CA	CACTAT	TTTCA	ATAT	2330
OY	2765	TT	CTG	AAAA	CA	AG	CACTTA	CTTAT	TTTAA	2824



Db 2331 GGTGGGGGGGGGACATATTTTACTCAAACTC--AAAGCATCATTTGAAACAC- 2387  
 QY 2825 TTTTACTATTCTTGATGATGATCAAAATGATCATTAAGCCAGTTTGCTTCACCTGCC 2884  
 Db 2388 TTTGACTATTTTGGACAGTACTC--AGTAGCAAGATTAAGTTAGCTTTTCTTCT 2445  
 QY 2885 TGAATAATTTTACTCAGATCATTTTGCAACAAGATAGCTTACTTATGTTAGGACTG 2944  
 Db 2446 TTAATTTATTCATTAARCTTATTTCAATAA-----ATCAACTGTTTAGGGGTT 2498  
 QY 2945 AACATTTATTTGGAGCAAACTCTTTATATGCTGAAGATCAATTTAAAGATGACTAC 3004  
 Db 2499 GTACATATTTGAGATCTGATCTTTATATGTAGATATACAGTTAAAGATTATCAT 2558  
 QY 3005 TTAGGC 3010  
 Db 2559 TTGGGC 2564  
 RESULT 15  
 ACC57951  
 ID ACC57951 standard; cDNA; 1726 BP.  
 AC ACC57951;  
 XX  
 DT 11-AUG-2003 (first entry)  
 DE Mouse interphotoreceptor matrix IPM 150, isoform D, cDNA.  
 XX  
 KM Mouse; interphotoreceptor matrix; IPM 150; chromosome 9; IPMC; receptor;  
 KM ophthalmological; gene therapy; gene; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 140..1540  
 FT /\*tag= a  
 FT /product= "IPM 150"  
 FT sig\_peptide 140..199  
 FT /\*tag= b  
 FT  
 PN WO2003039346-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-US036090.  
 XX  
 PR 08-NOV-2001; 2001US-00077270.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Hageman GS, Kuehn MH;  
 XX  
 DR MPI; 2003-441440/41.  
 DR P-PBDB; ABR42346.  
 XX  
 PT New interphotoreceptor matrix proteins and polynucleotides, useful for  
 PT treating or preventing photoreceptor death or retinal detachment, or for  
 PT treating ocular disorders.  
 XX  
 PS Claim 1; Page 82-83; 105pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding isoform D of novel mouse  
 CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
 CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
 CC is located on chromosome 9. Members of the IPMC gene family have been  
 CC identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and  
 CC rat. IPM 2 subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or  
 CC IPM2). The invention provides IPM 150 and IPM 200 polynucleotides and  
 CC polypeptides, antibodies that specifically bind the polypeptides, and  
 CC vectors comprising the polynucleotides. A claimed method of treating or  
 CC preventing photoreceptor death or retinal detachment involves  
 CC administering an IPMC polynucleotide, polypeptide or antibody. Also

CC claimed is a method for identifying a compound capable of modulating IPMC  
 CC gene expression  
 XX  
 SQ Sequence 1726 BP; 541 A; 383 C; 388 G; 414 T; 0 U; 0 Other;  
 Query Match 16.0%; Score 534; DB 9; Length 1726;  
 Best Local Similarity 72.0%; Pred. No. 8.7e-132;  
 Matches 792; Conservative 0; Mismatches 225; Indels 83; Gaps 4;  
 QY 396 TTTTAGACAGTCTTCAAGCTTATTTAGATTGAGAGTGTGACAGAGCATGATGGGAAG 455  
 Db 171 TTTTGGGATTTTCTCCAAAGTTCAAGAAATCAAGATGTGCAAGAAATCGTGGGAAG 230  
 QY 456 CATATCGGATCTTTCTGAGATGGCAATCCCTGACACAGGGGAAATATAGAGATCGGTCACA 515  
 Db 231 CATATCGATCTTCTTGAGCCGAATTCCTGACACAGAGAAATATCAAGCTGGATCCACC 290  
 QY 516 TCTGCCAGCAGAGACCTTCTGCTCTGCTTGAATTTGAATAAACTTCAGCAATTCCTCAGG 575  
 Db 291 TCTGCCAGAAAGAAACCTTCTGCTCTTGTGACATTTGGGAAAACTTCAGCAATTCCTCAGG 350  
 QY 576 AGCACTGGATCTTCTCCAGCAGAGAAATMAACAGAGAGTTTCCCTGACAGAAAAAGATG 635  
 Db 351 AGCACTGATCTTCTTCCAGCAGAGAAATMAACAGAGAGTTTCCCTGAGAGAAAGATG 410  
 QY 636 AATATCTGACAGAGAAAGCATTTGGAGAGCTCGTGAATCAATGTCTATTTCACAGCAA 695  
 Db 411 AGACAGCTCCATGAGACACTGGAAGCACTACTAGAGCCCTGTGTATCCAC----- 465  
 QY 696 TCTACATTTCAAGACTTGGGACAGATTTCTAAGAAACCTTCAGAAAGCAAAATTCAGA 755  
 Db 466 -----AGAA-----  
 QY 756 TGTGCCAAGCTCTCACTTGGGCTTTTCCCTGACTCTGATGACACCTCTGCAATGA 815  
 Db 469 TGTTCAGAGATGTCCTGGGGCCATTCCTCACTTCTGATGACAGACCTCAAGGA 528  
 QY 816 AATTCTGATATATACCTCAACGACCAAGATGCTTCAACAGAAAGAAACGAA-- 873  
 Db 529 GATTCTCAGTGTCAACCTCCAGAGACATTCMAAAGCCCAACAGAAATATATACGAAAC 588  
 QY 874 -----TTGCTGTGTGAGAGCAGAGGTGAGCTGAGCTCTCTGCTGTAA 923  
 Db 589 TATTCACTGTCTGATTTCTATGAGAGAGAAAGGTGAGATCTCTCTGCCAA 648  
 QY 924 CCAGAACTTCAAGCAGAGCTGCTGACTCCCACTCCCATATTTACAGAGCTTAGCAGG 983  
 Db 649 CCAGAGTTCAAGCAGAGCTCACCACTCTGGGTCACTATCTACAGAGAACTGTGGG 708  
 QY 984 AAGTCCCACTTCAGATGCAAAAGATATTTAAGAACTTCAGAGATTCMAAAATCCA 1043  
 Db 709 AAGTCCCACTTCAGATGCAAAAGATATTTAAGAACTTCAGAGATTCGGAATTCG 768  
 QY 1044 TGTGTAGGATTTTGAACCAAGAAAGAAAGATGCTCAAGCTTCACAGAGATGCAACT 1103  
 Db 769 TGTATAGGATTTTGAACCAAGAAAGAAAGATGCTCAAGCTTCACAGAAATCAAGCT 828  
 QY 1104 TACGSCCATCTTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGTGACTCTCTGTC 1163  
 Db 829 TATGCCATCTTTAAGAGGAGCATGCAAGAGCAAAAGCCCTGATATCTATCTATCTTC 888  
 QY 1164 TTTGATTCCAAAATTTGAAGTGAAGAGTATCATATGAAACCATGAGAGAGCA 1223  
 Db 889 TCTTGATTCCAAAATTTGAAGTGAAGAGATCATATGAGAGTCAAT--AGAAAGCA 945  
 QY 1224 GCAACCGAAATCTATCTCAAGCTACAGACTCAAAAGGCTGATCAGCAAGCACTTGA 1283  
 Db 946 ACAACCGAAACCTTACCTCAAGCTACAGACTCAAAAMCTCATCACTACACTTGA 1005  
 QY 1284 GGAAGCAAACTTTGAGATGGGGAACAATTCAGTTCACTGATGAATTTGCTGATCACT 1343  
 Db 1006 TGGAGACTGTCTTGGTGAAGGGAATTCATTCGATATGAATTAAGTTACTGGAGCACT 1065

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OY 1344 GCCAGCCTTGGTCCTGACACCCAAATCAGAGCTGCCCAATCTTTGCTGTATTAACAGA 1403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1066 -----CTTCAGACCTGTGCATGAAACAGATCTGCCCAAGCCCTTGGCTGATGTACAGA 1119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1404 GGATGCTACTTTGAGTCCAGAACTTCCTCTGTTGAAACCCAGCTTTGAGACAGTGGACGG 1463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1120 GGATGCCACTTTGAGTCCAGAACTTCCTCTGTTGAGCCTTAGCTTGAAGGCAGTGGACAG 1179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1464 AGCAGAGCATGSGTCTACCTG 1483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1180 AGAAGATCTGAGCTGCTG 1199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: January 14, 2006, 08:42:38  
Job time : 1928 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2006, 07:25:30 ; Search time 16555 Seconds  
(without alignment)

11433.929 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330  
Sequence: 1 taaccacgaaggtatcct.....tactatgatcataatcaat 3330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 26421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_rsc:\*  
11: gb\_by:\*  
12: gb\_un:\*  
13: gb\_vt:\*  
14: gb\_hvg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3196	96.0	3268	8	AF047492 Homo sapi
2	1713.2	51.4	3552	4	AB047844 Bos tauri
3	1604.2	48.2	2009	6	CQ725539 Sequence
4	1375.6	41.3	3668	9	AF266478 Mus muscu
5	1366.4	41.0	2924	9	BC022970 Mus muscu
6	1287.2	38.7	2850	9	AB047843 Rattus no
7	1255.2	37.7	3675	9	AF229929 Mus muscu
8	823.6	24.7	90766	8	AL392166 Human DNA
9	823.6	24.7	132145	14	AL359817 Homo sapi
10	814.2	24.5	1235	8	HSIMPG17
11	535.8	16.1	816	8	HSIMPG13
12	535.8	16.1	160719	14	AL157379 Homo sapi
13	481.2	14.5	4953	5	AB070714 Gallus ga
14	439	13.2	555	8	AF047491 Macaca fa
15	317.8	9.5	259413	14	AC161554 Bos tauri
16	282.6	8.5	157596	9	AC120388 Mus muscu
17	274.6	8.2	248573	14	AC096467 Rattus no
18	249	7.5	444	8	HSIMPG10

19	236.4	7.1	537	8	HSIMPG02	AF017761 Homo sapi
20	236.4	7.1	132145	14	AL359817	AL359817 Homo sapi
21	236.4	7.1	186301	8	AL359817	AL359817 Homo sapi
22	226	6.8	448	8	HSIMPG14	AF017773 Homo sapi
23	210.4	6.3	477	8	HSIMPG15	AF017774 Homo sapi
24	204.6	6.1	310	8	HSIMPG01	AF017760 Homo sapi
25	203.4	6.1	3326	6	CO728190	Sequence
26	203.4	6.1	3989	8	AF157624	Homo sapi
27	203.4	6.1	4165	6	CO870600	Sequence
28	203.4	6.1	4165	8	AF173155	Homo sapi
29	200.4	6.0	4368	9	RNU76717	Homo sapi
30	198.8	6.0	4010	9	AY174061	Mus muscu
31	198.8	6.0	6961	9	BC048863	Mus muscu
32	198.2	6.0	259413	14	AC161554	Bos tauri
33	169.8	5.1	422	8	HSIMPG03	Homo sapi
34	153	4.6	41220	9	AC148244	Mus muscu
35	145.6	4.4	159816	14	AC136044	Rattus no
36	143.2	4.3	214606	14	AC161819	Gallus ga
37	142.4	4.3	377	8	HSIMPG07	AF017766 Homo sapi
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## ALIGNMENTS

RESULT 1	AF047492	3268 bp	mRNA	linear	PRI 26-OCT-1999
LOCUS	AF047492				
DEFINITION	Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)				
ACCESSION	AF047492.2 GI:6118565				
VERSION	AF047492.2				
KEYWORDS	mRNA, complete cds.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Kuehn, M.H. and Hageman, G.S.				
TITLE	Expression and characterization of the IPM 150 gene (IMPG1) product, a novel human photoreceptor cell-associated chondroitin-sulfate proteoglycan				
JOURNAL	Matrix Biol. 18 (5), 509-518 (1999)				
PUBMED	10601738				
REFERENCE	2 (bases 1 to 3268)				
AUTHORS	Kuehn, M.H. and Hageman, G.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-FEB-1998) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 11190E PFP, Iowa City, IA 52240, USA				
REFERENCE	3 (bases 1 to 3268)				
AUTHORS	Kuehn, M.H. and Hageman, G.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-OCT-1999) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 11190E PFP, Iowa City, IA 52240, USA				
REMARK	Sequence update by submitter				
COMMENT	On Oct 26, 1999 this sequence version replaced gi:2906231.				
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 SOURCE  
 ORGANISM  
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 Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE  
 1 (bases)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Isolation and characterization of mucinlike glycoprotein associated  
 with photoreceptor cells  
 Invest. Ophthalmol. Vis. Sci. 41 (9), 2759-2765 (2000)  
 2 (bases 1 to 3552)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Direct Submision  
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 (E-mail: f.uehara@meds.kufm.kagoshima-u.ac.jp, Tel: 81-99-275-5402,  
 Fax: 81-99-265-4894)  
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## ORIGIN

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 Qy 1369 CACCAATGAGAGCTGGCCCAACATCTTTGCTGTATTAACAGAGATGCTACTTTAGATCC 1421  
 Db 1365 CACTGACCAAGATCTGGCCCAAGCCCTTGCTATGTCAAGAGAGATGCCACTTTAGATCC 1424  
 Qy 1422 AGAATCTCTCTGTTGAACCCCAAGCTTGAGACAGTGAAGAGAGAGATGCTCTACC 1481  
 Db 1425 AGAATCTCTCTGTTGAACCCCAAGCTTGAGAGAGTGAAGAGAGATGCTGAGCTGCC 1484  
 Qy 1482 T-----GACATTTCTTGTTCTCACTGCTATAGCTTCACTCCCTGTG 1526  
 Db 1485 TGGAAATGCTCCAAAGAGATGCTGTGCTCACCCTGTATCAAGCTCAATTTCCGATC 1544  
 Qy 1527 AGAAGCTCACTCTTTTATGAGCATCAAGCATCTTCTCTGAGTATCAAGGACCAAC 1586  
 Db 1545 AGAATATCTACCTTGTTA---CACTAGACATCTTCTCTAGATGCTCAAGGCCCC 1601  
 Qy 1587 AGATCAATGAGCACTGACCAAGACATGCTAGTACCAAGGCTCACCATCCCAAGTGA 1646  
 Db 1602 TCCCTTGATGACCACTGGCCCAAGCACTCATCCCAAGCCCACTCCCACTATGCA 1661  
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 Db 2142 ACCCTATCAATCTCAAGAGCTGTGACCGGGGTCTTGAGAGATTTTCTGTCTGACAC 2201  
 Qy 2187 CCAACAGCTCTCAATCTGAAATAGACAGTACTCTCTCAACATTTGAACCAAGCTGATCAAC 2246  
 Db 2202 TCAAGAGCTCTCAATCTGAAATAGACAGTACTCTCTCAACATTTGAACCAAGCTGATCAAC 2261  
 Qy 2247 AGATCCCTGCAAGTCTGTGCGCGGCGCAATTTGGCCCAATGTGTAAAGAAAGGAGC 2306  
 Db 2262 GGAATCCCTGCAAGTCTGTGCGCGGCGCAATTTGGCCCAATGTGTAAAGAAAGGAGC 2321  
 Qy 2307 TGAGAGAGGAGTGTGTCTGCAACCAAGATATGACAGCAGGAGGAGCTGGAACGATCT 2366  
 Db 2322 AGAGAGAGGAGTGTGTCTGCAACCAAGATATGACAGCAGGAGGAGCTGGAACGATCT 2381  
 Qy 2367 GGAACGAGGCTGTGTGCGCTGTGCAAAAGGATGCGAGGTCTCTCAAGGAAAGGAGC 2426

Db 2382 GACCTGAACCTGTGCCCCCTGG---AAAGACTGTGTGCGCGGCCGAGAACAGCAAC 2438  
 Qy 2427 TCCATGAGGTGTGCGAGATCACTGAAATCAAGCATACAAATAGTGTAAAGAT 2486  
 Db 2439 TCCATGAGGCGCACCGAGTCACTCTACAAACCAAGCTCAGGAACTGTGTTAAAGCT 2498  
 Qy 2487 CCAATATCAACAAATATCAAGGTATCATGTAAGAAATTTCTGAATTAAGTCCGTAGA 2546  
 Db 2499 AGCTGAGCA-----AATTAAGTATGCAAGAAAGAAATTTAACTATGATGATAGG 2552  
 Qy 2547 ATATGAAGATTTTAACATCAAGATTGGAGAAATTTAAATCTGAAA----- 2595  
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 Qy 2596 -----ATGTACATATATCACTAGGCTATCTCAAGAGATGATTGCT 2640  
 Db 2613 ATGTGCAAACTGTGTAAAGAAATTTTCTTAAAGAAAGGTATCTGTCTGT 2672  
 Qy 2641 TCTCAAGAAATATGAGACAGGATATTCATGGTCAATCAAAATCCAGACATACAGTCA 2700  
 Db 2673 TAACTTCTGAAABAAACAGAGGAGATTCAGTGTGCTTTGATGATACAGGATGATATCA 2732  
 Qy 2701 CACTGAGATGACACACATATTTCAATATGAAAGTCAATGATCTTGACACAG 2760  
 Db 2733 CTGAGAGACTGAG-----CATGCTTGAACAGGACAGGCGGTATTTGATGA-CAG 2784  
 Qy 2761 TAAATCTGAAABAAAGACACTTACTATTTATTA--AAACCCCAATGCAATCAGGAA 2818  
 Db 2785 TTAAGCTGTGTGGGCGGGGCGGAGCATATTTTATGCTAAACCTAAAGCAATCAATTGA 2844  
 Qy 2819 ACATATTTTACTATCTTGAATGATGATCAAAATGATCATAGGCAAGTGTCTTCAC 2878  
 Db 2845 ACACA-TTTGACTATTTTGGACAGTACTC--AGTACCAAGATTAAGTTAGCTTTT 2901  
 Qy 2879 CTCTCCGAAATTTTACTCACAGATCAATTGCAACAGCATGCTTACTTATGTTT 2938  
 Db 2902 CTCTCTTAAATTTATCATTAARCTTATTTCAATTAATACAC-----TTGTTT 2954  
 Qy 2939 GCACTGAACATTTATGGAAGCAACCTTATATGCTGAAAGTACATTTAAAGAT 2998  
 Db 2955 TGGGTTGACATATTTAGGATCTGATCTTTTATATGTTAGATATACAGTTAAAGAT 3014  
 Qy 2999 GACTACTTACG 3010  
 Db 3015 TATCATTTGGG 3026

RESULT 5  
 BC022970  
 LOCUS  
 DEFINITION Mus musculus interphotoreceptor matrix proteoglycan 1, mRNA (cdna  
 ACCESSION BC022970.1 GI:18606432  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Muridae; Mus.  
 REFERENCES  
 1 (bases 1 to 2924)  
 Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L.,  
 Scheetz T.E., Brownstein M.J., Ueding T.B., Toschyluk S.,  
 Carninci P., Prange C., Raha S.S., Iqbalulano N.A., Peters G.J.,  
 Abramson R.D., Mullen S.J., Bosak S.A., McSwan P.J.,  
 McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.,  
 Worley K.C., Hale S., Garcia A.M., Gay L.J., Hollyk S.W.,  
 Villalón J.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,



Db 778 AGGACATTCAAAAGCCCAACAGAAAGTAAAAAGAACTATTCATGTGTCTGAATCT 837  
Qy 884 TGGAGAGAGAGGGGTGAGCTCAGGCTCTCTGGTAAACAGAGATTCAGAGAGAGC 943  
Db 838 CATCAGAGAGAGAGGGATTCAGATCTCTGCAACACAGGTTCAGAGAGAGC 897  
Qy 944 TCGTGAATCTCCCATATTTACAGAGAGCTAGCAGAGAAAGTCCCACTTCAGATGC 1003  
Db 898 TCACCAACTCTGGGTACCACTACTACAGAGAGCTGGTGGACAGTCCCACTGCAGTTGC 957  
Qy 1004 AAAAGATTTTAAAGAACTTCAGAGATTCAGAGAAATTCATGTGTAGATTAAACCA 1063  
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Qy 1124 ACAGTGCAG 1183  
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Qy 1184 AAAGTGAAG 1243  
Db 1138 AAAGTGAAG 1194  
Qy 1244 CAGCTACAG 1303  
Db 1195 CAGCTACAG 1254  
Qy 1304 TGGAG 1363  
Db 1255 AAAGGAAATTCATCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1308  
Qy 1364 CCCAATCAG 1423  
Db 1309 CTGAACACAG 1368  
Qy 1424 AACTCTCTCTGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1482  
Db 1369 AACTCTCTCTGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1428  
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Db 1429 GAATGCTCCAAAG 1488  
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Qy 1649 ATTTCGAG 1708  
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Qy 1709 GCCGATCAG 1768  
Db 1666 GAGAGCTGATCAG 1725  
Qy 1769 ACACTCTGAG 1828  
Db 1726 ACACGAG 1785  
Qy 1829 TCTTGAAG 1888  
Db 1786 TCTTGAAG 1845  
Qy 1889 TTGCCCCAAG 1948  
Db 1846 TTGCCCCAAG 1905

Qy 1949 TCTCCAG 2008  
Db 1906 TCTCTTGAAG 1965  
Qy 2009 CAGAGCTGAG 2068  
Db 1966 CAGAGCTGAG 2025  
Qy 2069 TTAATTTCAAG 2128  
Db 2026 TCAGCTTGAAG 2085  
Qy 2129 GGTATTAACCTCAG 2188  
Db 2086 CCTTACAG 2145  
Qy 2189 AACATCTCATCTGAG 2248  
Db 2146 AAGGCTCATCTGAG 2205  
Qy 2249 ATCCCTGAG 2308  
Db 2206 ATCCCTGAG 2265  
Qy 2309 AGAAG 2368  
Db 2266 AGAAG 2325  
Qy 2369 AACAG 2428  
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Qy 2489 AAAATCAACAAATTAAG 2548  
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Qy 2549 ATGAAG 2595  
Db 2497 TTGAAG 2556  
Qy 2556 -----ATGTCATTAATTAAG 2642  
Db 2557 GTTGAAG 2616  
Qy 2643 TCAAG 2702  
Db 2617 ACTTGAAG 2676  
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Db 2677 TTGAAG 2728  
Qy 2763 AATTGAG 2820  
Db 2729 AAGCTGAG 2788  
Qy 2821 ATATTTTGAAG 2880  
Db 2789 ACA-TTGAAG 2845  
Qy 2881 TCCCTGAAG 2938  
Db 2846 TTCTTAATTAATTAAG 2993

RESULT 6  
AB047843  
LOCUS

AB047843

2850 bp

mRNA

linear

ROD 30-AUG-2000



Db	1279	GTTACTG-----AGCAGCTCTTGAGACTGTGACCCAAATCAGAGCTGCCAAGCCCTT	1332
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Db	1333	ACTGATGTCAAGAGAGATGTCACTTTGAGTCAGAGCTTCTCTTCAAGTAACCTAAGCTT	1392
QY	1450	GAGACAGTGAACGAGGACAGAGCATGGTCTACCTGTGACATTTCTTGAGTCTCCACCTGTATG	1509
Db	1333	GAGAGTGTGACATATATATGTCCGTACTGCTGTGACAGATCTTGATCTGTCTGTATACA	1452
QY	1510	GCCTTACCTCCCTGTGAGAAAGCTCCACTTTCTTTATGAGATCAAGCATCTTCTCTG	1569
Db	1453	GCCTTGACTTCCGAGGTGGGAAATCTACCTTCTCTTTA---GGCCTAGATCTTGCTCTC	1509
QY	1570	ACTGATCAAGGCACCAAGATACATGGCCACTGACAGACATATCTAATACAGGGCTC	1629
Db	1510	GATGATCAAAAGTCCCTCTCCCTGTGATGCGACTGGCCCAAGACATTCATCCCAAGCTC	1569
QY	1630	ACCAATCCCAACAGATATTATTCTGCATATACGCCAACTGGCTCTGGGAAATTTCACATCCA	1689
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QY	1690	CCTGCATCTTGAGATGACG--CCGATCAAGTGCAGGTGGCGAAGATATGTGACAGAC	1746
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QY	1747	CTAGATGAATGGATCTGTCTTGACACTCTCTGCCCATTTGAGTACAGAGCTACGGA	1806
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QY	1807	TATGTTCTGTGCCAGATCATTTCTTGAGAGATACACTCTGTCTGACTTTACAGAT	1866
Db	1750	TATGACTCTGCCCGGATCGGTTTGTGAGATGACACAGCCATCCGACATTCACAGAT	1809
QY	1867	ATCACCACTAGTTCTATGACCATTTGCCCCCAAGGGCCGAGAGCTGTATGTTCTTCACT	1926
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QY	1927	CTGCGTGTGCTACATAGCTTCTTCCACGACCTGTTCACACAGAGCTCTCTGAGTAC	1986
Db	1870	CTGCCGCTGCTTAACATGCCGTTCTCTATGACTTGTCAATATAGAATTTCCCTGGAGTAC	1929
QY	1987	CGAGCTCTGGAGCAACATTTACACAGCTGCTGTTCCATATCTTACGATCCAACTTTACA	2046
Db	1930	CAGGCTTGGAAACAAGATTCACACAGACTGTGTTCATTCACATGCAATCTTACG	1989
QY	2047	GGATTTAAGCAACTTGAATACTTAACTTCAGAAACGGGAGTGTGATTTGTGAATAGCAAA	2106
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QY	2107	ATGAAGTTTGCTAAGTCTGTGCGGTATTAACCTCACAAAGCTGTGTGACAGGGGTCTTGGAG	2166
Db	2050	GTGCGGTTTCGCCAAGGCGTACCTTACAACCTCACAGGCGGTGCGGGGTCTTGGAG	2109
QY	2167	GATTTTCGTTCTGTGCTGACGCCACAACTCCATCTTGAATATGACAGCTACTCTTCAAC	2226
Db	2110	GATCTTGGGTCCACTGACAGCTTCMAAGCTCAACTCGGAATATCGAAAGTTACTCTCTTGAT	2169
QY	2227	ATTGAACAGCTGATCAAGACAGATCCCTGCAAGTTCTGCGCTGCGGGAATTTGCCCA	2286
Db	2170	ATCGAACAGAGTATCAAGGAGATCTCTGTCCAAATTTCTTACATGTGTGGCAATTTGCCCAAG	2229
QY	2287	TGTGTAAAGAACGAACGGACTTGAGAGACGAGGTGCTGCTGCAACCAAGATATGACAGC	2346
Db	2230	TGTATTAAGAAATGAGATTGACAGAGGAAGAGGTGTCTGCTGACACAGGACATGAGAGC	2289
QY	2347	CAGGGGAGCTTGAACGGTCTGGAACCAAGGCTCTGTGGCCTTGGGCAAAAGATGCGAG	2406
Db	2290	CACGGGAGCTCTGGAAATCCAGGAACTGAAACCTGTCTCTCTGG---AAAAGCTTGTGAA	2346
QY	2407	GTCTCCAGGGGAAAGGAGCTCAATGCAAGTGTGACAGATCACTGGAATATCAGCAATAC	2466
Db	2347	GCCAGTCAAGACAGCAACCCCAATGCAAGGCCACAGAGTCACTTCAAAACCAAGCTCGG	2406

QY	2467	AAACTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2567	AAACTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2567	AAACTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2567	AAACTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2567	AAACTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2567	AAACTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2567	AAACTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT
DB	2407	CACCTAGTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2463	CACCTAGTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2463	CACCTAGTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2463	CACCTAGTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2463	CACCTAGTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2463	CACCTAGTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT	2463	CACCTAGTGTGTTAAAAAGTTCCAAATCAACAAATAAACAAGTAATCAGTAAGAAAT
QY	2527	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2586	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2586	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2586	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2586	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2586	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2586	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA
DB	2464	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2523	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2523	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2523	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2523	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2523	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA	2523	TCTGAATTTACTGACCGGTAGATATGATGAATTTTAACATCAAGATTGGAGAGAAATTTAA
QY	2587	AAACTGAAATGTA 2600		AAACTGAAATGTA 2600		AAACTGAAATGTA 2600		AAACTGAAATGTA 2600		AAACTGAAATGTA 2600		AAACTGAAATGTA 2600		AAACTGAAATGTA 2600
DB	2524	AGGCTGGAATCAT 2537		AGGCTGGAATCAT 2537		AGGCTGGAATCAT 2537		AGGCTGGAATCAT 2537		AGGCTGGAATCAT 2537		AGGCTGGAATCAT 2537		AGGCTGGAATCAT 2537
RESULT 7	AF229929	3675 bp	mRNA	linear	ROD 15-NOV-2000									
LOCUS	AF229929													
DEFINITION	Mus musculus staloaloprotein associated with cones and rods SPACR													
ACCESSION	AF229929													
VERSION	AF229929.1	GI:11177167												
KEYWORDS														
SOURCE	Mus musculus (house mouse)													
ORGANISM	Mus musculus													
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.													
AUTHORS	1 (bases 1 to 3675)													
TITLE	Lee, J.W., Chen, O., Rayborn, M.E., Shadrach, K.G., Crabbe, J.W., Rodriguez, I.R., and Hollyfield, J.G.													
JOURNAL	SPACR in the interphotoreceptor matrix of the mouse retina: molecular and biochemical characterization													
AUTHORS	Unpublished													
REFERENCE	2 (bases 1 to 3675)													
AUTHORS	Rodriguez, I.R., Lee, J.W., and Hollyfield, J.G.													
TITLE	Direct Submission													
JOURNAL	Submitted (31-JUN-2000) INCBM, NEI-NIH, 6 Center Drive MSC2740													
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	/codon_start=1													
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ORIGIN														
Query Match	37.7%	Score 1255.2;	DB 9;	Length 3675;										
Best local Similarity	69.0%;	Pred. No. 2.1e-274;												
Matches 2007;	Conservative 2;	Mismatches 746;	Indels 155;	Gaps 15;										
QY	154	TATTTTGTGTTTTCGAGTTTTCCTCCAAAGTTCAGAAACCAAGATATCTCCATTACAT	213	TATTTTGTGTTTTCGAGTTTTCCTCCAAAGTTCAGAAACCAAGATATCTCCATTACAT	213	TATTTTGTGTTTTCGAGTTTTCCTCCAAAGTTCAGAAACCAAGATATCTCCATTACAT	213	TATTTTGTGTTTTCGAGTTTTCCTCCAAAGTTCAGAAACCAAGATATCTCCATTACAT	213	TATTTTGTGTTTTCGAGTTTTCCTCCAAAGTTCAGAAACCAAGATATCTCCATTACAT	213	TATTTTGTGTTTTCGAGTTTTCCTCCAAAGTTCAGAAACCAAGATATCTCCATTACAT	213	TATTTTGTGTTTTCGAGTTTTCCTCCAAAGTTCAGAAACCAAGATATCTCCATTACAT

## ORIGIN

Query Match	37.78;	Score 1255.2;	DB 9;	Length 3675;
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Matches 2007; Conservative 2; Mismatches 746; Indels 155; Gaps 15;

154 TATTTTGTGATTTTCTCCAAGTCAAGGACCAAGATATCTCCATTACAT 213

Db 84 TGTCTGATTTTTCAGAAATTACGATATACAGAACGAAATGAATTTTCAATTTAAAC 143  
 QY 214 ATACATCTGAAACTTAAAGACATAGACATCCCCAGAAATGAACAATGAAAGTAC 273  
 Db 144 ATGCTATCTTTGTTTGGGATTTTCTCCAGTTTCAGAGATCAACAATGAAAGTAC 203  
 QY 274 TGAATAAATGTCAAAATGTCAACTATGAGAGAAATATTGATTTGGGCAAGCATCGAAC 333  
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 QY 334 AAAAAATCCGCAATTTTCCCAACGAGGTTTAAAGTGTCTCCACAGAGATCCATGAACA 393  
 Db 264 CAAAAGATCAGCACTTTTCCCA--GCTGCTAAACATGTGTCCCGAGAACTCTTAGACA 320  
 QY 394 GATTTTAAACAGTCTTCAAGCTTATTATATGATTGAGGTGTCAAGAAACGATATGGA 453  
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 QY 514 CATCTGCAGACAGAGACCTTCTGCTCTTTGACATTTGAAAAAATTCAAGCAATTTCCA 573  
 Db 441 CCTCTGCCAGAAAGAACTTCTGCTCTTTGACATTTGGGAAAACTTCAGCACTCCCA 500  
 QY 574 GAGGACCTGGATCTTCTCAGCAGAGAAATTAACAGAGAGTTTCTCTGACAGAAAA 633  
 Db 501 GAGAGACCTAGATCTTCTCAGCAGAGAAATTAACAGAGAGTTTCTCTGAGAGAAAA 560  
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 QY 694 AATCTACATTTCAAAAGACTTGGGCAGTATTTCTAAGAAAACTCTCAGAAAGCAATTCAA 753  
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RESULT 8
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the 3' end of the IMPG1 gene for Interphotoreceptor matrix
proteinolytan 1, complete sequence.
ACCESSION AL392166
VERSION AL392166.19 GI:13396652
KEYWORDS HTG; IMPG1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 90766)
AUTHORS Clark,S.
TITLE Direct Submision
JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Mar 20, 2001 this sequence version replaced gi:13224983.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi, EMBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information

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## FEATURES

## source

on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping  
 Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr6>  
 RP11-758J17 is from the library RP11-11.3 constructed by the group  
 of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [vegas@sanger.ac.uk](mailto:vegas@sanger.ac.uk)  
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This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one subclone; and the assembly was confirmed by restriction digest,  
 except on the rare occasion of the clone being a YAC.

## Location/Qualifiers

## misc\_feature

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## mRNA

## polyA\_site

## polyA\_signal

## gene



AUTHORS  
TITLE  
JOURNAL  
COMMENT

McLay, K.  
Direct Submission  
Submitted (09-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
Requests: clonerequest@sanger.ac.uk  
On Jan 14, 2001 this sequence version replaced gi:12214326.

----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: BA505B21  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 11761 bases at least Q40  
Consensus quality: 12343 bases at least Q30  
Consensus quality: 126505 bases at least Q20  
Insert size: 12645; sum-of-coverage  
Insert size: 166195; 8.3% error; agarose-  
Quality coverage: 3.05x in Q20 bases; sum-of-coverage  
Quality coverage: 2.65x in Q20 bases; agarose-  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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FEATURES  
source

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Matches 835; Conservative	0;	Mismatches 19;	Indels 0;	Gaps 0;

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DEFINITION	Homo sapiens interphotoreceptor matrix gene (IPM150), exon 17 and complete cds.
ACCESSION	AF017776
VERSION	AF017776.1 GI:3800731
KEYWORDS	.
SEGMENT	17 of 17
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	1 (bases 1 to 1235)		
Felbro, U., Gehrig, A., Sauer, C.G., Margardt, A., Kohler, M., Schmid, M., and Weber, B.H.		Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for eg-linked retinopathies	Cytogenet. Cell Genet. 81 (1), 12-17 (1998)

PUBMED REFERENCE AUTHORS	9691169 2 (bases 1 to 1235) Gehrigh,A., Felsbor,U., Kelsell,R., Hunt,D.M., Maumenee-Husels,I.B. and Weber,B.H.F.
TITLE	Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)
JOURNAL REFERENCE AUTHORS	Unpublished 3 (bases 1 to 1235) Felsbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
TITLE	Direct Submission
JOURNAL	Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Hblland, Wuerzburg D-97074, Germany

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RESULT 12  
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 ACCESSION AL157379  
 VERSION AL157379.14 GI:15590763  
 KEYWORDS HTG; HTGS PHASE2; HTGS\_CANCELLED.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1  
 Wall, M.  
 Direct Submission  
 Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 Requester: clonequest@sanger.ac.uk  
 On Sep 12, 2001 this sequence version replaced gi:11991356.  
 ----- Genome Center  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: duf2L18  
 ----- Summary Statistics  
 Sequencing program: XGAP4, version 4.5  
 Sequencing vector: plasmid; 108752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 160382 bases at least Q40  
 Consensus quality: 160493 bases at least Q30  
 Consensus quality: 160578 bases at least Q20  
 Insert size: 160719; sum-of-contigs  
 Insert size: 158939; 9.3% error; agarose-fp  
 Quality coverage: 8.32x in Q20 bases; sum-of-contigs Quality  
 coverage: 8.41x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 Location/Qualifiers

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Query Match 16.1%; Score 535.8; DB 14; Length 160719;  
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 Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 7344 GCCGAGAGCTGTAGTGTCTTCTCAGTCTGCGTGTGCTAACATGAGCTTTCTCCAGACC 7285  
 Qy 1961 TGTTCACAGAGCTCTCTGAGTACCGAGCTCTGAGAGCAATTCACACAGCTGTG 2019  
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RESULT 13  
 AB070714  
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 DEFINITION Gallus gallus mRNA for SPACR, complete cds.  
 ACCESSION AB070714  
 VERSION AB070714.1 GI:21623676  
 KEYWORDS  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
AUTHORS  
REFERENCE  
TITLE  
JOURNAL  
FEATURES  
source

1  
Zako, M., Iwaki, M., Yoneda, M., Miyajishi, O., Zhao, J., Suzuki, Y.,  
Takeuchi, M., Miyake, G., Ikegawa, H., and Kimura, K.,  
Molecular Cloning and Characterization of Chick Staloprotein  
Associated with Cones and Rods, a Developmentally Regulated  
Glycoprotein of Interphotoreceptor Matrix  
J. Biol. Chem. 277 (28), 25592-25600 (2002)  
11991949  
2 (bases 1 to 4953)  
Zako, M. and Iwaki, M.  
Direct Submission  
Submitted (28-AUG-2001) Maaehiro Zako, Aichi Medical University,  
Department of Ophthalmology, Nagakute-cho, Aichi-gun, Aichi  
480-1195, Japan (E-mail: zako@aiichi-med-u.ac.jp.  
Tel:81-52-264-4811(ex.2181), Fax:81-561-63-7255)  
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ORIGIN

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QY 99 GTTATCAGATTACCAATGACAAAAAGCAGATGATTGAAAATAGAGATATT 158  
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DB 254 TGGCCATTTGGCTTGCTCTCAAGTTCAAGAAACGAGAAATCCCAATTAACAAATC 313  
QY 219 ATTCTGAACCTAAAGCATGACATCCCCCAAGAAATGAAAACAATGAAAGTACTGAAA 278  
DB 314 ATGGTGAACCAACAACTTGACATGCTCCTCAGGGGTCAAGAAAACAGAAACAAACA 373

QY 279 AATGTACAAAATGTCACTATGAGAGAAATATTGATTTGGCAAGCATGAAACAAA 338  
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DB 434 GATCACCTTTTTCCTATCTGTGTGAAAAATTTGGCCCAAGAAATCACTGAAAGCAGATT 493  
QY 399 TAGACATCTTCAAGCTTATATATGATTGAGAGTGTGACAGAAACAGTATGGAAAGAT 458  
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QY 459 ATCCGATTTCTGTGATGTGATCCCTGACACAGGAGAAATATCAGAGCTGGGTGACATCT 518  
DB 554 TTCTGATTTTCTGTGATGTGATCCCGATACCTCTGAAATATCAAGATCGGTACTGCT 613  
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QY 699 ACATTTCAAGACCTTGGCAGTATTTCAAGAAAAACCTCAGAAAGCAAAATTCAGATGT 758  
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DB 969 TGAACCTTAGTATCCAACTCCCAACATATCGAATTAAGCTGCAAAATTCACATGCA 1028  
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QY 1353 TGGCTCGACCCCAATCAGAGCTGGCCCACTTTTGTGTTATACAGAGATGCTAC 1412  
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 QY 1413 TTTGAGTCGAACTTCTCTCTGTTGAACCCGAGCTTGAGACAGTGAGCGAGC 1466  
 DB 1449 CATTAAGCGGAACTCCCACTGGTTTATCCAGCCCAATACAGTGAGCAAC 1502

RESULT 14  
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 LOCUS Macaca fascicularis interphotoreceptor matrix proteoglycan 150  
 DEFINITION mRNA, partial cds.  
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 VERSION AF047491.1 GI:2906229  
 KEYWORDS Macaca fascicularis (crab-eating macaque)  
 SOURCE Macaca fascicularis  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
 REFERENCE 1 (bases 1 to 555)  
 Kuehn, M.H. and Hageman, G.S.  
 Characterization And Complete cDNA Sequence Of IPM 150, A Novel Human Photoreceptor Cell-Associated Chondroitin-Sulfate Proteoglycan  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 555)  
 Kuehn, M.H. and Hageman, G.S.  
 Direct Submission  
 JOURNAL Submitted (10-FEB-1998) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 1190E PP, Iowa City, IA 52240, USA

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 DB 4 TTTCTTCCGAAAGGGGTTAAAGTCTGTCCACAGAAATCCAGATTTTACAGACT 63  
 QY 407 CTTCAAGCTTATTATAGATTGAGTGTCTCGAAGAGCATGTGGGAAGCATTTGGGATC 466  
 DB 64 CTTCAAGCTTATTATAGATTGAGTGTCTCGAAGAGCATGTGGGAAGCATTTGGGATC 123  
 QY 467 TTTCTGATCGATCCCTGACACAGGGGAATATCAGACTGGGTGAGCATCTGCAGAG 526  
 DB 124 TTTCTGATCGATCCCTGACACAGGGGAATATCAGACTGGGTGAGCATCTGCAGAG 183  
 QY 527 GAGACCTTGTGCTCTTTGACATTGAAAAAATTCAGCAATTTCCAGAGACCTGGAT 586  
 DB 184 GAGACCTTGTGCTCTTTGACATTGAAAAAATTCAGCAATTTCCAGAGACCTGGAT 243  
 QY 587 CTTCTCGACGACGATTAACAGAGAAATTTCCCTGACAGAAAGATGAAATATCTGCA 646

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 QY 707 AAGACTTGGGACGATTTCTTAAGAAAAACCTCAAGAGACCAATTTCAAGTGTGGCAAG 766  
 DB 348 -----AGATGTGGCCAGG 361  
 QY 767 TCTCACTTGGGCTTTCCCTCTCACTCTCGATGACACCCCTCTCAATGAAATTTGATGATA 826  
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 QY 887 AGGACGAGAGGTGAGCTCAGCTCTCTGTGTTAAACCAAGTTCAAGGACGAGCTCG 946  
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 QY 947 CTGACTCCGAGTC 959  
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 DEFINITION unordered pieces.  
 AC161554  
 AC161554.2 GI:68303115  
 VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 259413)  
 REFERENCE 1  
 Murny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Angilano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, P., Bawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Cerner, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Ande, C., Dederich, D., Delgado, O., Denison, S., Dexamio, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, T., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Geghegoris, B., Geer, K., Gill, R., Gentry, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huix, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheya, L., Louisseged, H., Lorado, R.J., Lu, X., Ma, J., Maneshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, B., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

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 Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,  
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 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von  
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 Weinstein, G. and Gibbs, R.A.  
 Unpublished  
 Direct Submission  
 2 (bases 1 to 259413)  
 Morley, K.C.  
 Direct Submission  
 Submitted (17-MAY-2005) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 259413)  
 Cow Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (01-JUN-2005) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jun 29, 2005 this sequence version replaced gi:65811890.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Project name: PCOV  
 Center clone name: CH240-104J3  
 ----- Summary Statistics  
 Assembly program: Atlas 3.0  
 Consensus quality: 237131 bases at least Q40  
 Consensus quality: 240855 bases at least Q30  
 Consensus quality: 244386 bases at least Q20  
 Estimated insert size: 249035; sum-of-contigs estimation  
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 47 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 3634: contig of 3634 bp in length  
 3635 3767: gap of 133 bp



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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2006, 16:49:15 ; Search time 532 Seconds

(without alignments)  
5066.034 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taacacgaagaggtatcctc.....tactatgatcattatcaat 3330

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:\*  
1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq4:\*  
10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119.4	3.6	1219	6 US-10-750-185-30474	Sequence 30474, A
2	119.4	3.6	1219	6 US-10-750-623-30474	Sequence 30474, A
3	84.8	2.5	554	6 US-10-750-185-30481	Sequence 30481, A
4	84.8	2.5	554	6 US-10-750-623-30481	Sequence 30481, A
5	46.6	1.4	1288	6 US-10-750-185-46240	Sequence 46240, A
6	46.6	1.4	1288	6 US-10-750-623-46240	Sequence 46240, A
7	44.8	1.3	5562	6 US-10-240-708-63	Sequence 63, Appl
8	43.2	1.3	8607	6 US-10-240-708-72	Sequence 72, Appl
9	42.8	1.3	105550	6 US-10-995-561-13235	Sequence 13235, A
10	41.6	1.2	1902	6 US-10-750-185-29751	Sequence 29751, A
11	41.6	1.2	1902	6 US-10-750-623-29751	Sequence 29751, A
12	41.6	1.2	7304	6 US-10-240-708-43	Sequence 43, Appl
13	41.2	1.2	10467	6 US-10-240-708-2	Sequence 2, Appl
14	41.2	1.2	53641	6 US-10-995-561-13238	Sequence 13238, A
15	41.2	1.2	1125000	6 US-10-995-561-13286	Sequence 13286, A
16	40.6	1.2	316	7 US-11-000-688-348	Sequence 348, App
17	40.6	1.2	1045	6 US-10-750-185-49935	Sequence 49935, A
18	40.6	1.2	1045	6 US-10-750-623-49935	Sequence 49935, A
19	40	1.2	6306	6 US-10-240-708-50	Sequence 50, Appl
20	39.6	1.2	600	7 US-11-136-527-4832	Sequence 4832, Ap
21	39.6	1.2	2475	7 US-11-136-527-736	Sequence 736, App
22	39.6	1.2	6113	6 US-10-240-708-14	Sequence 14, Appl
23	39.6	1.2	19513	6 US-10-240-708-39	Sequence 39, Appl

C 24	39.6	1.2	645179	6 US-10-995-561-13293	Sequence 13293, A
C 25	39.2	1.2	135019	6 US-10-849-438-11	Sequence 11, Appl
C 26	39	1.2	2419	6 US-10-750-185-49215	Sequence 49215, A
C 27	39	1.2	2419	6 US-10-750-623-49215	Sequence 49215, A
C 28	39	1.2	100000	7 US-11-124-368A-2883	Sequence 2883, Ap
C 29	39	1.2	148935	6 US-10-995-561-13308	Sequence 13308, A
C 30	39	1.2	285300	6 US-10-857-780-6	Sequence 6, Appl
C 31	38.8	1.2	5152	6 US-10-240-708-74	Sequence 74, Appl
C 32	38.8	1.2	8537	6 US-10-240-708-41	Sequence 41, Appl
C 33	38.6	1.2	5360	6 US-10-240-708-65	Sequence 65, Appl
C 34	38.4	1.2	134499	7 US-11-117-187-192	Sequence 192, App
C 35	38.2	1.1	57073	6 US-10-995-561-13275	Sequence 13275, A
C 36	37.8	1.1	1240	6 US-10-750-185-60335	Sequence 60335, A
C 37	37.8	1.1	1240	6 US-10-750-623-60335	Sequence 60335, A
C 38	37.8	1.1	1483	6 US-10-750-185-39052	Sequence 39052, A
C 39	37.8	1.1	1483	6 US-10-750-623-39052	Sequence 39052, A
C 40	37.8	1.1	4128	6 US-10-995-561-253	Sequence 253, App
C 41	37.8	1.1	95832	6 US-10-995-561-13273	Sequence 13273, A
C 42	37.6	1.1	600	6 US-10-750-185-809	Sequence 809, App
C 43	37.6	1.1	600	6 US-10-750-623-809	Sequence 809, App
C 44	37.6	1.1	1741	6 US-10-750-185-26423	Sequence 26423, A
C 45	37.6	1.1	1741	6 US-10-750-623-26423	Sequence 26423, A

## ALIGNMENTS

```

RESULT 1
US-10-750-185-30474
; Sequence 30474, Application US/10750185
; Publication No. US20050260603M1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30474
; LENGTH: 1219
; TYPE: DNA
; ORGANISM: Bovine 19866880607526
US-10-750-185-30474

Query Match          3.6%; Score 119.4; DB 6; Length 1219;
Best Local Similarity 89.0%; Pred. No. 5.2e-23;
Matches 129; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 430 AGTGTGAGAGAGAGATGGAAGCATTCGATCTTTGATCCGATCCGACAC 489
DB 1075 AGTGTGAGAGAGAGAGATGGAAGCATTCGATCTTTGATCCGATCCGACAC 1134
OY 490 AGGGAATATATGAGACTGGTTCAGCATTCGACAGAGACCTTTCCTTTGACAT 549
DB 1135 GGGGGAATATATGAGACTGGTTCAGCATTCGACAGAGACCTTTCCTTTGACAT 1194
OY 550 TGGAAAAAATTCAGCAATTCGACAG 574
DB 1195 CGGAAAAAATTCAGCAATTCGACAG 1219

RESULT 2
US-10-750-623-30474
; Sequence 30474, Application US/10750623

```

Oy 888 GGAGCAGAGGCTGAACCTCAACGGTTCCTGTAAACCGAAGTTCAAGGCAGACTCCG 947

Dd 369 GGAGCAGAAAGTAGAGCTTAAGTATCTCTCTGCGAACCAACGAAAGTTCAAAGTCAGAGCTTGG 310

Query Match	1.4%;	Score 46.6;	DB 6;	Length 1288;
Best Local Similarity	59.4%;	Pred. No. 0.016;		

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Query Match      1.4%; Score 46.6; DB 6; Length 1289;
Best Local Similarity 59.4%; Pred. No. 0.016;
Matches 79; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY      2235 AGCTGATCAGACAGATCCCTCGAAGTTCCTGCCTCGCGGCAATTGTGCCAATGTGTA   2294
          |||
Db       275 AGGGATTCACACCACCTTGCAAGTTTCAAGCATGTGCATTAATTTTCTGAGTGTGTTG   216

QY      2295 GAATGAACGCACTAGAGAAAGCGAGATGTCGCTGTCAAAACAGATATATGACAGCCAGGGAG   2354
          |||
Db       215 CAATTCCTCGAGTGGAGAGGCGAGATGTGACATGTCTACTCCTGGGTAACCTGATGTGTGAAGA   156

QY      2355 CCTGAGCGGTCTG   2367
          |||
Db       155 TCTGCCCTGTGAG   143

RESULT 7
US-10-240-708-63/c
: Sequence 63, Application US/10240708
: Publication NO. US20050282157A1
: GENERAL INFORMATION:
: APPLICANT: OLEK, Alexander
: APPLICANT: PIPENBROCK, Christian
: APPLICANT: BERLIN, Kurt
: TITLE OF INVENTION: Diagnosis of diseases Associated with DNA Replication
: FILE REFERENCE: 5013_1012
: CURRENT APPLICATION NUMBER: US/10/240,708
: PRIOR APPLICATION NUMBER: PCT/EP01/03971
: PRIOR FILING DATE: 2001-04-06

```

Query Match	1.3%;	Score 44.8;	DB 6;	Length 5562;
Best Local Similarity	44.9%;	Pred. No. 0.14;		
Matches 210;	Conservative 0;	Mismatches 257;	Indels 1;	Gaps 1;
QY	2394	AAAGAAATGCGAGTCTCCAGGGAAGGAGCTCCATGCAAGTGGCCAGATCATCTCTGA	2453	
Db	1956	AAATATTTACGACGACGCAAAAACAAATATCCATTAACCAATATTAACCTTACACATATACA	1897	
QY	2454	AAATCAAGCATACAAAACCTAGTGTATTAAGTTCCAAATATCAACAAATATTAACAGTAAAT	2513	
Db	1896	AAAACACATATATATCTCTTATGCAAAAACCTACTTCAATATTAATAAATATTAACCTTAAA	1837	
QY	2514	CAGTAAAGAAATTCGAAATTAAGTCCGATGAGATATGAAGAAATTTAACATCAAGATTG	2573	
Db	1836	CCTATATATAAAATTAATATATACCTTCAAAATATTAATAAATCAATCATATTAATAAATAAT	1777	
QY	2574	GGAAGAAATTAATAAACTGAAAAATGTACATTAATCACTTAGGCTATTCAGAGAGATGA	2633	
Db	1776	CATCATATATTCCTCAAAACGAAAAAGTAAAAAAATCAATATTAATAAACAATAAAAAA	1717	
QY	2634	TTTGCTCTTCAAGAAATGAGAGACAGCATTAATTCATGGGTGATCCAAATCCAGA-CAT	2692	
Db	1716	AAACCATCATTAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1657	
QY	2693	ACAGTCAACCTGGAATCGACACACCCATATTTCAAATATATGAGAGATCATGTAATTG	2752	
Db	1656	AAATTTCTAAAAATTAACATCATCTCTAAAAAATAAATAAATAAATAAATAAATAA	1597	
QY	2753	GCAACGAGTAATTTCTGAATAAATAAAGACACTTACTTATTAATAAACCCCAATATGCATC	2812	
Db	1596	TAAATCTTCTTAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1537	
QY	2813	AGCGAAACATATTTTATATATCTTCTTGATGATAGTCAAAATGATCATTA	2860	
Db	1536	AAAAAAAAAAAAATCTAATAACAAAAAATAAATAAATAAATAAATAAATAA	1489	
RESULT 8				
US-10-240-708-72/c				
Sequence 72, Application US/10240708				
Publication No. US20050282157A1				
GENERAL INFORMATION:				
APPLICANT: OLEK, Alexander				
APPLICANT: PIERENBROCK, Christian				
APPLICANT: BERLIN, Kurt				
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication				
TITLE OF INVENTION: by Assessing DNA Methylation				
FILE REFERENCE: 5013.1012				
CURRENT APPLICATION NUMBER: US/10/240, 708				
CURRENT FILING DATE: 2002-10-03				
PRIOR APPLICATION NUMBER: PCT/EP01/03971				
PRIOR FILING DATE: 2001-04-06				
PRIOR APPLICATION NUMBER: DE 10019058.8				
PRIOR FILING DATE: 2000-04-06				
PRIOR APPLICATION NUMBER: DE 10019173.8				
PRIOR FILING DATE: 2000-04-07				



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/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 72
/ LENGTH: 8607
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-72
```

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Query Match      1.3%; Score 43.2; DB 6; Length 8607;
Best Local Similarity 50.4%; Pred. No. 0.54;
Matches 131; Conservative 0; Mismatches 128; Indels 1; Gaps 1;
```

```
QY 2454 AATTCAGATCAAAAAGTGTAAAGTTCCAAAATCAACAATAACAGATAT 2513
DB 7055 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6996
QY 2514 CAGTAAAGAAATTCGATTAAGTCCGATAGATATGAGATTTAACCATCAAGATTG 2573
DB 6996 AAAAAAAAAAAAAAAAAAAAAAAAAACATATCAAAATTAACATTAACATTAACATTA 6936
QY 2574 GGAAGAAATTAACATGAATAATGATCAATTA-TCAGTTAGGCTATCTCAAGAGATG 2632
DB 6936 CAATTTCTCTCACTATACATAATCTCCATTAATCTCTTACCAATCTTATTAATAAATA 6876
QY 2632 ATTGCTCTCTCAAGAAATGAGACAGCATATTCAGGTCTATCAAAATCCAGACAT 2692
DB 6875 TTTTAACTAAACCGATTAATCACTATTAATCCACAGCTTAAATAAATCTAAAT 6816
QY 2692 ACAGTCAACACGAGAAATCA 2712
DB 6815 AACGATCACTAAATCA 6796
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RESULT 9  
US-10-995-561-13235

```
/ Sequence 13235, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13235
/ LENGTH: 105550
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-13235
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Query Match      1.3%; Score 42.8; DB 6; Length 105550;
Best Local Similarity 45.1%; Pred. No. 4;
Matches 155; Conservative 1; Mismatches 188; Indels 0; Gaps 0;
```

```
QY 14 TTATCCATCATCTGATATCATATATATTTTTCACATTTCTGTACTTTTAA 73
DB 48951 WTATATTTAAATATATATATATATATATATATATATATATATATATATAT 49010
QY 74 TGAGATTTGAGGTGTTCTGTGATTTGTTATCAAGATTTACCAATGCAAGACCAAGATG 133
DB 49011 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 49070
QY 134 TATTTGGAAGACTGAGAGACTATTTTGTGTTTGTGATTTTCTCCAGATTCAGGAC 193
DB 49071 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 49130
```

```
QY 194 AAGATATCTCCATTAACATATACCATTTGAAAATAAGACATGACATCCCCCAGA 253
DB 49131 AATTTATATTTATATATATATATATATATATATATATATATATATATATATAT 49190
QY 254 AATGAAACACTGAAAGTACTGAAAAATGTACAAATATGTCACATGAGACGAAATATTC 313
DB 49191 AAAATCAAGATATACAGATATATATATATATATATATATATATATATATATATAT 49250
QY 314 GATTTGGAAAGCATCGAAGAAAAATCCGATTTTCCCAAC 357
DB 49251 TATATATGTTAGTAAATATATATATATATATATATATATATATATATATATAT 49294
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RESULT 10  
US-10-750-185-29751

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/ Sequence 29751, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENNIS, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 29751
/ LENGTH: 1902
/ TYPE: DNA
/ ORGANISM: Bovine
US-10-750-185-29751
```

```
Query Match      1.2%; Score 41.6; DB 6; Length 1902;
Best Local Similarity 49.5%; Pred. No. 0.54;
Matches 107; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
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```
QY 2517 TAAAGAAATCTGATTAAGTACCGGTAGATATGAGAAATTTAACATCAAGATGGGA 2576
DB 459 TAAAGAAATCTGATTAAGTACCGGTAGATATGAAATATATATATATATATATATAT 518
QY 2577 AGGAATTTAAAGTGAATGTATCAATATCACTTAGGCTATCTCAAGAGATGATTT 2636
DB 519 ATGTCATCATCAAGAGAAATGTAAAGTTCTGTTTGTGTTTTCACACAAACATTT 578
QY 2637 GCCTTCTCAAGAAATGGAAGACAGCATATTCATGGTCAATCAAAATCCAGACATACG 2696
DB 579 GAAATTCGAAAGAAATGAGGTAGGCTTCTTACTTAAAGCTTAAAGAAAGTCTAGGACAT 638
QY 2697 TCAACACTGAGATCAGACACACCATATTTCAAT 2732
DB 639 CTGGTCTGGGCAATTCGTAGAGGTTCAATGTTCAAT 674
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RESULT 11

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US-10-750-623-29751
/ Sequence 29751, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENNIS, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
```

; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
 ; FILE REFERENCE: MM1100-1  
 ; CURRENT APPLICATION NUMBER: US/10/750,623  
 ; CURRENT FILING DATE: 2003-12-31  
 ; PRIOR APPLICATION NUMBER: US 60/437,482  
 ; PRIOR FILING DATE: 2002-12-31  
 ; NUMBER OF SEQ ID NOS: 64922  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 29751  
 ; LENGTH: 1902  
 ; TYPE: DNA  
 ; ORGANISM: Bovine  
 ; US-10-750-623-29751

Query Match 1.2%; Score 41.6; DB 6; Length 1902;  
 Best Local Similarity 49.5%; Pred. No. 0.54;  
 Matches 107; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 2517 TAAAGAAATTCGATTACTGACCGTAGAATAGAAATTTAACCATCAAGATTGGGA 2576  
 DB 459 TAAAGAAATTCGAAATATCTGATTGCAAAATATGAAATATATTCCAACCAACATGTG 518  
 QY 2577 AGAAATTTAAAGCTGAAATATGACATTTATCACTTAGCGCTATCTCAAGAGATGATTT 2636  
 DB 519 ATGTCAATCACTCAAGAGAAATGTAAGTTTCTGTTTGTGTTTTCACACACAAACATTT 578  
 QY 2637 GCCTTCTCAGAGAAATGAGACAGGCATATTCATGCGTCAATCAAAATTCAGACATPACG 2696  
 DB 579 GAAATTTCAAGAAATAGGCTAGGCTTCTTACTTAATAGCTTAAGAAAGTACTGACCAT 638  
 QY 2697 TCAACACTGAGAAATCAGACACACATATTTCAAT 2732  
 DB 639 CTGGCTGGGCAATCGAGGTTCAATAGTTCAAT 674

RESULT 12  
 US-10-240-708-43/c  
 ; Sequence 43, Application US/10240708  
 ; Publication No. US20050282157A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIPENBROCK, Christian  
 ; APPLICANT: BERLIN, Kurt  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
 ; FILE REFERENCE: 5013.1012  
 ; CURRENT APPLICATION NUMBER: US/10/240,708  
 ; CURRENT FILING DATE: 2002-10-03  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: DE 10019058.8  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: DE 10019173.8  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: DE 10032529.7  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: DE 10043826.1  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SEQ ID NO 43  
 ; LENGTH: 7304  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 ; US-10-240-708-43

Query Match 1.2%; Score 41.6; DB 6; Length 7304;  
 Best Local Similarity 46.4%; Pred. No. 1.4;  
 Matches 170; Conservative 0; Mismatches 194; Indels 2; Gaps 1;  
 QY 2464 TACAAACTAGTGTAAAGTTCCAAATCAACAAATTAACAGATATCATGTAAGA 2523

DB 619 TAAAAAGCTAAACAAAAAATTACTTAAACATTAATAAACAATAATTAACATTAACCGAT 560  
 QY 2524 AATTCTGAATTACTGACCGTAGAATATGAAAGATTTAAACATCAAGATTGGAGAAAT 2583  
 DB 559 ATTATTAACACTTACTCCAAACCTTAACGACAAAAAATACTCAATCAAAAAACAAC 500  
 QY 2584 TAAAAAGCTAAATGTAATTAATGACTTAACTAGCTATCTCAAGAGATGATTGGCTTCT 2643  
 DB 499 AAAACAAAAAATAATTAATTAATAAATAAATACGAAATTAATCTTTATATATTTAT 440  
 QY 2644 CAAGAAAAATGAGACAGGCAATATTCATGCGTATCAAAATCAGACATACAGTCAAC 2703  
 DB 439 TTTCTTAATTAATCAACATTAATCTT-ATTAATTAATTAATTAATTAATTAATTAAC 382  
 QY 2704 TGAAATAGACACACCAATATTTCAAAATATGAAAGTCAATGATCTTGGCAACAGTAA 2763  
 DB 381 TCTAAAACTAAATCACTAAACAAATTAATTAATTAATTAATTAATTAATTAATTAAC 322  
 QY 2764 ATTCGAAAAAAGACACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2823  
 DB 321 ATTAACAAATTAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 262  
 QY 2824 TTTTAA 2829  
 DB 261 TTATTA 256

RESULT 13  
 US-10-240-708-2/c  
 ; Sequence 2, Application US/10240708  
 ; Publication No. US20050282157A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIPENBROCK, Christian  
 ; APPLICANT: BERLIN, Kurt  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
 ; FILE REFERENCE: 5013.1012  
 ; CURRENT APPLICATION NUMBER: US/10/240,708  
 ; CURRENT FILING DATE: 2002-10-03  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: DE 10019058.8  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: DE 10019173.8  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: DE 10032529.7  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: DE 10043826.1  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 98  
 ; SEQ ID NO 2  
 ; LENGTH: 10467  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 ; US-10-240-708-2

Query Match 1.2%; Score 41.2; DB 6; Length 10467;  
 Best Local Similarity 45.4%; Pred. No. 2.3;  
 Matches 186; Conservative 0; Mismatches 223; Indels 1; Gaps 1;  
 QY 2447 ACTCGAAATCAAGCATACAAACTAGTGTAAAGTTCCAAAATCAACAAATTAACA 2506  
 DB 8253 ACTATATTAATTTTAAAAATTAATAAATAATCAATTCAAAAAATAAATAAATAAATA 8194  
 QY 2507 AGGTAAATCAATTAAGAAATTTCTGAATTACTGACCGTAGAATATGAAAGATTTAACATC 2566  
 DB 8193 AAAAAACACGTAAAAAACAATTAATAAATAAATAAATAAATAAATAAATAAATAAATA 8134  
 QY 2567 AAGATTGGAGGAATTAATAAAGTAAATGTAATTAATTAATTAATTAATTAATTAATTA 2626

```

Db      8133 TATTGATTAATCGAATTAATAA-TTATTAATCTCAAAACAAAAAATTAATCAAC 8075
Qy      2627 GAGATGATTTGCTTCTCAAGAAAATGAGACAGGCATATTCATGGTCATCAAAATCC 2686
Db      8074 CAATATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8015
Qy      2687 AGACATACAGTCAACAGTGAATGACACACACATATTTCAAAATATGAAAGTCATG 2746
Db      8014 TAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7955
Qy      2747 TACTGGCAGCAGCAATTAATTTGAAAAAAGACCTTACTTATTTAAACCCCAAT 2806
Db      7954 ATAAATATATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 7895
Qy      2807 GCATTCAGGAAACATATTTTACTTCTTGATGATAGTCAAAATGAT 2856
Db      7894 TTCTCCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 7845

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## RESULT 14

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US-10-995-561-13238
; Sequence 13238, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13238
; LENGTH: 53641
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13238

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Query Match 1.2%; Score 41.2; DB 6; Length 53641;

Best Local Similarity 48.0%; Pred. No. 7; Matches 118; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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Qy      2581 AATTAAAACTGAAAAATGACATTAATCACTTAGGCTATCTCAAGAGATGATTTGCT 2640
Db      14714 AAGCAACAAAGCAAACTAGCAAGTAGGTTAGCTAAATTAATTAATTAATTAATTA 14773
Qy      2641 TCTCAAGAAAATGAGACAGGCATATTCATGGTCATCAAAATCCAGATACAGTCA 2700
Db      14774 TAAAGAAAACAATCAAGACATGAAGGCAAGCTACAAATATGTAATAATTAATTA 14833
Qy      2701 CACTGAGATCAACACACATATTTCAAAATATGAAAGTCATGCTAGTCAACG 2760
Db      14834 ACCCTATTAAGTATGTTGTTCAATTCAAATATATATAGAACTCTTAACCAATAGC 14893
Qy      2761 TAAATTTGAAAAAAGACACTTACTTATTAATAAACCCTAATGATCAGCAAC 2820
Db      14894 AAAAAAAAAAAAAAAAAAACAAGATTTTAAAAACAAGCAAGAACCAATATGAC 14953
Qy      2821 ATATTT 2826
Db      14954 AATTCT 14959

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## RESULT 15

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US-10-995-561-13286/c
; Sequence 13286, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

```

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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13286
; LENGTH: 1125000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1125000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13286

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Query Match 1.2%; Score 41.2; DB 6; Length 1125000;

Best Local Similarity 48.0%; Pred. No. 55; Matches 118; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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Qy      2581 AATTAAAACTGAAAAATGACATTAATCACTTAGGCTATCTCAAGAGATGATTTGCT 2640
Db      66237 AAGCAACAAAGCAAACTAGCAAGTAGGTTAGCTAAATTAATTAATTAATTAATTA 66178
Qy      2641 TCTCAAGAAAATGAGACAGGCATATTCATGGTCATCAAAATCCAGATACAGTCA 2700
Db      66177 TAAAGAAAACAATCAAGACATGAAGGCAAGCTACAAATATGTAATAATTAATTA 66118
Qy      2701 CACTGAGATCAACACACATATTTCAAAATATGAAAGTCATGCTAGTCAACG 2760
Db      66117 ACCCTATTAAGTATGTTGTTCAATTCAAATATATATAGAACTCTTAACCAATAGC 66058
Qy      2761 TAAATTTGAAAAAAGACACTTACTTATTAATAAACCCTAATGATCAGCAAC 2820
Db      66057 AAAAAAAAAAAAAAAAAAACAAGATTTTAAAAACAAGCAAGAACCAATATGAC 65998
Qy      2821 ATATTT 2826
Db      65997 AATTCT 65992

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Search completed: January 14, 2006, 22:47:11  
Job time : 538 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	3330	100.0	3330	5	US-10-007-270-1	Sequence 1, Appl1
2	3124.6	93.8	3261	5	US-10-007-270-27	Sequence 27, Appl1
3	2765.8	83.1	2887	5	US-10-007-270-5	Sequence 3, Appl1
4	2184.2	65.6	2244	5	US-10-007-270-5	Sequence 5, Appl1
5	1375.6	41.3	3668	5	US-10-007-270-8	Sequence 8, Appl1
6	534	16.0	1726	5	US-10-007-270-10	Sequence 10, Appl1
7	491.6	14.8	1321	5	US-10-007-270-12	Sequence 12, Appl1
8	439	13.2	355	5	US-10-007-270-14	Sequence 14, Appl1
9	204.6	6.1	536	5	US-10-027-632-286848	Sequence 14, Appl1
10	204.6	6.1	1858	5	US-10-027-632-286848	Sequence 286848, Appl1
11	204.6	6.1	1585	5	US-10-007-270-7	Sequence 7, Appl1
12	203.4	6.1	4165	8	US-10-073-528-9	Sequence 9, Appl1
13	203.4	6.1	4166	5	US-10-007-270-15	Sequence 15, Appl1
14	197.8	5.9	4204	5	US-10-007-270-23	Sequence 23, Appl1
15	184.8	5.5	2964	5	US-10-007-270-18	Sequence 18, Appl1
16	103.4	3.1	592	9	US-10-972-079-61156	Sequence 61156, Appl1
17	103.4	3.1	599	9	US-10-972-079-61152	Sequence 61152, Appl1
18	103.4	3.1	600	9	US-10-972-079-61153	Sequence 61153, Appl1
19	103.4	3.1	600	9	US-10-972-079-61154	Sequence 61154, Appl1
20	103.4	3.1	600	9	US-10-972-079-61155	Sequence 61155, Appl1
21	79	2.4	429	4	US-09-925-065A-223807	Sequence 223807, Appl1
22	69	1.9	536	4	US-09-925-065A-462444	Sequence 462444, Appl1
23	62.4	1.1	448	9	US-10-972-079-61157	Sequence 61157, Appl1

C	24	61	1.8	113515	6	US-10-311-455-2147	Sequence 2147, Ap
C	25	60	1.8	60	3	US-09-908-975-16399	Sequence 16399, A
C	26	56.4	1.7	434	8	US-10-357-930-58550	Sequence 58550, A
C	27	54.6	1.6	3683	8	US-10-473-126-339	Sequence 339, App
C	28	53.2	1.6	6255	6	US-10-311-455-833	Sequence 933, App
C	29	52.6	1.6	516	3	US-09-960-352-57885	Sequence 5785, A
C	30	52.6	1.6	673	7	US-10-424-599-578785	Sequence 57885, A
C	31	52.6	1.6	6775	7	US-10-433-793-189	Sequence 189, App
C	32	52.2	1.6	5596	7	US-10-257-166-86	Sequence 86, App
C	33	52.2	1.6	11155	6	US-10-311-455-577	Sequence 577, App
C	34	52.2	1.6	15674	6	US-10-311-455-335	Sequence 335, App
C	35	52.2	1.6	15674	6	US-10-240-485-29	Sequence 29, App1
C	36	52.2	1.6	3673778	6	US-10-312-841-2	Sequence 2, App1
C	37	52	1.6	4654	6	US-10-311-455-1196	Sequence 2196, App
C	38	52	1.6	4654	7	US-10-221-714A-508	Sequence 508, App
C	39	51.8	1.6	1243	6	US-10-425-115-17217	Sequence 112717, App
C	40	51.6	1.5	533	8	US-10-311-455-533	Sequence 533, App
C	41	50.6	1.5	2308	8	US-10-602-494-264	Sequence 264, App
C	42	50.4	1.5	457	3	US-09-814-353-18778	Sequence 18778, A
C	43	50.4	1.5	15387	6	US-10-311-455-157	Sequence 157, App
C	44	50.2	1.5	4424	6	US-10-108-846-2925	Sequence 2257, App
C	45	49.8	1.5	6668	6	US-10-311-455-1669	Sequence 1669, App

QY 241 CAATCCCCAGAAATGAAACAACTGAAGTACTGAAAAATGTACAAATGTCAACTAT 300  
DB |||||  
241 CAATCCCCAGAAATGAAACAACTGAAGTACTGAAAAATGTACAAATGTCAACTAT 300  
QY 301 GAGACGAATATTGCAATTTGGCAAAAGCATGAAACAAAAGATCCGATTTTCCCAACGGG 360  
DB |||||  
301 GAGACGAATATTGCAATTTGGCAAAAGCATGAAACAAAAGATCCGATTTTCCCAACGGG 360  
QY 361 GGTAAAGCTGTGCCAAGAAATCCATGAACAGATTTTGAACAGCTTCAAGCTTATTA 420  
DB |||||  
361 GGTAAAGCTGTGCCAAGAAATCCATGAACAGATTTTGAACAGCTTCAAGCTTATTA 420  
QY 421 TAGATTGAGAGTGTGCAGAGAACAGTATGGAAGCATATCCGATCTTCTGATCGCAT 480  
DB |||||  
421 TAGATTGAGAGTGTGCAGAGAACAGTATGGAAGCATATCCGATCTTCTGATCGCAT 480  
QY 481 CCTTGACACAGGGGAATATCAGAGCTGGGTCAAGCATCTGCCAGACAGAGACCTTCTGCT 540  
DB |||||  
481 CCTTGACACAGGGGAATATCAGAGCTGGGTCAAGCATCTGCCAGACAGAGACCTTCTGCT 540  
QY 541 CTTTGACATTGGAAAAAACTTGACGAATCCGAGAGACCTGGAATCTTCTGACAGAG 600  
DB |||||  
541 CTTTGACATTGGAAAAAACTTGACGAATCCGAGAGACCTGGAATCTTCTGACAGAG 600  
QY 601 AATAAAAACAGAAAGTTTCCCTGACAGAAAGATGAATATCTGACAGAGAACATTTGGG 660  
DB |||||  
601 AATAAAAACAGAAAGTTTCCCTGACAGAAAGATGAATATCTGACAGAGAACATTTGGG 660  
QY 661 AAGAGCTGGTGAACCATTTGTCTCAACAGCATCTACATTTCAAGACTTTGGGCGAT 720  
DB |||||  
661 AAGAGCTGGTGAACCATTTGTCTCAACAGCATCTACATTTCAAGACTTTGGGCGAT 720  
QY 721 ATTCTAAGAAAAACCTCAGAAAGCAAAATTCAGAGATGTTGCCAGCTCTCACTTGGGCT 780  
DB |||||  
721 ATTCTAAGAAAAACCTCAGAAAGCAAAATTCAGAGATGTTGCCAGCTCTCACTTGGGCT 780  
QY 781 TTCCCTCTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATTAATCACTACAGAC 840  
DB |||||  
781 TTCCCTCTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATTAATCACTACAGAC 840  
QY 841 ACCAAGATGCTTCAACAGAAAGAGAAACAGAAATTCGCTGTGTGAGAGACAGAGGTTG 900  
DB |||||  
841 ACCAAGATGCTTCAACAGAAAGAGAAACAGAAATTCGCTGTGTGAGAGACAGAGGTTG 900  
QY 901 GAGCTCAGGCTCTCTGTGTAACAGAGTTCAAGGCTGAGCTGCTGCTCCAGTCC 960  
DB |||||  
901 GAGCTCAGGCTCTCTGTGTAACAGAGTTCAAGGCTGAGCTGCTGCTCCAGTCC 960  
QY 961 CCATATTACAGAGAGCTAGCAGAGAAAGTCCAACTTCAGATGCAAAAGATTTTAAGAA 1020  
DB |||||  
961 CCATATTACAGAGAGCTAGCAGAGAAAGTCCAACTTCAGATGCAAAAGATTTTAAGAA 1020  
QY 1021 CTTTCCAGATTTCAAAAAATCCATGTGTTAGATTGAACAAAGAAAGAAAGATGGC 1080  
DB |||||  
1021 CTTTCCAGATTTCAAAAAATCCATGTGTTAGATTGAACAAAGAAAGAAAGATGGC 1080  
QY 1081 TCAAGCTCAGAGAGTGAACCTTAAGGCACTTTAAGAGACACAGTSCAAGAGAA 1140  
DB |||||  
1081 TCAAGCTCAGAGAGTGAACCTTAAGGCACTTTAAGAGACACAGTSCAAGAGAA 1140  
QY 1141 AGCCCTGCAAGTGAACCTCTGTCTTGTGATTCACAAATTTGAAGTGAAGTCTAT 1200  
DB |||||  
1141 AGCCCTGCAAGTGAACCTCTGTCTTGTGATTCACAAATTTGAAGTGAAGTCTAT 1200  
QY 1201 CATGGAACATGAGAGAGACAAAGCAACAGAAATCTATCTCAAGCTCAAGACCTCAA 1260  
DB |||||  
1201 CATGGAACATGAGAGAGACAAAGCAACAGAAATCTATCTCAAGCTCAAGACCTCAA 1260  
QY 1261 AAGGCTGATCAGAGAGACCTAAGAGAGAAACAATCTTTGATGTGGGCAATTCAGTTTC 1320  
DB |||||  
1261 AAGGCTGATCAGAGAGACCTAAGAGAGAAACAATCTTTGATGTGGGCAATTCAGTTTC 1320  
QY 1321 ACTGATGAATTTGCTGATCACTGCGAGCTTGTGCTGACACCAATCAGAGCTGCC 1380

DB |||||  
1321 ACTGATGAATTTGCTGATCACTGCGAGCTTTGCTCTGACACCAATCAGAGCTGCC 1380  
QY 1381 ACATTTTGTCTGTTATTAACAGAGATGCTACTTTGATCCAGAACTTCTCTGTTGA 1440  
DB |||||  
1381 ACATTTTGTCTGTTATTAACAGAGATGCTACTTTGATCCAGAACTTCTCTGTTGA 1440  
QY 1441 CCCGAGCTTGAACAGTGAACGAGACAGAGATGCTTACCTGACACTTCTTGTGCTCA 1500  
DB |||||  
1441 CCCGAGCTTGAACAGTGAACGAGACAGAGATGCTTACCTGACACTTCTTGTGCTCA 1500  
QY 1501 CCTGCTATGAGCTTCACTCTCTGTGAGAGCTCCACTTTCTTTATGACATCAAGATC 1560  
DB |||||  
1501 CCTGCTATGAGCTTCACTCTCTGTGAGAGCTCCACTTTCTTTATGACATCAAGATC 1560  
QY 1561 TTCTCTGATCTGATCAAGGACCCACATATCAATGAGCACTGACACAGAAATGCTAGTA 1620  
DB |||||  
1561 TTCTCTGATCTGATCAAGGACCCACATATCAATGAGCACTGACACAGAAATGCTAGTA 1620  
QY 1621 CAGAGGCTCAGCATCCCAAGAGTATTTCTGCAATCAGGCAACTGAGCTCTGGAAAT 1680  
DB |||||  
1621 CAGAGGCTCAGCATCCCAAGAGTATTTCTGCAATCAGGCAACTGAGCTCTGGAAAT 1680  
QY 1681 TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGAAGTGGGAAATATGATC 1740  
DB |||||  
1681 TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGAAGTGGGAAATATGATC 1740  
QY 1741 AGACACTGATGAATGAATGATCTGTCTGACACTCTGCCCCATCTGAGATACAGAGCTC 1800  
DB |||||  
1741 AGACACTGATGAATGAATGATCTGTCTGACACTCTGCCCCATCTGAGATACAGAGCTC 1800  
QY 1801 AGCGAATATGTTTCTGCTCCAGATCATTTCTTGAAGATCAACACTCTGCTCAGCTTTA 1860  
DB |||||  
1801 AGCGAATATGTTTCTGCTCCAGATCATTTCTTGAAGATCAACACTCTGCTCAGCTTTA 1860  
QY 1861 CAGTATATCACCACTAGTTCTATGACATTTGCCCAAGGGCCGAGAGCTGATGTTTC 1920  
DB |||||  
1861 CAGTATATCACCACTAGTTCTATGACATTTGCCCAAGGGCCGAGAGCTGATGTTTC 1920  
QY 1921 TTCACTGCTGCTGTTGCTTACATGAGCTTCTTCCACAGACTGTTTACAGAGCTCTG 1980  
DB |||||  
1921 TTCACTGCTGCTGTTGCTTACATGAGCTTCTTCCACAGACTGTTTACAGAGCTCTG 1980  
QY 1981 GAGTACGAGCTCTGAGACCAATTCACAGAGCTGAGTTCATATCTAGATCAAT 2040  
DB |||||  
1981 GAGTACGAGCTCTGAGACCAATTCACAGAGCTGAGTTCATATCTAGATCAAT 2040  
QY 2041 CTTACAGATTTTAAGCACTTGAAATTACTTAATCTTCAAGAAACGAGAGTGTGAT 2100  
DB |||||  
2041 CTTACAGATTTTAAGCACTTGAAATTACTTAATCTTCAAGAAACGAGAGTGTGAT 2100  
QY 2101 AGCAAAATGAAGTTGCTTAAAGTCTGTGCTGATTAACCTTCAACAGAGCTGTGACGGGTC 2160  
DB |||||  
2101 AGCAAAATGAAGTTGCTTAAAGTCTGTGCTGATTAACCTTCAACAGAGCTGTGACGGGTC 2160  
QY 2161 TTGAGAGATTTTCTGCTGAGCCCAACATCTCACTGAGAAATGAACGACTACT 2220  
DB |||||  
2161 TTGAGAGATTTTCTGCTGAGCCCAACATCTCACTGAGAAATGAACGACTACT 2220  
QY 2221 CTCAACATTTGAACAGCTGATCAAGCAATCTTCAAGTTCGAGCTGCGGCAATTT 2280  
DB |||||  
2221 CTCAACATTTGAACAGCTGATCAAGCAATCTTCAAGTTCGAGCTGCGGCAATTT 2280  
QY 2281 GCCCAATGTTTGAAGAT 2340  
DB |||||  
2281 GCCCAATGTTTGAAGAT 2340  
QY 2341 GACAGCAGAGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
DB |||||  
2341 GACAGCAGAGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
QY 2401 TGCGAGTCTTCAAGGATCA 2460

	1	CURRENT APPLICATION NUMBER: US/10/007,270	
	1	CURRENT FILING DATE: 2001-11-08	
	1	PRIOR APPLICATION NUMBER: US 09/430,195	
	1	PRIOR FILING DATE: 1999-10-29	
	1	PRIOR APPLICATION NUMBER: US 09/183,972	
	1	PRIOR FILING DATE: 1998-10-29	
	1	NUMBER OF SEQ ID NOS: 37	
	1	SOFTWARE: PatentIn Ver. 2.1	
	1	SEQ ID NO 27	
	1	LENGTH: 3261	
	1	TYPE: DNA	
	1	ORGANISM: Homo sapiens	
	1	FEATURE:	
	1	OTHER INFORMATION: Human IPW 150 Isoform A variant CDNA sequence	
	1	FEATURE:	
	1	NAME/KEY: CDS	
	1	LOCATION: (1128)..(2440)	
	1	US-10-007-270-27	
Query Match	93.8%; Score 3124.6; DB 5; Length 3261;		
Best Local Similarity	97.8%; Pred. No. 0;		
Matches 3256; Conservative	0; Mismatches 5; Indels 69; Gaps 6		
Dn	1	TAAACCAAGAGTTATCTCAATCATCTGATATCATATATTAATTTTTCACATTTC	60
Dn	1	TAAACCAAGAGTTATCTCAATCATCTGATATCAATATATTAATTTTTCACATTTC	58
Dn	61	TGTACTTTTTAAGAGATTGAGTGTTCTGATATGTAATCGAATTCGAATGCAC	120
Dn	59	TGTACTTTTTAAGAGATTGAGTGTTCTGATATGTAATCGAATTCGAATGCAC	117
Dn	121	AAAAGCCAGATGATTTGGAAACTAGAAGACTATTTTGTTTTGGATTTTCTCCA	180
Dn	118	AAAAGCCAGATGATTTGGAAACTAGAAGACTATTTTGTTTTGGATTTTCTCCA	177
Dn	181	AGTTCAAGAACCAAGATATCTCCATTAAATATACATATTCATTCTGAATCTAAAGACATAGA	240
Dn	178	AGTTCAAGAACCTAAAGATATCTCCATTAAATATACATATTCATTCTGAATCTAAAGACATAGA	237
Dn	241	CAATCCCCCAGAAATGAAACAATGAAAGTACTGAAAAATGTAACAAAATGTCACATCT	300
Dn	238	CAATCCCCCAGAAATGAAACAATGAAAGTACTGAAAAATGTAACAAAATGTCACATCT	297
Dn	301	GAGACGAATATTCGATTTGGCAAAGCATCGAACAAAAAGATCCGATTTTCCAAACGGG	360
Dn	298	GAGACGAATATTCGATTTGGCAAAGCATCGAACAAAAAGATCCGATTTTCCAAACGGG	357
Dn	361	GATTAAAGTCTGTCCACAGAAATCATGAAAACAGATTTTGAACAGTCTTCAAGCTTAATTA	420
Dn	358	GATTAAAGTCTGTCCACAGAAATCATGAAAACAGATTTTGAACAGTCTTCAAGCTTAATTA	417
Dn	421	TAGATTGAGATGTGTCAAGAGCATATGAGAACATATGGATCTTTCTGATCGCAT	480
Dn	418	TAGATTGAGATGTGTCAAGAGCATATGAGAACATATGGATCTTTCTGATCGCAT	477
Dn	481	CCCAGACACAGGGGAATATACAGATCGGGGTAGCATCTGCCAGCAGAGACCTTCTGCT	540
Dn	478	CCCAGACACAGGGGAATATACAGATCGGGGTAGCATCTGCCAGCAGAGACCTTCTGCT	537
Dn	541	CTTTGACATTGGAATAAACTTCAGCAATTCACAGAGACCTGATCTTCTCACAGAG	600
Dn	538	CTTTGACATTGGAATAAACTTCAGCAATTCACAGAGACCTGATCTTCTCACAGAG	597
Dn	601	AATTAACACAGAGATTTCTCTGACAGAAAGATGAATATCTGACAGAGACATTTGGG	660
Dn	598	AATTAACACAGAGATTTCTCTGACAGAAAGATGAATATCTGACAGAGACATTTGGG	657
Dn	661	AGAGCCGTGGTAAACCATGTCATTTCAACAGCAATCTACATTTCAAGAATTTGGGCAGT	720
Dn	658	AGAGCCGTGGTAAACCATGTCATTTCAAC-----	687
Dn	721	ATTCTAAGAAAACCCTCAGAGAGCAAAATTCAGATGTTGCCAAGTCTCATTTGGGCT	780

Db 688 -----AGATGTTGCCAAGCTCTCACTTGGGCT 715  
Qy 761 TTCCCTCTCACTCTGATGACACCCCTCCATGAAATTTCTGATTAATCACTCAAGAC 840  
Db 716 TTCCCTCTCACTCTGATGACACCCCTCCATGAAATTTCTGATTAATCACTCAAGAC 775  
Qy 841 ACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTGTTGAGAGACAGAGGTTG 900  
Db 776 ACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTGTTGAGAGAGAGAGGTTG 835  
Qy 901 GAGCTCAGGCTCTCTCTGTGTAACCAAGAAATTGAGAGAGAGCTGCTGATCCAGTCC 960  
Db 836 GAGCTCAGGCTCTCTCTGTGTAACCAAGAAATTGAGAGAGAGCTGCTGATCCAGTCC 895  
Qy 961 CCAATTAACAGAGAGCTGAGAGAAAGTCCCAATTCAGATGCAAAAGATTTTAAGAA 1020  
Db 896 CCAATTAACAGAGAGCTGAGAGAAAGTCCCAATTCAGATGCAAAAGATTTTAAGAA 955  
Qy 1021 CTTCCAGAGATTCAAAAAAATCCATGTGTAGATTGACCAAGAAAGAAAGAAATGAGC 1080  
Db 956 CTTCCAGAGATTCAAAAAAATCCATGTGTAGATTGACCAAGAAAGAAAGAAATGAGC 1015  
Qy 1081 TCAAGCTCACAAGATGCACTTAACGCTCATCTTTAAGAGACACATGTCAGAGCAAAA 1140  
Db 1016 TCAAGCTCACAAGATGCACTTAACGCTCATCTTTAAGAGACACATGTCAGAGCAAAA 1075  
Qy 1141 AGCCCTGCAAGTGAAGCTCTCTGTCTTTTGAATTCACAAATGAAAGTGAAGTCTAT 1200  
Db 1076 AGCCCTGCAAGTGAAGCTCTCTGTCTTTTGAATTCACAAATGAAAGTGAAGTCTAT 1135  
Qy 1201 CATGGAACCATGAGAGAGAGACAGAACCAAGAAATCTATCTCAAGCTACAGACCTCAA 1260  
Db 1136 CATGGAACCATGAGAGAGAGACAGAACCAAGAAATCTATCTCAAGCTACAGACCTCAA 1195  
Qy 1261 AGGCTGATGAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGCAATTCAGTTC 1320  
Db 1196 AGGCTGATGAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGCAATTCAGTTC 1255  
Qy 1321 ACTGATGAAATTTGCTGATCACTGACAGCTTTGGCTTGACACCAATCAAGAGTGGCC 1380  
Db 1256 ACTGATGAAATTTGCTGATCACTGACAGCTTTGGCTTGACACCAATCAAGAGTGGCC 1315  
Qy 1381 ACATCTTTTGTCTGTTAATAACAGAGATGCTACTTTGAGTCCAGAACTTCTCTGTGA 1440  
Db 1316 ACATCTTTTGTCTGTTAATAACAGAGATGCTACTTTGAGTCCAGAACTTCTCTGTGA 1375  
Qy 1441 CCCGAGCTTGAAGACAGTGAACGAGACAGACATGCTTACTGACACTTCTTGTCTCA 1500  
Db 1376 CCCGAGCTTGAAGACAGTGAACGAGACAGACATGCTTACTGACACTTCTTGTCTCA 1435  
Qy 1501 CCGTGTATGGCTCTACCTCCCTGTGACAGAGCTCCACTTTCTTTATGGCATCAAGCATC 1560  
Db 1436 CCGTGTATGGCTCTACCTCCCTGTGACAGAGCTCCACTTTCTTTATGGCATCAAGCATC 1495  
Qy 1561 TTCTCTGTGATGATCAAGGACCAACAGATACATGAGCCATGACAGACATGCTAGTA 1620  
Db 1496 TTCTCTGTGATGATCAAGGACCAACAGATACATGAGCCATGACAGACATGCTAGTA 1555  
Qy 1621 CCAAGGCTCAACATCCCAACAGATGATTAATTCGCAATCAGCCAACTGCTCTGGAAAT 1680  
Db 1556 CCAAGGCTCAACATCCCAACAGATGATTAATTCGCAATCAGCCAACTGCTCTGGAAAT 1615  
Qy 1681 TCACATCCACCTGACATCTTCAATGACAGCGATCAAGTGAAGTGGCGAATATGTC 1740  
Db 1616 TCACATCCACCTGACATCTTCAATGACAGCGATCAAGTGAAGTGGCGAATATGTC 1675  
Qy 1741 AGACACTGATGAAATGATCTGTCTGACACTCTGCTCCCACTGAGGTACAGAGCTC 1800  
Db 1676 AGACACTGATGAAATGATCTGTCTGACACTCTGCTCCCACTGAGGTACAGAGCTC 1735  
Qy 1801 AGGAAATATGTTTCTGTCCCAATCAATTTCTTGAAGATACCACTCTGTCTCACTTTA 1860  
Db 1736 AGGAAATATGTTTCTGTCCCAATCAATTTCTTGAAGATACCACTCTGTCTCACTTTA 1795

Qy 1861 CAGTATATCACCACTAGTTTCTATGACCATGCCCCCAAGGGCCGAGAGCTGTAGTTC 1920  
Db 1796 CAGTATATCACCACTAGTTTCTATGACCATGCCCCCAAGGGCCGAGAGCTGTAGTTC 1855  
Qy 1921 TTCAGTCTGCGTGTGTCTAATGAGCTTCTTCAACGACCTGTTCAACAGAGCTCTGTG 1980  
Db 1856 TTCAGTCTGCGTGTGTCTAATGAGCTTCTTCAACGACCTGTTCAACAGAGCTCTGTG 1915  
Qy 1981 GAGTACCGAGCTCTGAGACCAATTCACACAGCTGCTGTTCCATATCTACGATCCAT 2040  
Db 1916 GAGTACCGAGCTCTGAGACCAATTCACACAGCTGCTGTTCCATATCTACGATCCAT 1975  
Qy 2041 CTTACAGAGTTTAAAGCACTTGAATATCTTAATCTTCAAGAAACGAGAGTGTATGTAAT 2100  
Db 1976 CTTACAGAGTTTAAAGCACTTGAATATCTTAACTTCAAGAAACGAGAGTGTATGTAAT 2035  
Qy 2101 AGCAAAATGAAGTTTGTAGTCTGTGCGGTATTAACCTCACCAAGGCTGTGACCGGGTC 2160  
Db 2036 AGCAAAATGAAGTTTGTAGTCTGTGCGGTATTAACCTCACCAAGGCTGTGACCGGGTC 2095  
Qy 2161 TTGAGAGATTTTCTGTTCTGTGACAGCCCAACAATCTCCATCTGGAATTAAGACCTACT 2220  
Db 2096 TTGAGAGATTTTCTGTTCTGTGACAGCCCAACAATCTCCATCTGGAATTAAGACCTACT 2155  
Qy 2221 CTCAACATTTGAACAGCTGATCAAGCAGATCCCTGCAAGTTCTTGAGCTGCGGCAATTT 2280  
Db 2156 CTCAACATTTGAACAGCTGATCAAGCAGATCCCTGCAAGTTCTTGAGCTGCGGCAATTT 2215  
Qy 2281 GCCCAATGTGTAAAGAACGAACGACCTGAGAGAGAGTGTGCTGCAACAGAGATAT 2340  
Db 2216 GCCCAATGTGTAAAGAACGAACGACCTGAGAGAGAGTGTGCTGCAACAGAGATAT 2275  
Qy 2341 GACAGCCAGGGAGCTGTGAGAGGTTGGAACCAAGGCTCTGTGGCCCTGGCAAAAGAA 2400  
Db 2276 GACAGCCAGGGAGCTGTGAGAGGTTGGAACCAAGGCTCTGTGG - CCTGGCAAAAGAA 2334  
Qy 2401 TGCGAGGCTCTCAAGGAAAGGAGCTCATGACAGGTTGCCAGATCACTTGAATAATCA 2460  
Db 2335 TGCGAGGCTCTCAAGGAAAGGAGCTCATGAC - GCTTCCAGATCACTTGAATAATCA 2392  
Qy 2461 GCATCAAAACTAGTGTAAAAAGTTCCAAATCAACAAATCAACAGATATCACTGATAA 2520  
Db 2393 GCATCAAAACTAGTGT - AAAAGTTCCAAATCAACAAATCAACAGATATCACTGATAA 2451  
Qy 2521 AGAAATTTGAAATTTCTGACCGGTAGAAATTAAGAAATTTAACCATCAAGATTTGGAAAG 2580  
Db 2452 AGAAATTTGAAATTTCTGACCGGTAGAAATTAAGAAATTTAACCATCAAGATTTGGAAAG 2511  
Qy 2581 AATTAAAACTGAAATGTAACAATTAATGAGCTATCTCAAGAGAGATGATTGCT 2640  
Db 2512 AATTAAAACTGAAATGTAACAATTAATGAGCTATCTCAAGAGAGATGATTGCT 2571  
Qy 2641 TCTCAAGGAAATGAGACAGGCAATATCATGGGTATCAAAATCCAGACATACAGTCA 2700  
Db 2572 TCTCAAGGAAATGAGACAGGCAATATCATGGGTATCAAAATCCAGACATACAGTCA 2631  
Qy 2701 CACTGAGATGACACACATATTTCAATTAATTAAGAGATCATGTACTTGGCAACAG 2760  
Db 2632 CACTGAGATGACACACATATTTCAATTAATTAAGAGATCATGTACTTGGCAACAG 2691  
Qy 2761 TAAATTTGAAAAAAAAGACACTTACTTAATTAATTAATTAATTAATTAATTAATTAAT 2820  
Db 2692 TAAATTTGAAAAAAAAGACACTTACTTAATTAATTAATTAATTAATTAATTAATTAAT 2751  
Qy 2821 ATATTTTACTATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880  
Db 2752 ATATTTTACTATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2811  
Qy 2881 TCCCTGAAATTTTACTGACAGATATTTGCAACAGATAGCTTATTTGTTAGG 2940  
Db 2812 TCCCTGAAATTTTACTGACAGATATTTGCAACAGATAGCTTATTTGTTAGG 2871



Db	195	AGCACC	GTGGATCTTCTCCAGACAGAGAAATTA	AAACAGAGAAAGTTTCCCTGCACGAAAAGATG	254
Oy	636	AAATAT	ATCTGCAGAGAAAGCATTTGGAGAGCC	CTGTGAAACCATTTGTCAATTTCAACGACGA	695
Db	255	AAATAT	CTGCAGAGAAAGCATTTGGAGAGCC	CTGTGAAACCATTTGTCAATTTCAAC	309
Oy	696	TC	TACATTTCAAAGACTTTGGGAGATTTCTA	AGAAAACCTCAGAAAGCAATTTCAAGA	755
Db	310	-----	-----	-----AGA	312
Oy	756	TGTTGCC	AAGCTCTCACTTGGGGCTTTTCCCTCTCA	CTCTGATGACACCTCTCAATGA	815
Db	313	TGTTGCC	AAGCTCTCACTTGGGGCTTTTCCCTCTCA	CTCTGATGACACCTCTCTCAATGA	372
Oy	816	AATTCT	CGATATATCACTTCAACGACACCAAGATG	CTTACAAACAGAAAGAGAAACGAATTT	875
Db	373	AATTCT	CGATATATCACTTCAACGACACCAAGATG	CTTACAAACAGAAAGAGAAACGAATTT	432
Oy	876	CGCTGT	TGTGGAGAGACAGAGGGTGGAGCTCA	GGCTCTCTTGGTAAACCGAAGTTTCA	935
Db	433	CGCTGT	TGTGGAGAGACAGAGGGTGGAGCTCA	GGCTCTCTTGGTAAACCGAAGTTTCA	492
Oy	936	GGCAGAG	TCGCTGACTCCGAGTCCCAATATTACAG	AGAGCTAGACGAGAAAGTCCCAACT	995
Db	493	GGCAGAG	TCGCTGACTCCGAGTCCCAATATTACAG	AGAGCTAGACGAGAAAGTCCCAACT	552
Oy	996	TC	CAATGCMAAAGATATTTAAGAAACTTCC	AGATTCAAAAAAAATTCATGTGTAGGATT	1055

576 P. Oy

[illegible]

QY 1716 AAGTCAGGTGGCGAAGATATGTCAGACCTAGATGAATGATCTGTGACACTCC 1775  
DB 1273 AAGTCAGGTGGCGAAGATATGTCAGACCTAGATGAATGATCTGTGACACTCC 1332  
QY 1776 TGGCCCATTTGAGATCCAGAGCTCAGCAATATGTTCTGTCCAGATCATTTCTTGA 1835  
DB 1333 TGGCCCATTTGAGATCCAGAGCTCAGCAATATGTTCTGTCCAGATCATTTCTTGA 1392  
QY 1836 GGAATACCATCTCGTGTGAGCTTTAGATATACACTAGTGTATGACCAATGGCCCC 1895  
DB 1393 GGAATACCATCTCGTGTGAGCTTTAGATATACACTAGTGTATGACCAATGGCCCC 1452  
QY 1896 CAAAGGCCAGAGCTGTGATGTTCTTCACTGCTGTGCTTAAATGAGCTTCTCCA 1955  
DB 1453 CAAAGGCCAGAGCTGTGATGTTCTTCACTGCTGTGCTTAAATGAGCTTCTCCA 1512  
QY 1956 CCACTGTTCACCAAGAGCTCTCTGAGATCCAGAGCTTGGAGCAACAAATTCACAGCT 2015  
DB 1513 CCACTGTTCACCAAGAGCTCTCTGAGATCCAGAGCTTGGAGCAACAAATTCACAGCT 1572  
QY 2016 GCTGGTTCATATATCAAGATCCAAATCTTACAGATTTAGCACTTGAATCTTAATCT 2075  
DB 1573 GCTGGTTCATATATCAAGATCCAAATCTTACAGATTTAGCACTTGAATCTTAATCT 1632  
QY 2076 CAGAAACGGAGATGATGATGTAATAGCAAAATGAAATTTGCTAGTCTGTCCGATTA 2135  
DB 1633 CAGAAACGGAGATGATGATGTAATAGCAAAATGAAATTTGCTAGTCTGTCCGATTA 1692  
QY 2136 CCTCACCAAGCTGTGACCGAGGCTTGGAGAGATTTTCTGTCTGACGCCCAACT 2195  
DB 1693 CCTCACCAAGCTGTGACCGAGGCTTGGAGAGATTTTCTGTCTGACGCCCAACT 1752  
QY 2196 CCATCTGGAATATGACAGCTACTCTCTCAACATTTGAACAGCTGATCAAGCATCCCTG 2255  
DB 1753 CCATCTGGAATATGACAGCTACTCTCTCAACATTTGAACAGCTGATCAAGCATCCCTG 1812  
QY 2256 CAAAGTCTGAGCTGTGCGAGAAATTTGCCAATGTGTAAAGAAAGCAAGCACTGAGGAAGC 2315  
DB 1813 CAAAGTCTGAGCTGTGCGAGAAATTTGCCAATGTGTAAAGAAAGCAAGCACTGAGGAAGC 1872  
QY 2316 GGAATGTCTCTGCAAAACAGATATGACAGCAAGGAGCTTGGAGCGTCTGAAACGAG 2375  
DB 1873 GGAATGTCTCTGCAAAACAGATATGACAGCAAGGAGCTTGGAGCGTCTGAAACGAG 1932  
QY 2376 CCTGTGAGCTGTGCGAGAAATGCGAGGCTTCCAGAGGAGGAGGCTCCATGCG 2435  
DB 1933 CCTGTGAGCTGTGCGAGAAATGCGAGGCTTCCAGAGGAGGAGGCTCCATGCG 1992  
QY 2436 GTTGCAGATCACTCTGAAATTCAGCATACAAACTAGTGTAAATTTCCAAATCA 2495  
DB 1993 GTTGCAGATCACTCTGAAATTCAGCATACAAACTAGTGTAAATTTCCAAATCA 2052  
QY 2496 ACAAATTAACAAGATATGATGTAAGAAATTTCTGAATTACTGACCGTATGATGAGA 2555  
DB 2053 ACAAATTAACAAGATATGATGTAAGAAATTTCTGAATTACTGACCGTATGATGAGA 2112  
QY 2556 ATTTAACCATCAAGATTTGGAGAGAAATTTAAATCTGAAATATGATCACTTAG 2615  
DB 2113 ATTTAACCATCAAGATTTGGAGAGAAATTTAAATCTGAAATATGATCACTTAG 2172  
QY 2616 CTATCTCAAGAGATGATTTGCTTCTCAAGGAAATGAGAGCAGGCTATTTCAATGAGT 2675  
DB 2173 CTATCTCAAGAGATGATTTGCTTCTCAAGGAAATGAGAGCAGGCTATTTCAATGAGT 2232  
QY 2676 CATCAAAATTCAGACATACATGACACTGAGATGAGACACACCATATTTCAATATAT 2735  
DB 2233 CATCAAAATTCAGACATACATGACACTGAGATGAGACACACCATATTTCAATATAT 2292  
QY 2736 GAAAGTCAATGATCTTGGAGCAAGATATTTCTGAAATTAAGCACTTACTTATATTA 2795  
DB 2293 GAAAGTCAATGATCTTGGAGCAAGATATTTCTGAAATTAAGCACTTACTTATATTA 2352

QY 2796 AAACCCCAATGATCATGAGCAAAATATTTTACTATTTCTGATGATGATCAAAATGA 2855  
DB 2353 AAACCCCAATGATCATGAGCAAAATATTTTACTATTTCTGATGATGATCAAAATGA 2412  
QY 2856 TCATAGCCAGGTTTGTCTTCCACTTCCCTGAAAAATTTTACTCACAGATCATTTGCAACA 2915  
DB 2413 TCATAGCCAGGTTTGTCTTCCACTTCCCTGAAAAATTTTACTCACAGATCATTTGCAACA 2472  
QY 2916 AGCATAGCTTATATGTTTGAAGGAGTGAACCAATTTATTTGGAGAGCAACCTTATAT 2975  
DB 2473 AGCATAGCTTATATGTTTGAAGGAGTGAACCAATTTATTTGGAGAGCAACCTTATAT 2532  
QY 2976 GCTAGAAAGTACATTTAAAGATGACTATTACGAGGAGATGACAGGTCTCTTAAACG 3035  
DB 2533 GCTAGAAAGTACATTTAAAGATGACTATTACGAGGAGATGACAGGTCTCTTAAACG 2592  
QY 3036 CATGATGATATGATGTTGTGAGGAGCTGTATGATGATATATGCTTCACTACAGTCT 3095  
DB 2593 CATGATGATATGATGTTGTGAGGAGCTGTATGATGATATGCTTCACTACAGTCT 2652  
QY 3096 GATTAACCAAACTCAGTATTTCAAGTTATTTAGGACACTAGTTTATACGCACTACG 3155  
DB 2653 GATTAACCAAACTCAGTATTTCAAGTTATTTAGGACACTAGTTTATACGCACTACG 2712  
QY 3156 TTACATAGTACAGTGTGTTGTTGCCAATATCTTGAATGTTCTTTAAAGAACTGAG 3215  
DB 2713 TTACATAGTACAGTGTGTTGTTGCCAATATCTTGAATGTTCTTTAAAGAACTGAG 2772  
QY 3216 GTTCAGATACATATCATGAGAAATTTTACTTTCTTTGTTATACACAAAGCTATTTT 3275  
DB 2773 GTTCAGATACATATCATGAGAAATTTTACTTTCTTTGTTATACACAAAGCTATTTT 2832  
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DB 2833 AAAGAGATGCTATGTTGGAGAGAGGAGGAGGAGTTGACTATATGACATATCAAT 2887

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US-10-007-270-5  
Sequence 5, Application US/10007270  
Publication No. US20020160954A1  
GENERAL INFORMATION:  
APPLICANT: Hegeman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
APPLICANT: University of Iowa Research Foundation  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
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PRIOR APPLICATION NUMBER: US 09/430,195  
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PRIOR APPLICATION NUMBER: US 09/183,972  
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NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 2244  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(2244)  
OTHER INFORMATION: n 1s a, c, g, or t.  
US-10-007-270-5

Query Match 65.6%; Score 2184.2; DB 5; Length 2244;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
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Db 22 TAAACGAGAGTTATCTCATCATCTGTATCAATATATATATTTTCACATTTTC 81  
Qy 61 TTTTATCTTTTATAGATTTTGAAGTGTCTCTGTATTTGTATCAGAAATTACCAATGCAC 120  
Db 82 TGTTCCTTTTATAGATTTTGAAGTGTG-TCTGTGTATGTATACAAATTACCAATGCAC 140  
Qy 121 AAAAGCCAGAAATGTATTTGAAAAGTGAAGAGTATTTTGTTTTGTGATTTTTCCTCA 180  
Db 141 AAAAGCCAGAAATGTATTTGAAAAGTGAAGAGTATTTTGTTTTGTGATTTTTCCTCA 200  
Qy 181 AGTTCAAGGAACCAAGATATCTCCATTTAATATACATTCCTGAATTAAGACATAGA 240  
Db 201 AGTTCAAGGAACCAAGATATCTCCATTTAATATACATTCCTGAATTAAGACATAGA 260  
Qy 241 CAATCCCCCAAGAAATGAAACAAGTGAAGTGAAGAAATGTACAAATGTCAATAT 300  
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Qy 301 GAGACGAATATTCGATTTGGCAAAAGCATGCAAAAGATCCGATTTTTCCTCAACGGG 360  
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Qy 361 GGTAAAGTCTGTCCAAGAAATCCATGAACAGATTTTGAACAGTCTTCAAGCTTATTA 420  
Db 381 GGTAAAGTCTGTCCAAGAAATCCATGAACAGATTTTGAACAGTCTTCAAGCTTATTA 440  
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Qy 661 AGAGCTGGTGAACCATTCGATTCATTCAGAGCATTCATTCCTTCAAGACTTGGGCACT 720  
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Db 801 TTTCCCTCTCATCTCTGATGACACCTCTCTCAATGAATTTCTGATATACACTCAACGAC 860  
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Db 861 ACCAAGATGCTCAACAGAAAGAGAAAGAAATTCGCTGTTGAGAGAGAGAGGGTG 920  
Qy 901 GAGCTCAGGCTCTCTCTGTTAAACAGAGATTCAGAGCAGAGCTGCTGCTCCAGTCC 960  
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Qy 1741 AGACACTAGATGAATGGAATCTGTCTGACACTCTGCGCCCATCTGAGGTACAGAGCTC 1800  
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Qy 1801 AGCGAATATGTTTCTGTCCAGATCATTTCTTGAAGATACCACTCTGTCTCAGCTTTA 1860  
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Qy 1861 CAGTATATCAACACTAGTTCATATGACATTCGCCCCCAAGGGCCGAGACTGGTATGTTTC 1920  
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Qy 1921 TTCAGTCTGCGGTGCTCAACATGCGCTTCCACAGACCTGTTCAAGAGGCTCTGTC 1980  
Db 1940 TTCAGTCTGCGGTGCTCAACATGCGCTTCCACAGACCTGTTCAAGAGGCTCTGTC 1999  
Qy 1981 GAGTACCGAGCTCTGAGCAACAATTCACAGAGCTGCTGTTCCATATCTACATCCAT 2040  
Db 2000 GAGTACCGAGCTCTGAGCAACAATTCACAGAGCTGCTGTTCCATATCTACATCCAT 2059  
Qy 2041 CTTACAGATTTTAAAGCACTTGAAATTAATCTTCAAGAAACGGAAGTGTATGTGAAT 2100  
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Qy 2101 AGCAAAATGAAGTTCATAGTCTGTGCGCTGCTTAACTTCAACAGGCTGTGACAGGGTTC 2160  
Db 2120 AGCAAAATGAAGTTCATAGTCTGTGCGCTGCTTAACTTCAACAGGCTGTGACAGGGTTC 2179  
Qy 2161 TTTGAGATTTTCTGTTCTGTGACAGCCCAACACTCTCTGAAATATGACAGCTACTCT 2220  
Db 2180 TTTGAGATTTTCTGTTCTGTGACAGCCCAACACTCTCTGAAATATGACAGCTACTCT 2239



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DB 1602 TCCCTTGATGACATCGGCCCAACAGACATCAATCCCAAGCCCACTCCCACTATGCA 1661
QY 1647 TTATTCGCAATCAGCCCAATGCTCTGCGGAATTTCAACATCCAGCTGCATCTTCAGATGA 1706
DB 1662 TTATTCATCATCCGCAATTCCTCTGGAATCGTCACTATGGCTGCATCTCCAGTGA 1721
QY 1707 CAGCGCATCAAGTCAGGTGGCGAAAGATATGCTCAGACACTTGAATGAAATGATCTGTC 1766
DB 1722 CAGAGAGTCATCAAGACGACCAAGACAATCCGAGACTGATGAGATGATGTC 1781
QY 1767 TGACATCTCCGCCATCTGAGTACAGAGCTCAGCCAAATATGTTCTGTCCCAAGTCA 1826
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DB 1842 GTTCTTGAGATGACCAACCAATCCCAAGATAGGTTCACTACCAACAGCTCCGAGAC 1901
QY 1887 CATTGCCCCCAAGGCCGAGAGCTGTAGTGTCTTCAGTCTGCGTGTGCTACATGAC 1946
DB 1902 CATTCACCAAGGCGCAGAGACTAGTGATTTCTTCAGCCGTGCGTGTGCTACATGCC 1961
QY 1947 CTTCTCCACAGACCTGTTCAACAAGAGCTCTTGAATACGAGCTCTGAGCAACAAT 2006
DB 1962 GTTCTCTATGACCTGTTCACAAAGATCTCTGAGATCAAGCCCTGGAACAACGAT 2021
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QY 2067 ACTTAATCTCAGAAACGAGAGTGTATGTGAATAGCAAAATGAATGATGCTAGTCTGT 2126
DB 2082 ACTCAGCTTCAGAAACGAGAGTGTATGTGAACGAAAGTGGGTTTGCAAAAGCGGT 2141
QY 2127 GCCGTATACCTCACCAGAGCTGTGACAGGGGCTTTGAGAGATTTTCTGCTGTCAGC 2186
DB 2142 ACCCTCAACCTCACCAGGCGGTGCGGGCTTTGAGAGATCTTCGCTCACCAGC 2201
QY 2187 CCAACAACTCCATCTGGAATATGACAGCTACTCTCAACATTTGAACAGAGCTGATCAAGC 2246
DB 2202 TCAAGGCTCAATCTGGAATATGAAAGCTACTCTCCATGATGAACAGCTGATCAGGC 2261
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DB 2262 GGATCCCTGCAAACTCTGAGACTGTGGAATTTGCCAGTGTGTAAAGATGATGAGAC 2321
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DB 2322 AGAGGAACAGAGTGTCTGCAAGAGGACATGAGAGCCAGGACCTTGAATCAACA 2381
QY 2367 GGAACAGGCTCTGTGGCGCTGCGCAAAAGGAATGCGAGTCTCTCAGGGAAGGAGC 2426
DB 2382 GACCTGAACCTGTCTCCCTCGG---AAAGCTGTGTGGCGGCGCAGAAACAAGCAAC 2438
QY 2427 TCCATGAGGTTGCAAGATCACTCTGAAATCAAGACATACAAATTAAGTGTAAAGATT 2486
DB 2449 TCCATGAGGCGCACAGATCACTCAAAACCAACTCAGAACTGTGTTTAAAGAGCT 2498
QY 2487 CCAAAATCAAAATAACAAGTATACATGTAAGAAATTTCTGAATTAAGACCGTGA 2546
DB 2499 ACGTCAAGCA---AATAAGTGTGCAAGAAAGAAATTTCTAACTACAGTATAGG 2552
QY 2547 ATATGAGAAATTTAACAATCAAGATTGGAGAGAAATTTAAACCTGAAA----- 2595
DB 2553 ATTTAAGAAATTTGAAGACAGGACTGGAGGGAATTTAAAGCTGGAATCATATGCAAT 2612
QY 2596 -----ATGTACAATTTATCACTTGGCTATCTCAAGAGATGATTTGGCT 2640
DB 2613 ATGTTCAAACCTGTGTGAAGGAACCTTAATTTCTTAAAGAAAGTGTATCTGTCTGT 2672

```

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QY 2641 TCTCAAGAAATATGAGACAGGCATATTCATGGCTCATCAAAATCCAGACATACAGTCA 2700
DB 2673 TAACTTCTGAAAACACAGAGGAGATTCAGTGTCAATTTGAAATACAGGACATGATCA 2732
QY 2701 CACTGAGATACAGCACACCATATTTCAAAATATGAAAGATCATGTACTTGGCAACAG 2760
DB 2733 CTTTGAAGCTAG-----CATGCTTGAACAAAGACACAGCGGTGTATTTGATGA-CAG 2784
QY 2761 TAAATCTGAAAAAAAAGACACTTACTATTAATTA--AAACCCCAATGCAATCAGCGAA 2818
DB 2785 TTAAGCTGTGTGGGCGCGGGGACATATTTTATGTCAAAACCTCAAGCAATCAATGGA 2844
QY 2819 AATATTTTCTATCTCTGTGATGATGACTCAAAATGATCATTAAGCAGTTTGTCTCAC 2878
DB 2845 ACACA-TTGTACTATTTTGTGACAGTACTC--AGTACAAAAGATTAAGTTAGCTTTT 2901
QY 2879 CTTCCCTGAAAATTTTACTCAGATCAATTTGCAACAGCAAGCTTACTTATTTGTTAG 2938
DB 2902 CTTTCTTAAATTTATTAATTAARCTTATTTCAAAATTAATCAAC-----TTGTTAG 2954
QY 2939 GCACTGAACAAATTAATTTGGAAGCAAACTTTATATGCTAAGAAATACATTTAAAGAT 2998
DB 2955 TGGGTGTGACAATATTTGAGATGATGATCTTTATATGTTGAATATACAGTTAAAGAT 3014
QY 2999 GACTACTTAAGC 3010
DB 3015 TATCATTTGGGC 3026

RESULT 6
US-10-007-270-10
; Sequence 10, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 CDNA sequence, isoform D
US-10-007-270-10

Query Match 16.0%; Score 534; DB 5; Length 1726;
Beech Local Similarity 72.0%; Pred. No. 1.2e-11;
Matches 792; Conservative 0; Mismatches 225; Indels 83; Gaps 4;

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Db 351 AGCAGTATCTTCTTTCAGACAGAAATTAACAGAGAAGCTTCCCTGGAGAAAGATG 410
Qy 636 AATATCTGACAGAAACATTTGGAGAGCCCTGGTAAACCTTTCATTTTCAACAGCA 695
Db 411 AGACAGCTCCATGAGACATGAAAGCACTTACGAAAGCCCTGGTGAACCAAC----- 465
Qy 636 TCTACATTTCAAAAGACTTGGGAGATTTCTAAGAAAACCCCTGAGAAAGCAATTCAGAA 755
Db 466 -----AGAA----- 468
Qy 756 TGTTCGCAAGCTCTCACTTGGGCTTTCCTCTCACTCTGTATGACACCTCTCAATGA 815
Db 469 TGTTCGCAAGATGCTCTGGGGCAATTCCTCACTCTGTATGACACGACCTCAAGGA 528
Qy 816 AATTCGCAATATACCTCAAGACCAAGATGCTCTCAAGAAAGAAAGCAAGAA-- 873
Db 529 GATTCGAGTGTACCTTCAAGACATTCAAAAGCCCAAGAAAGATATACAGAAC 588
Qy 874 -----TTCGCTGTGGAGAGAGAGGAGGAGCTCAGCGTCTCTGTAA 923
Db 589 TATTCAGCTGTCTGAATTTCTCATAGAGAGAAAGTGAAGTTCAAGATCTCTGCCAA 648
Qy 924 CCAGAAATTCAGAGCAGAGCTCTGCTGCTCCAGTCCCATATTAACAGAGCTAGCAG 983
Db 649 CCAGAGTTCAAGAGCAGAGCTCAACCACTCTGGGTCAACATCTACAGAGAACTGTGG 708
Qy 984 AAGTCCCACTTCAGATGCAAAAGATTTTAAGAACTTCCAGATTCAAAATACTCA 1043
Db 709 AAGTCCCACTTCAGATGCAAAAGATTTTAAGAACTTCCAGATTCAAAATACTCA 768
Qy 1044 TGTGTAGATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTCAGAGATGCAACT 1103
Db 769 TGTATTAAGATTTAGACCAAAAGAAAGATGCTCAAGCTCAGAGATGCAACT 828
Qy 1104 TACGCGCATCTTTAAGAGACAGTGCAGAGAGAAAGCCCTGCAAGTGCCTCTGTC 1163
Db 829 TATGCGCATCTTTAAGAGAGAGACCATGCAAGAGCAAAAGCCCTGATGATCTACTGTC 888
Qy 1164 TTTTGTTCGCAAAATTTGAAGTGAAGAGTCTATCATGGAACCATGAGAGAGACA 1223
Db 889 TCTGTATTCGCAAAATTTGAAGTGAAGAGTCTATCATGGAACCATGAGAGAGACA 945
Qy 1224 GCAACGCAAAATCTATCTCAGACTCAGAGCTCAAAAGCTGATCAGCAAGCACTAGA 1283
Db 946 ACAAACGAAACCTTACTCTCAGACTCAGAGCTCAAAAGCTGATCAGCAAGCACTAGA 1005
Qy 1284 GGAAGAAACATCTTGGATGAGGAGCAATTCAGTCTGATGAATGCTGATCACT 1343
Db 1006 TGGAGACCTGTCTGTGAGAGAGGAAATTCATTCGTGATGAAGTTACTGGGACACT 1065
Qy 1344 GCCAGCTTTGTCTCGAACAACCAATCAGAGCTGCCCACTTTTGTCTGTATTAACGA 1403
Db 1066 -----CTTCAGACCTGTCACTGAAACCAATCTGCCAAGCCCTTGTGATGTCACAGA 1119
Qy 1404 GGATGTAATTTGAGTCCAGAACTTCTCTGTGTAACCCAGCTGAGACAGTGAACG 1463
Db 1120 GGATGTAATTTGAGTCCAGAACTTCTCTGTGTAACCCAGCTGAGACAGTGAACG 1179
Qy 1464 AGCAGAGATGCTTACTG 1483
Db 1180 AGAAGATCTGAGCTGCTG 1199

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## RESULT 7

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US-10-007-270-12
; Sequence 12, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: University of Iowa Research Foundation
; FILE REFERENCE: 020618-000120US

```

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; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPW 150 cDNA sequence, isoform E
US-10-007-270-12

Query Match 14.8%; Score 491.6; DB 5; Length 1321;
Best Local Similarity 76.0%; Pred. No. 2,4e-120;
Matches 634; Conservative 1; Mismatches 190; Indels 9; Gaps 2;

Qy 1767 TGACACTCTGCTCCCATCTGAGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCA 1826
Db 319 TGAACGCGCAGCTTGTCAAAATATCAGAACTGAGTGAATACATTCGCTCGGGTCA 378
Qy 1827 TTTCTTGAGAGATACCACTCTGCTCAGCTTTACAGATATACCACTAGTTCTATGAC 1886
Db 379 GTTCTGAGATGACCAACCACTCCCAAGTACGTTTCACTACCACTGAGAC 438
Qy 1887 CATTCGCCCAAGGCGCAGAGCTGTGATGTTCTTCAGTCTGCTGTTCTACATGAC 1946
Db 439 CATTCGCCCAAGGCGCAGAGCTGTGATGTTCTTCAGTCTGCTGTTTACATGCC 498
Qy 1947 GTTCTCCAGAGACCTGTTCAACAAGAGCTCTGAGATACCGAGCTGAGCACAAT 2006
Db 499 GTTCTCTATGACCTGTTCACACAGAGTTCTTGAAGTACAGCTGAGCAACAT 558
Qy 2007 CACACAGCTGTGTTCCATATCTAGATCCAACTTACAGATTTAAGCACTTGAAT 2066
Db 559 CACAGACCTGTGTTCCATATCTAGATCCAACTTACAGATTTAAGCACTTGAAT 618
Qy 2067 ACTTAATTCAGAAACGAGAGTGTGATGTAATGCAAAATGAAGTTTCTAGTCTGT 2126
Db 619 ACTCACTTCAGAAACGAGAGTGTGATGTAATGCAAAAGTGTGCAAAAGCGGT 678
Qy 2127 GCCGATTAACCTCAACAGAGCTGTGACAGGGCTTGAAGATTTTCTGTCTGACAGC 2186
Db 679 ACCCTAACAACCTCAACAGAGCTGTGACAGGGCTTGAAGATTTTCTGTCTGACAGC 738
Qy 2187 CCAACAATCTCATCTGAAATTAAGACAGTACTCTCTCAACATTTGAACAGCTGATCAAGC 2246
Db 739 TCAAGGCTCAATCTGAAATTAAGACAGTACTCTCTCAACATTTGAACAGCTGATCAAGC 798
Qy 2247 AGATCTCTGCAAGTTCTGTGCTGTGAGGAGAAATTTGCGCAATGTGTAAAGAACGAGC 2306
Db 799 GGATCTCTGCAAGTTCTGTGCTGTGAGGAGAAATTTGCGCAATGTGTAAAGAACGAGC 858
Qy 2307 TGAAGAACGAGTGTGCTGTGAAACAGAGATTAACAGCCAGGAGAGCTGGAAGGCT 2366
Db 859 AAGAGAACGAGTGTGCTGTGAAACAGAGATTAACAGCCAGGAGAGCTGGAAGGCT 918
Qy 2367 GGAACGAGGCTGTGTGAGGCTGTGCAAAAGAAATGCAAGGCTCTCCAGGAAAGGAGC 2426
Db 919 GACCTGAACCTGTGTGAGGCTGTGCAAAAGAAATGCAAGGCTCTCCAGGAAAGGAGC 975
Qy 2427 TCCATGCAAGTTGCGAGATCACTGAAATTAAGCAATTAAGCAATTAAGTTAAAGTT 2486
Db 976 TCCATGCAAGGCGACAGATCACTTAACAACCAAGCTCAGGAACCTGTGTAAAGAGT 1035
Qy 2487 CCAAAATCAACAAATTAACAGTAAATCAAGTAAAGAAATTTGATTAAGTCCGTAGA 2546
Db 1036 ACGTACGAA-----AATTAAGTGTGCAAGAAAGAAATTTTAACATACATGATGAG 1089
Qy 2547 ATATGAAGATTTAATCAATCAAGATTTGGAGAGAAATTAAGAAATGTA 2600

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Db 1090 ATTGAATAATTGAGACCGAGACTGGAGGGAATTAAAGCTGCAATCATA 1143

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RESULT 8
US-10-007-270-14
; Sequence 14, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Monkey ipm 150 cdna (partial)
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Monkey species
US-10-007-270-14

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D<sub>b</sub>  
Qy  
D<sub>b</sub>

482	AGGANGAGGGGTGAAGCTCAGCATCTCTCTATTAACAGAGGTTCAAGCAGAAGCTCG	541
947	CTGACTCCCAATC	959
542	CTGACTTCAATC	554

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RESULT 9
US-10-027-632-286848/c
Sequence 286848, Application US/10027632
Publication No. US20020198372A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIORITY FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 286848
LENGTH: 596
TYPE: DNA
ORGANISM: Human
US-10-027-632-286848

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Db	362	TCTCACTTGGGCTTTTCCTTCATCTCTGATGACACCCTCCTCAATGAATTTCTCGATA	421
Oy	827	ATTACATCAACGACACCAAGATGCTTCACACAGAAAGAAACAGAAATTCGCTGTGTGG	886
Ddb	422	ATGCATCTACAGACACACAGATGCTTCACACAGAAAGAAAGAAACAGAAATTCGCTGTGTGG	481
Oy	887	AGAGACAGACGGTGGAGCTCAGCGTCTCTCTGTGTAAACAGAAATTCAAGGCAGAGCTCG	946

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RESULT 10
US-10-027-633-286848/c
; Sequence 286848, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```



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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 286848
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-286848

Query Match      6.1%; Score 204.6; DB 6; Length 596;
Best Local Similarity 86.9%; Pred. No. 1.4e-43;
Matches 225; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

OY 1 TAAACCAAGAGGTTATCTCATCATCTGTATCAATATATATATTTTTCACATTTC 60
DB 525 TAAACCAAGAGGTTATCTCATCATCTGTATCAATATATATATTTTTCACATTTC 466
OY 61 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAAGAAATTCACATTC 120
DB 465 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAAGAAATTCACATTC 406
OY 121 AAAAGCCGAATGTTATTTGGAACCTAAGAAAGCTATTTTGTGTTTGGATTTCCTCA 180
DB 405 AAAAGCCGAATGTTATTTGGAACCTAAGAAAGCTATTTTGTGTTTGGATTTCCTCA 346
OY 181 AGTTCAAGAACCAAGATATCTCCATTAACTATATACATTCGAAACTAAAGACATAGA 240
DB 345 AGTTCAAGAACCAAGATATCTCCATTAACTATATACATTCGAAACTAAAGACATAGA 286
OY 241 CAATCCCCCAAGAAATGAA 259
DB 285 ATCTACCGATAGAGTGAA 267

RESULT 11
US-10-007-270-7
; Sequence 7, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: University of Iowa Research Foundation
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1858
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: Human IMPG1 gene, regulatory region
; NAME/KEY: misc feature
; LOCATION: (1)..(1858)
; OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-7

Query Match      6.1%; Score 204.6; DB 5; Length 1858;
Best Local Similarity 86.9%; Pred. No. 2.9e-43;
Matches 225; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

OY 1 TAAACCAAGAGGTTATCTCATCATCTGTATCAATATATATATTTTTCACATTTC 60
DB 1070 TAAACCAAGAGGTTATCTCATCATCTGTATCAATATATATATTTTTCACATTTC 1129
OY 61 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAAGAAATTCACATTC 120
DB 1130 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAAGAAATTCACATTC 1189
OY 121 AAAAGCCGAATGTTATTTGGAACCTAAGAAAGCTATTTTGTGTTTGGATTTCCTCA 180
DB 1190 AAAAGCCGAATGTTATTTGGAACCTAAGAAAGCTATTTTGTGTTTGGATTTCCTCA 1249
OY 181 AGTTCAAGAACCAAGATATCTCCATTAACTATATACATTCGAAACTAAAGACATAGA 240
DB 1250 AGTTCAAGAACCAAGATATCTCCATTAACTATATACATTCGAAACTAAAGACATAGA 1309
OY 241 CAATCCCCCAAGAAATGAA 259
DB 1310 ATCTACCGATAGAGTGAA 1328

RESULT 12
US-10-783-528-9
; Sequence 9, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4165
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4076)..(4076)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (4091)..(4091)
; OTHER INFORMATION: n is a, c, g, or t
US-10-783-528-9

Query Match      6.1%; Score 203.4; DB 8; Length 4165;
Best Local Similarity 63.7%; Pred. No. 1e-42;
Matches 309; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

OY 1883 TGACCATGGCCCGGAGGCGGAGCTGAGTGTCTTCAGTCTGGGTGTGCTAACA 1942
DB 2860 TGAGTTATCCAGACCTTCAGAGAGCTTTGGTGTTTCTTACGCTCCGAGTACTAACA 2919
OY 1943 TGGCCTTCTCCAGACCTGTTCACACAGAGCTCTTGAGAGTACGAGCTCTGAGCAAC 2002
DB 2920 TGATGTTTTCAGAGAGATCTGTTTAAATAAACTCCTTGAGATATAAACCTCGAGCAAA 2979
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OM nucleic - nucleic search, using sw model

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(without alignments)  
12325.052 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 ttaaccagaaggtatcct.....tactatatgacataatcaat 3330

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 2339354128 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hic: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_gse1: \*  
10: gb\_gse2: \*  
11: gb\_gse3: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2472	74.2	5829	4	CR749572 Homo sapi
2	1456	43.7	1665	10	AY415971 Homo sapi
3	634	19.0	690	5	BX510244 DKFZ06866
4	626	18.8	626	5	BQ639265 h33404.Y
5	558	16.8	675	5	BM630735 UI-E-CKO-
6	480	14.4	633	3	BM695987 UI-E-CKO-
7	472	14.2	472	5	BX097138 BX097138
8	469	14.1	472	5	BQ638902 h429406.Y
9	467	14.0	653	3	BM685921 UI-E-CKO-
10	433	13.0	836	3	BT752112 603022362
11	409	12.3	422	3	BM726533 UI-E-EJO-
12	402	12.1	508	6	CA393958 CA44404.Y
13	395	11.9	801	2	BG196799 RST16026
14	380	11.4	598	5	BQ636596 h41102.Y
15	373	11.2	683	5	BT732814 UI-E-COI-
16	340	10.2	698	5	BT792227 UI-E-COI-
17	332	9.4	405	8	H38604 yP4604.r1
18	306	9.2	448	3	BM681190 UI-E-EJO-
19	284	8.8	368	3	BM694699 UI-E-CII-
20	282	8.5	521	3	BM691879 UI-E-CL1-
21	282	8.5	548	5	BT728582 UI-E-CL1-
22	268	8.0	515	5	BT726282 UI-E-CKO-

C	23	266	8.0	561	8	W26960	W26960 16b10 Human
C	24	263	7.9	618	6	CA391789	CA391789 CA1807.Y
C	25	249	7.5	340	1	AV656968	AV656968 AV656968
C	26	241	7.2	510	1	AL713229	AL713229 DKFZP686P
C	27	228	6.8	641	5	BT734170	BT734170 UI-E-CK1-
C	28	213	6.4	298	1	AA296278	AA296278 RST10795
C	29	204	6.1	393	5	BQ636351	BQ636351 h407h06.Y
C	30	188	5.6	1587	10	AY415972	AY415972 Pan trog1
C	31	168	5.0	309	8	H38594	H38594 yP4606.r1
C	32	156	4.7	322	1	AA326863	AA326863 RST30113
C	33	152	4.6	527	5	BT731220	BT731220 UI-E-CII-
C	34	113	3.4	701	1	AG128736	AG128736 Pan trog1
C	35	81	2.4	647	9	AQ234080	AQ234080 HS 2057.A
C	36	40	1.2	626	5	BK646053	BK646053 DKFZP781B
C	37	32	1.0	624	7	CK619878	CK619878 mk29d09.Y
C	38	32	1.0	754	8	CX568203	CX568203 UI-M-IBO-
C	39	32	1.0	797	4	AK020862	AK020862 Mus muscu
C	40	32	1.0	802	3	BT735091	BT735091 603356230
C	41	32	1.0	1647	10	AY415973	AY415973 Mus muscu
C	42	30	0.9	654	10	CS664832	CS664832 t1gr-g88-
C	43	28	0.8	753	3	BT735383	BT735383 603356869
C	44	25	0.8	393	6	CB774211	CB774211 AMGNNUC:S
C	45	25	0.8	409	6	CB770207	CB770207 AMGNNUC:S
C	46	24	0.7	269	7	CO506867	CO506867 CGEZR201
C	47	24	0.7	400	5	BU255882	BU255882 603745523
C	48	24	0.7	471	5	BU201300	BU201300 604155385
C	49	24	0.7	866	5	BY742200	BY742200 BY742200
C	50	24	0.7	624	3	BT738733	BT738733 603358767
C	51	24	0.7	851	3	BT733865	BT733865 603353151
C	52	24	0.7	963	5	BU506195	BU506195 AGENCOURT
C	53	24	0.7	1090	5	BU295512	BU295512 603742306
C	54	23	0.7	779	9	BH357376	BH357376 CH230-175
C	55	23	0.7	814	10	C2814676	C2814676 OC Ba019
C	56	22	0.7	320	2	BB251690	BB251690 BB251690
C	57	22	0.7	387	1	A1632451	A1632451 WP09C01.X
C	58	22	0.7	387	2	BP059396	BP059396 7K59A06.X
C	59	22	0.7	391	1	A1695882	A1695882 t687b06.X
C	60	22	0.7	446	1	A1093483	A1093483 q015b03.X
C	61	22	0.7	497	2	BE378318	BE378318 601236351
C	62	22	0.7	503	1	AM303461	AM303461 xv19d01.X
C	63	22	0.7	520	3	BM168779	BM168779 RST571302
C	64	22	0.7	549	3	BT509853	BT509853 BB1700248
C	65	22	0.7	562	7	CO617781	CO617781 DG9-179e1
C	66	22	0.7	569	7	CN694482	CN694482 E0351C10-
C	67	22	0.7	611	7	CK621236	CK621236 ml22a05.Y
C	68	22	0.7	626	5	BU456998	BU456998 603218530
C	69	22	0.7	646	5	BU736728	BU736728 UI-E-CK1-
C	70	22	0.7	647	5	BU742303	BU742303 UI-E-EOI-
C	71	22	0.7	658	9	BZ211527	BZ211527 CH230-379
C	72	22	0.7	682	5	BU681181	BU681181 UI-CF-ECL1
C	73	22	0.7	703	5	BH471398	BH471398 BOGET55TR
C	74	22	0.7	732	9	BX871618	BX871618 BX871618
C	75	22	0.7	781	11	CR906529	CR906529 Sus scrofa
C	76	22	0.7	917	10	C2525050	C2525050 GMD2-64N1
C	77	22	0.7	963	5	BU287197	BU287197 603604306
C	78	22	0.7	1305	9	CC314264	CC314264 TAM32-311
C	79	22	0.6	201	6	CA931592	CA931592 MTU2PA.P9
C	80	22	0.6	227	9	BH817561	BH817561 BACP1-P2
C	81	21	0.6	269	2	BB279156	BB279156 BB279156
C	82	21	0.6	310	6	CA304286	CA304286 Ae adfo.1
C	83	21	0.6	310	6	CB921817	CB921817 VVD075H12
C	84	21	0.6	312	6	CA304907	CA304907 Ae adfo.2
C	85	21	0.6	333	11	CNS040D5	AL99588 Tetradon
C	86	21	0.6	343	6	CB379587	CB379587 rqt7d07.Y
C	87	21	0.6	369	10	CB317252	CB317252 t1gr-g88-
C	88	21	0.6	374	5	BO797217	BO797217 RST 6155
C	89	21	0.6	410	3	BM677324	BM677324 UI-E-EOI-
C	90	21	0.6	448	10	CU882307	CU882307 AbE54b08.
C	91	21	0.6	456	9	AO871114	AO871114 nbe0042A
C	92	21	0.6	474	8	DT035848	DT035848 VTL109B05
C	93	21	0.6	483	8	CX917235	CX917235 JGI CAAN6
C	94	21	0.6	486	5	BO796326	BO796326 RST 5264
C	95	21	0.6	487	6	CF405842	CF405842 CSECS059H

C 96	21	0.6	522	2	BE951912	UI-M-CCO-	C 169	20	0.6	411	9	BH619076	BH619076	0402
C 97	21	0.6	526	8	DT032872	VVL074E08	C 170	20	0.6	415	7	CN993429	CN993429	MDfW20471
C 98	21	0.6	526	8	DT034159	VVL089H07	C 171	20	0.6	424	5	A0842252	A0842252	T16193b
C 99	21	0.6	526	8	DT037143	VVL124C01	C 172	20	0.6	425	5	BY453108	BY453108	
C 100	21	0.6	526	8	DT038689	VVL142A03	C 173	20	0.6	425	5	AA550505	AA550505	1662m3 gm
C 101	21	0.6	535	10	CG828766	ZMMBBD035	C 174	20	0.6	426	2	B0376040	B0376040	UI-R-C90-
C 102	21	0.6	564	3	BI344794	373373 MA	C 175	20	0.6	428	10	CG603376	CG603376	OB87277852
C 103	21	0.6	572	6	CB515345	88A19B51	C 176	20	0.6	430	10	CG556157	CG556157	OB87171460
C 104	21	0.6	583	6	CB977622	CBA40004	C 177	20	0.6	431	10	CG655365	CG655365	OB87425581
C 105	21	0.6	622	10	CL380760	RPCI44_31	C 178	20	0.6	435	10	BY452502	BY452502	
C 106	21	0.6	629	6	CB968634	CAB10002	C 179	20	0.6	438	10	CL410684	CL410684	RPCI44_41
C 107	21	0.6	633	6	CF767493	CE5007726	C 180	20	0.6	439	10	CW853357	CW853357	OG_BB608
C 108	21	0.6	638	7	CV332095	IL3-HT061	C 181	20	0.6	440	2	BE332178	BE332178	u098a04.y
C 109	21	0.6	641	7	CN549008	EST 16647	C 182	20	0.6	443	1	A1843103	A1843103	UI-M-AK1-
C 110	21	0.6	645	5	BO795258	EST 4196	C 183	20	0.6	444	7	CO047626	CO047626	Lt ATTICP
C 111	21	0.6	648	10	CW312286	CM12286 104_802.1	C 184	20	0.6	446	7	CK648707	CK648707	C.T7.13.5
C 112	21	0.6	655	10	CZ624870	OM_Ba016	C 185	20	0.6	446	7	CC055335	CC055335	SALK_0937
C 113	21	0.6	658	10	CE756240	CE756240 L1gr-g88-	C 186	20	0.6	449	10	CB412164	CB412164	L1gr-g88-
C 114	21	0.6	661	5	B0800405	EST 7440	C 187	20	0.6	453	5	BY364364	BY364364	
C 115	21	0.6	669	5	AZ802391	2M0061H13	C 188	20	0.6	456	5	B79720	B79720	CIT-HSP-204
C 116	21	0.6	675	5	BX673585	BX673585	C 189	20	0.6	463	3	B3381985	B3381985	
C 117	21	0.6	679	9	AZ101786	RPCI-23-3	C 190	20	0.6	464	2	BP454115	BP454115	ma858002.
C 118	21	0.6	681	9	AZ507532	AZ507532 1M0349009	C 191	20	0.6	464	2	B0629908	B0629908	B0629908 B0629908.
C 119	21	0.6	682	9	CC944557	BO1BQ231P	C 192	20	0.6	464	5	A0504415	A0504415	RPCI-23-4
C 120	21	0.6	683	10	CL412012	CL412012 RPCI44_43	C 193	20	0.6	468	5	BQ562452	BQ562452	H4076A11-
C 121	21	0.6	702	8	BO795268	EST 4206	C 194	20	0.6	482	2	BE924401	BE924401	EST428266
C 122	21	0.6	722	5	DN897153	DN897153 nap1b09.	C 195	20	0.6	482	2	AZ627247	AZ627247	RPCI-23-1
C 123	21	0.6	725	1	AA199203	mw43d02.r	C 196	20	0.6	487	9	A0766440	A0766440	HS.2145_A
C 124	21	0.6	755	5	CC132217	NDL.6885.	C 197	20	0.6	490	8	CK730414	CK730414	OC03B01.y
C 125	21	0.6	772	5	BO797221	EST 6159	C 198	20	0.6	494	6	CA531456	CA531456	OC03B01.y
C 126	21	0.6	783	7	CO924291	AGENCOURT	C 199	20	0.6	500	1	A1197745	A1197745	u070F04.r
C 127	21	0.6	793	6	CB977200	CAB40003	C 200	20	0.6	502	1	AU283596	AU283596	AU283596 AU283596
C 128	21	0.6	808	8	CV821817	80975.130	C 201	20	0.6	502	2	AZ521464	AZ521464	RPCI-11-8
C 129	21	0.6	815	10	CG354293	CG354293 OXKEXU41TH	C 202	20	0.6	503	2	BG692747	BG692747	342554_BA
C 130	21	0.6	815	10	CG909956	ZMMBBD034	C 203	20	0.6	504	10	CE650178	CE650178	L1gr-g88-
C 131	21	0.6	827	8	DR504412	DR504412 WS02710.C	C 204	20	0.6	506	6	A0926673	A0926673	RPCI-23-4
C 132	21	0.6	828	8	CV821732	80890.130	C 205	20	0.6	508	2	BE556656	BE556656	BQ09a06.y
C 133	21	0.6	849	4	CN80GCOU	CR712466 Tetradon	C 206	20	0.6	509	9	A0798460	A0798460	HS.3212_B
C 134	21	0.6	870	4	CX070374	UCRC08.1	C 207	20	0.6	515	1	AV521136	AV521136	AV521136
C 135	21	0.6	872	9	CC567485	CH240.441	C 208	20	0.6	519	5	AZ562922	AZ562922	RPCI-23-2
C 136	21	0.6	937	10	CG202550	PURD0571TB	C 209	20	0.6	520	5	BS14287	BS14287	BX514287
C 137	21	0.6	954	11	CNS07103	clone BAO	C 210	20	0.6	520	7	CK527205	CK527205	rw87A0.00
C 138	21	0.6	984	10	CG387901	ZMMBBD056	C 211	20	0.6	521	10	CL158195	CL158195	CL158195
C 139	21	0.6	1038	6	CA183445	SC08T312	C 212	20	0.6	522	1	AU294267	AU294267	AU294267
C 140	21	0.6	1049	11	CNS05FB9	AL334782 Tetradon	C 213	20	0.6	534	2	BF190921	BF190921	RPCI44_41
C 141	21	0.6	1055	3	BMS63823	AGENCOURT	C 214	20	0.6	534	2	BF190921	BF190921	
C 142	21	0.6	1081	11	CNS08S02	AG175404 Pan. t1091	C 215	20	0.6	535	2	BF190921	BF190921	
C 143	21	0.6	1127	10	AG175404	AG175404 Pan. t1091	C 216	20	0.6	535	2	BE635222	BE635222	
C 144	21	0.6	1129	8	DN734691	DN734691 CNB77-B07	C 217	20	0.6	538	2	BG284885	BG284885	
C 145	21	0.6	1175	8	DN659881	CECA3-E09	C 218	20	0.6	539	1	AL921767	AL921767	
C 146	21	0.6	1321	8	DN670614	CEM57-H06	C 219	20	0.6	539	2	BP440402	BP440402	
C 147	20	0.6	164	9	AO284104	AO284104 RPCI11-80	C 220	20	0.6	542	3	BM367799	BM367799	NXUV_056_
C 148	20	0.6	200	7	CO156880	CO156880 EN09505.5	C 221	20	0.6	542	9	CS128419	CS128419	L1gr-g88-
C 149	20	0.6	202	2	BB803363	BB803363	C 222	20	0.6	546	5	BX726424	BX726424	BX726424
C 150	20	0.6	228	9	AQ264725	CITB1-EI-	C 223	20	0.6	547	1	AZ563047	AZ563047	
C 151	20	0.6	233	9	AZ860783	2M0166M24	C 224	20	0.6	556	9	BH225736	BH225736	
C 152	20	0.6	249	5	BO740878	ap88e02.	C 225	20	0.6	557	9	AZ982835	AZ982835	
C 153	20	0.6	255	3	B3383608	B3383608	C 226	20	0.6	565	9	BZ299094	BZ299094	
C 154	20	0.6	275	1	AV267846	AV267846	C 227	20	0.6	566	10	CW844897	CW844897	GTL1434.D
C 155	20	0.6	275	1	AV267846	AV267846	C 228	20	0.6	573	1	AA522085	AA522085	
C 156	20	0.6	288	1	BG630814	CC-e8f1Ct	C 229	20	0.6	574	6	CD225102	CD225102	CCCI_38.C
C 157	20	0.6	293	2	BB364413	BB364413	C 230	20	0.6	574	9	BZ293682	BZ293682	
C 158	20	0.6	316	8	TS3905	TS3905 yb83f06.r1	C 231	20	0.6	576	2	BB021893	BB021893	
C 159	20	0.6	324	6	CD699153	EST15676	C 232	20	0.6	578	10	CZ828758	CZ828758	
C 160	20	0.6	324	8	BH814509	BH814509 SALK_0665	C 233	20	0.6	579	9	BZ949175	BZ949175	
C 161	20	0.6	328	8	CV733778	CV733778 oc48H02.y	C 234	20	0.6	580	9	AZ980451	AZ980451	
C 162	20	0.6	352	7	CN821102	HRO4427.E	C 235	20	0.6	580	9	CC775800	CC775800	CH240.130
C 163	20	0.6	368	1	AI266177	AI266177 QG87B12-x	C 236	20	0.6	581	1	AJ755911	AJ755911	
C 164	20	0.6	381	2	BF321976	BF321976 w459A10.x	C 237	20	0.6	581	8	CK733660	CK733660	oc47D04.y
C 165	20	0.6	382	6	CF373518	CF373518 CSECS088E	C 238	20	0.6	584	3	BP104182	BP104182	
C 166	20	0.6	390	5	BW536747	BW536747	C 239	20	0.6	587	8	CK730244	CK730244	OB16909.y
C 167	20	0.6	393	7	CN580229	MDfW2037f	C 240	20	0.6	588	8	CK732041	CK732041	OC25f05.y
C 168	20	0.6	397	6	CB772157	AMGNNUC:IM	C 241	20	0.6	589	2	BB640516	BB640516	





C 534	19	0.6	442	9	A0054640	A0054640 CTT-HSP-2	607	19	0.6	501	5	BX311952	BX311952
535	19	0.6	444	8	DR566736	DR566736 WS0268.B2	C 608	19	0.6	504	1	AV523816	AV523816
536	19	0.6	446	1	AW465903	AW465903 BE230021A	C 609	19	0.6	504	2	BF402435	BF402435
537	19	0.6	446	8	DR576573	DR576573 WS00743.C	C 610	19	0.6	504	3	BJ381538	BJ381538
538	19	0.6	447	1	DR586481	DR586481 WS0342.B2	C 611	19	0.6	506	5	BK474504	BK474504
C 539	19	0.6	447	11	TA230D1P	TA230D1P	C 612	19	0.6	506	9	AK391032	AK391032
C 540	19	0.6	450	9	B2158538	B2158538 CH230-244	C 613	19	0.6	507	3	BJ380941	BJ380941
C 541	19	0.6	452	2	BF407032	BF407032 UT-R-BJ2-	C 614	19	0.6	507	3	BJ382102	BJ382102
C 542	19	0.6	452	9	AQ820005	AQ820005 HS-5270.A	C 615	19	0.6	507	3	BF422579	BF422579
C 543	19	0.6	453	3	BU440205	BU440205 BU440205	C 616	19	0.6	508	3	BJ443622	BJ443622
C 544	19	0.6	454	2	BE207110	BE207110 ba10q12.Y	C 617	19	0.6	508	7	CK493883	CK493883
C 545	19	0.6	454	3	BJ443131	BJ443131 BJ443131	C 618	19	0.6	509	3	BM043320	BM043320
C 546	19	0.6	454	6	CB785072	CB785072 AMGNNUC.N	C 619	19	0.6	509	10	CE718291	CE718291
C 547	19	0.6	455	2	BE991926	BE991926 UT-M-BZ1-	C 620	19	0.6	510	3	BJ382009	BJ382009
C 548	19	0.6	455	3	BU440612	BU440612 AZ720214 RPCI-24-1	C 621	19	0.6	511	10	CL661095	CL661095
C 549	19	0.6	459	9	CE053899	CE053899 t1gr-g88-	C 622	19	0.6	512	3	BJ446579	BJ446579
C 550	19	0.6	460	2	BE206908	BE206908 ba05g11.Y	C 623	19	0.6	512	3	BJ446579	BJ446579
C 551	19	0.6	461	1	AA143625	AA143625 z065g08.T	C 624	19	0.6	512	5	BJ446579	BJ446579
C 552	19	0.6	461	1	AA143625	AA143625 z065g08.T	C 625	19	0.6	512	5	BJ446579	BJ446579
553	19	0.6	461	1	AA143625	AA143625 z065g08.T	C 626	19	0.6	512	6	CA768372	CA768372
554	19	0.6	462	1	AM740850	AM740850 uq93e08.X	C 627	19	0.6	513	1	AW249387	AW249387
555	19	0.6	462	2	BF898935	BF898935 RC4-MT013	C 628	19	0.6	513	3	BJ439229	BJ439229
C 556	19	0.6	462	3	BM942848	BM942848 UT-M-BZ1-	C 629	19	0.6	514	6	CD296394	CD296394
C 557	19	0.6	462	10	CM565514	CM565514 OA_ABA009	C 630	19	0.6	514	2	BM764576	BM764576
C 558	19	0.6	463	2	BG126428	BG126428 EST472074	C 631	19	0.6	514	7	CK991337	CK991337
C 559	19	0.6	463	3	BU445943	BU445943 BU445943	C 632	19	0.6	514	11	TA101D06P	TA101D06P
C 560	19	0.6	464	8	DN162818	DN162818 SGP268789	C 633	19	0.6	516	6	BJ442338	BJ442338
C 561	19	0.6	466	3	BJ436797	BJ436797 BJ436797	C 634	19	0.6	516	6	CD007461	CD007461
C 562	19	0.6	466	9	AQ222723	AQ222723 HS-2012.A	C 635	19	0.6	517	6	CA768445	CA768445
C 563	19	0.6	467	5	BY015974	BY015974 BY015974	C 636	19	0.6	517	6	CA768445	CA768445
C 564	19	0.6	468	8	DR564838	DR564838 WS02631.C	C 637	19	0.6	518	3	BJ442523	BJ442523
C 565	19	0.6	469	9	AQ820320	AQ820320 HS-5316.A	C 638	19	0.6	519	3	BJ444638	BJ444638
C 566	19	0.6	470	8	T21911	T21911 3919_Lambda	C 639	19	0.6	519	2	BG226324	BG226324
C 567	19	0.6	470	8	T21911	T21911 3919_Lambda	C 640	19	0.6	519	3	BP422465	BP422465
C 568	19	0.6	472	2	BE314829	BE314829 601147484	C 641	19	0.6	520	6	CF603787	CF603787
C 569	19	0.6	472	2	BE314829	BE314829 601147484	C 642	19	0.6	520	6	CF603787	CF603787
C 570	19	0.6	472	2	BE314829	BE314829 601147484	C 643	19	0.6	520	8	DR539946	DR539946
C 571	19	0.6	473	8	DR544945	DR544945 WS01045.B	C 644	19	0.6	521	3	BJ446264	BJ446264
C 572	19	0.6	474	2	BI041006	BI041006 113-NT028	C 645	19	0.6	521	10	CM446004	CM446004
C 573	19	0.6	475	9	AZ272169	AZ272169 RPCI-23-4	C 646	19	0.6	522	2	BG299088	BG299088
C 574	19	0.6	476	2	BE991683	BE991683 UT-M-BZ1-	C 647	19	0.6	522	9	AO958704	AO958704
C 575	19	0.6	476	3	BJ437568	BJ437568 BJ437568	C 648	19	0.6	522	9	AO958704	AO958704
C 576	19	0.6	477	11	CR332264	CR332264 mcl-61P3	C 649	19	0.6	523	2	BE110065	BE110065
C 577	19	0.6	477	11	CR332264	CR332264 mcl-61P3	C 650	19	0.6	523	3	CB152379	CB152379
C 578	19	0.6	477	11	TA232A12Q	TA232A12Q	C 651	19	0.6	523	7	CK225617	CK225617
C 579	19	0.6	478	8	DR806621	DR806621 2M_BRF003	C 652	19	0.6	524	9	AG255062	AG255062
C 580	19	0.6	479	10	CG992546	CG992546 CH240_152	C 653	19	0.6	524	9	AZ074207	AZ074207
C 581	19	0.6	480	7	CK534974	CK534974 rbgp00_00	C 654	19	0.6	525	5	BK645922	BK645922
C 582	19	0.6	481	1	A1510373	A1510373 mp95e12.Y	C 655	19	0.6	525	10	CE857088	CE857088
C 583	19	0.6	481	5	BX865430	BX865430 BX865430	C 656	19	0.6	525	10	CE857088	CE857088
C 584	19	0.6	482	3	BU351397	BU351397 BU351397	C 657	19	0.6	526	8	CK215834	CK215834
C 585	19	0.6	483	3	BU445152	BU445152 BU445152	C 658	19	0.6	527	10	CM287043	CM287043
C 586	19	0.6	483	3	BX881262	BX881262 BX881262	C 659	19	0.6	529	8	CK509438	CK509438
C 587	19	0.6	484	5	BQ613291	BQ613291 rD05809.Y	C 660	19	0.6	530	8	DR539918	DR539918
C 588	19	0.6	485	5	AZ296738	AZ296738 RPCI-23-1	C 661	19	0.6	531	11	CNS032KU	CNS032KU
C 589	19	0.6	486	5	BX913331	BX913331 BX913331	C 662	19	0.6	532	10	CM476688	CM476688
C 590	19	0.6	487	2	BI198872	BI198872 602759933	C 663	19	0.6	533	8	CK699694	CK699694
C 591	19	0.6	487	2	BI198872	BI198872 602759933	C 664	19	0.6	534	10	CM641834	CM641834
C 592	19	0.6	487	5	BX878084	BX878084 BX878084	C 665	19	0.6	534	3	BJ437154	BJ437154
C 593	19	0.6	487	5	BX909101	BX909101 BX909101	C 666	19	0.6	535	3	BJ442578	BJ442578
C 594	19	0.6	487	5	AZ021649	AZ021649 RPCI-23-3	C 667	19	0.6	536	2	BG047045	BG047045
C 595	19	0.6	488	3	BU381314	BU381314 BU381314	C 668	19	0.6	537	2	BE581317	BE581317
C 596	19	0.6	489	3	BU439213	BU439213 BU439213	C 669	19	0.6	537	5	BJ378637	BJ378637
C 597	19	0.6	490	7	CM438285	CM438285 BE04015B1	C 670	19	0.6	537	5	BK477495	BK477495
C 598	19	0.6	495	1	AA116463	AA116463 mp95e12.X	C 671	19	0.6	539	3	BJ438516	BJ438516
C 599	19	0.6	495	9	AO153617	AO153617 HS-2346.A	C 672	19	0.6	539	8	CK222301	CK222301
C 600	19	0.6	496	3	BU442310	BU442310 BU442310	C 673	19	0.6	541	3	BJ438578	BJ438578
C 601	19	0.6	498	8	DR557071	DR557071 WS02610.B	C 674	19	0.6	541	3	BX885283	BX885283
C 602	19	0.6	500	3	BP114396	BP114396 BP114396	C 675	19	0.6	542	3	BJ446522	BJ446522
C 603	19	0.6	500	3	BP114684	BP114684 BP114684	C 676	19	0.6	542	10	CM099409	CM099409
C 604	19	0.6	500	3	BP114685	BP114685 BP114685	C 677	19	0.6	543	3	BJ438952	BJ438952
C 605	19	0.6	500	3	BP114716	BP114716 BP114716	C 678	19	0.6	545	2	BP723252	BP723252
C 606	19	0.6	500	6	CD568290	CD568290 RK046A1H0	C 679	19	0.6	545	3	BJ371709	BJ371709

C 680	19	0.6	545	9	BZ212961	BZ212961 CH230-342	753	19	0.6	591	7	CK534355	CK534355 rwwb0.00
C 681	19	0.6	546	10	C2812620	C2812620 OC_Ba018	C 754	19	0.6	592	2	BG815534	BG815534 dad6803.
C 682	19	0.6	547	10	B1301062	B1301062 UI-R-CV2-	C 755	19	0.6	592	2	B435364	B435364 B435364
C 683	19	0.6	547	9	AZ764151	AZ764151 1M0559N20	C 756	19	0.6	592	5	B0521154	B0521154 N19C_n109
C 684	19	0.6	548	1	AL387243	AL387243 MeBC41C07	C 757	19	0.6	593	2	BG047109	BG047109 baa76102.
C 685	19	0.6	548	1	AM423908	AM423908 sh57E08.Y	C 758	19	0.6	593	3	BM308006	BM308006 bka40f06.
C 686	19	0.6	548	7	CR551424	CR551424 CR551424	C 759	19	0.6	594	6	CA768485	CA768485 ssa1p1C15
C 687	19	0.6	549	7	CR551424	CR551424 CR551424	C 760	19	0.6	594	5	BX304856	BX304856 BX304856
C 688	19	0.6	550	11	DR140386	DR140386 Oryzias 1	C 761	19	0.6	595	3	B1383602	B1383602 B1383602
C 689	19	0.6	552	10	CM485250	CM485250 fdbb001f2	C 762	19	0.6	595	10	CM349401	CM349401 fdbb001f0
C 690	19	0.6	554	3	B0383700	B0383700 B0383700	C 763	19	0.6	595	11	DE040648	DE040648 Brenchiof
C 691	19	0.6	554	3	B0630245	B0630245 sakp9G05.	C 764	19	0.6	596	3	B0383496	B0383496 B0383496
C 692	19	0.6	556	5	BM528831	BM528831 sakp9G05.	C 765	19	0.6	596	7	CJ417931	CJ417931 A0722909
C 693	19	0.6	556	5	B0637599	B0637599 hel2B08.Y	C 766	19	0.6	596	9	A0722909	A0722909 HS_5309_A
C 694	19	0.6	556	7	CK536785	CK536785 rwwb0.00	C 767	19	0.6	597	3	B1378587	B1378587 B1378587
C 695	19	0.6	556	9	CE262345	CE262345 tigt-g88-	C 768	19	0.6	598	5	BX315421	BX315421 BX315421
C 696	19	0.6	557	3	B0444030	B0444030 B0444030	C 769	19	0.6	598	5	BX861372	BX861372 BX861372
C 697	19	0.6	557	5	BX304857	BX304857 BX304857	C 770	19	0.6	598	5	BX912644	BX912644 BX912644
C 698	19	0.6	557	8	DN165680	DN165680 SGP275253	C 771	19	0.6	598	6	CA162195	CA162195 SC08R2303
C 699	19	0.6	557	8	AZ889361	AZ889361 RPT-24-1	C 772	19	0.6	598	7	CK534393	CK534393 rwwb0.00
C 700	19	0.6	559	1	AM019857	AM019857 fd57G06.X	C 773	19	0.6	598	8	CK693547	CK693547 ydC83A09.
C 701	19	0.6	559	7	CM075137	CM075137 EC1CBA002	C 774	19	0.6	600	3	B1987071	B1987071 3191-40_M
C 702	19	0.6	560	8	CV889994	CV889994 41A1586_B	C 775	19	0.6	600	9	A2835957	A2835957 2M0130P20
C 703	19	0.6	560	9	AZ271596	AZ271596 RPT-23-1	C 776	19	0.6	601	1	AM027901	AM027901 AM027901
C 704	19	0.6	560	9	BH873279	BH873279 hp43G03.b	C 777	19	0.6	602	8	CK193949	CK193949 25-B02357
C 705	19	0.6	561	9	BH327557	BH327557 CH230-80L	C 778	19	0.6	603	2	B1198736	B1198736 602759748
C 706	19	0.6	562	8	CK215179	CK215179 MNS22917	C 779	19	0.6	603	2	B2887048	B2887048 CK240_189
C 707	19	0.6	563	5	BM888281	BM888281 BM888281	C 780	19	0.6	604	7	CK716729	CK716729 16450_Swo
C 708	19	0.6	563	8	DR448999	DR448999 WS0062.B2	C 781	19	0.6	605	2	BF296000	BF296000 032BDF12
C 709	19	0.6	564	6	CD009721	CD009721 VVB059D12	C 782	19	0.6	605	2	BF297106	BF297106 047PB812
C 710	19	0.6	564	6	CD510832	CD510832 onerfxy00	C 783	19	0.6	606	1	AM263637	AM263637 xm81b12.x
C 711	19	0.6	565	3	BJ446382	BJ446382 BJ446382	C 784	19	0.6	606	3	BJ041429	BJ041429 B0041429
C 712	19	0.6	565	7	CV046303	CV046303 RST_8010	C 785	19	0.6	607	9	A0552773	A0552773 RPT-11-3
C 713	19	0.6	566	3	B1855827	B1855827 603382276	C 786	19	0.6	610	9	A0523119	A0523119 HS_5225_A
C 714	19	0.6	566	3	BH453773	BH453773 BOH1H93TR	C 787	19	0.6	611	1	AL786354	AL786354 AL786354
C 715	19	0.6	567	5	BJ398523	BJ398523 BJ398523	C 788	19	0.6	611	8	CK888756	CK888756 SGP160753
C 716	19	0.6	567	5	BX315420	BX315420 BX315420	C 789	19	0.6	611	7	DR109168	DR109168 USDA-FP.1
C 717	19	0.6	568	3	BJ441773	BJ441773 BJ441773	C 790	19	0.6	612	2	BE346790	BE346790 B31C02.Y
C 718	19	0.6	568	3	BM102179	BM102179 fvi4a11.X	C 791	19	0.6	612	10	CZ664314	CZ664314 OM_Ba021
C 719	19	0.6	570	3	B1501908	B1501908 tm06f08.Y	C 792	19	0.6	613	11	DE038834	DE038834 Brenchiof
C 720	19	0.6	570	8	DR017499	DR017499 STRS1_16-	C 793	19	0.6	614	3	B1871167	B1871167 60335056
C 721	19	0.6	571	3	BP257239	BP257239 BP257239	C 794	19	0.6	615	5	B0379464	B0379464 603612195
C 722	19	0.6	571	6	CB501492	CB501492 ssa1ga504	C 795	19	0.6	615	7	CK225711	CK225711 704377058
C 723	19	0.6	571	9	AZ491333	AZ491333 1M0324P16	C 796	19	0.6	615	10	CM169909	CM169909 104_580_1
C 724	19	0.6	572	2	B1196895	B1196895 602756042	C 797	19	0.6	616	5	B0383652	B0383652 N19C-tm02
C 725	19	0.6	572	11	DR4U16T	DR4U16T Dantio rex	C 798	19	0.6	616	5	BE517267	BE517267 BOMR109TR
C 726	19	0.6	574	3	B0446758	B0446758 B0446758	C 799	19	0.6	619	3	B0381554	B0381554 B0381554
C 727	19	0.6	575	2	BF520075	BF520075 EST457543	C 800	19	0.6	619	3	CR339582	CR339582 m6a1-71E7
C 728	19	0.6	575	9	AZ981550	AZ981550 2M0262G03	C 801	19	0.6	619	11	FR0005517	FR0005517 F_rubripes
C 729	19	0.6	577	8	CV993112	CV993112 IPGFR2_1	C 802	19	0.6	620	1	B0382952	B0382952 B182952
C 730	19	0.6	579	9	BZ561221	BZ561221 PAC82-14	C 803	19	0.6	621	1	AM027370	AM027370 AM027370
C 731	19	0.6	580	3	B1921317	B1921317 EST541220	C 804	19	0.6	621	2	BG933813	BG933813 SK1-0085
C 732	19	0.6	580	3	BM042038	BM042038 603616036	C 805	19	0.6	622	8	DN165414	DN165414 SGP274985
C 733	19	0.6	580	9	BH447662	BH447662 BCGP877TR	C 806	19	0.6	622	8	BS517806	BS517806 BS517806
C 734	19	0.6	581	2	BG202714	BG202714 RST22080	C 807	19	0.6	623	7	CK961454	CK961454 1402545_B
C 735	19	0.6	581	2	BP214435	BP214435 BP214435	C 808	19	0.6	623	7	AZ709950	AZ709950 RPT-24-1
C 736	19	0.6	581	3	BP215536	BP215536 BP215536	C 809	19	0.6	623	9	BH168513	BH168513 VV_SBA000
C 737	19	0.6	582	3	BP214297	BP214297 BP214297	C 810	19	0.6	624	3	B0440119	B0440119 B0440119
C 738	19	0.6	582	3	BP222685	BP222685 BP222685	C 811	19	0.6	625	6	CA767825	CA767825 ssa1e1a00
C 739	19	0.6	582	3	BP293425	BP293425 BP293425	C 812	19	0.6	625	6	CA768179	CA768179 ssa1imga00
C 740	19	0.6	582	3	BP294277	BP294277 BP294277	C 813	19	0.6	625	6	AZ718349	AZ718349 RPT-24-1
C 741	19	0.6	582	3	BP294281	BP294281 BP294281	C 814	19	0.6	626	9	BH168239	BH168239 B0168239
C 742	19	0.6	582	3	BP376655	BP376655 BP376655	C 815	19	0.6	626	9	BH168513	BH168513 VV_SBA000
C 743	19	0.6	583	1	AU262739	AU262739 AU262739	C 816	19	0.6	627	5	CA045007	CA045007 ssa1p1Ind5
C 744	19	0.6	583	8	BP215710	BP215710 BP215710	C 817	19	0.6	628	3	B0385399	B0385399 B0385399
C 745	19	0.6	585	8	DR545737	DR545737 WS0011.B2	C 818	19	0.6	628	3	B0440733	B0440733 B0440733
C 746	19	0.6	587	3	BJ381331	BJ381331 BJ381331	C 819	19	0.6	628	5	BX316959	BX316959 BX316959
C 747	19	0.6	587	3	BJ437182	BJ437182 BJ437182	C 820	19	0.6	628	5	BZ126781	BZ126781 CH230-309
C 748	19	0.6	588	5	B0083790	B0083790 sarr31a01.	C 821	19	0.6	629	3	B0608089	B0608089 B0608089
C 749	19	0.6	588	5	B0355579	B0355579 B0355579	C 822	19	0.6	629	3	B0379241	B0379241 B0379241
C 750	19	0.6	588	6	CB440909	CB440909 691222_MA	C 823	19	0.6	629	3	B0625121	B0625121 B0625121
C 751	19	0.6	589	6	CF125591	CF125591 UI-HR-EL0	C 824	19	0.6	629	10	CG798678	CG798678 ZMMBBD342
C 752	19	0.6	590	11	DR13B1T	DR13B1T Dantio rex	C 825	19	0.6	630	11	DE090220	DE090220 Oryzias 1



C 826	19	0.6	631	7	CV046305	CV046305 EST 8012	C 899	19	0.6	665	7	CO257262	CO257262 WS0085.B2
C 827	19	0.6	631	10	AC340743	AC340743 Lotus CCR	C 900	19	0.6	666	3	B0378796	B0378796
C 828	19	0.6	633	5	CA037935	CA037935 sea11na01	C 901	19	0.6	666	6	CD814557	CD814557 BN15.023H
C 829	19	0.6	634	2	BF269910	BF269910 044PDD08	C 902	19	0.6	666	8	CD814557	CD814557 BN15.023H
C 830	19	0.6	636	5	BX856958	BX856958 BX856958	C 903	19	0.6	666	6	CD814557	CD814557 BN15.023H
C 831	19	0.6	637	7	CK225647	CK225647 704268151	C 904	19	0.6	667	11	CR232846	CR232846 Forward s
C 832	19	0.6	638	1	AL895643	AL895643 AL895643	C 905	19	0.6	667	11	CR277407	CR277407 Forward s
C 833	19	0.6	638	2	BF297822	BF297822 056PDD10	C 906	19	0.6	668	7	CR372282	CR372282
C 834	19	0.6	639	5	BX869740	BX869740 BX869740	C 907	19	0.6	669	3	B0384573	B0384573
C 835	19	0.6	639	9	BH256749	BH256749 CH230-243	C 908	19	0.6	669	6	CD511102	CD511102 oneErfy00
C 836	19	0.6	640	2	BF296061	BF296061 030PBG01	C 909	19	0.6	669	10	CR332869	CR332869
C 837	19	0.6	640	5	BUS73145	BUS73145 PA_Ea000	C 910	19	0.6	670	6	CA361761	CA361761 635651 NC
C 838	19	0.6	640	6	CA363170	CA363170 637671 NC	C 911	19	0.6	670	6	CB925035	CB925035
C 839	19	0.6	641	6	CB377311	CB377311 CmaB1_36	C 912	19	0.6	671	3	B0381149	B0381149
C 840	19	0.6	641	10	CB692050	CB692050 t1gr-g88-	C 913	19	0.6	672	5	BX867950	BX867950
C 841	19	0.6	642	1	AL641723	AL641723 AL641723	C 914	19	0.6	672	10	CL318100	CL318100
C 842	19	0.6	642	3	B0405405	B0405405 B0405405	C 915	19	0.6	673	3	B0378456	B0378456
C 843	19	0.6	642	7	CV029287	CV029287 8011_Full1	C 916	19	0.6	673	3	B0384065	B0384065
C 844	19	0.6	643	2	BF297337	BF297337 050PDD02	C 917	19	0.6	674	8	DR552513	DR552513
C 845	19	0.6	643	3	B0441266	B0441266 BX441266	C 918	19	0.6	674	8	DR552513	DR552513
C 846	19	0.6	643	5	BX316958	BX316958 BX316958	C 919	19	0.6	674	8	BX186586	BX186586
C 847	19	0.6	645	1	AW348152	AW348152 GM210001A	C 920	19	0.6	675	5	BX863222	BX863222
C 848	19	0.6	645	3	B0911906	B0911906 B0911906	C 921	19	0.6	675	5	B0601934	B0601934
C 849	19	0.6	645	10	CM166128	CM166128 104_574_1	C 922	19	0.6	676	10	CM286496	CM286496
C 850	19	0.6	645	11	DE028101	DE028101 Branch108	C 923	19	0.6	677	7	CM675929	CM675929
C 851	19	0.6	647	2	BF297165	BF297165 048PDA11	C 924	19	0.6	678	7	CK559907	CK559907
C 852	19	0.6	647	3	B0437409	B0437409 B0437409	C 925	19	0.6	679	9	BH965026	BH965026
C 853	19	0.6	648	2	BF296658	BF296658 040PDD02	C 926	19	0.6	681	3	B0373057	B0373057
C 854	19	0.6	648	2	BF297726	BF297726 055PDD06	C 927	19	0.6	681	3	B0408091	B0408091
C 855	19	0.6	648	3	B0378497	B0378497 B0378497	C 928	19	0.6	681	8	DR429252	DR429252
C 856	19	0.6	650	2	BF113497	BF113497 B8T441087	C 929	19	0.6	681	10	AG276945	AG276945
C 857	19	0.6	650	6	CD595531	CD595531 RK097A2C0	C 930	19	0.6	682	3	B0528261	B0528261
C 858	19	0.6	650	6	CD595647	CD595647 RK097A4C0	C 931	19	0.6	682	6	CD510873	CD510873
C 859	19	0.6	650	7	CK243455	CK243455 B8T727102	C 932	19	0.6	682	7	CR789861	CR789861
C 860	19	0.6	650	9	AQ898457	AQ898457 HS_3135_B	C 933	19	0.6	682	8	CK079050	CK079050
C 861	19	0.6	650	9	CE141998	CE141998 t1gr-g88-	C 934	19	0.6	683	10	CM532704	CM532704
C 862	19	0.6	650	10	BX174747	BX174747 Danilo rex	C 935	19	0.6	683	3	B0385279	B0385279
C 863	19	0.6	651	6	CB455691	CB455691 727754_MA	C 936	19	0.6	684	3	B0358242	B0358242
C 864	19	0.6	651	6	CD415012	CD415012 Gm_CK5042	C 937	19	0.6	684	7	CK225713	CK225713
C 865	19	0.6	651	8	DN091459	DN091459 JGI_CABE4	C 938	19	0.6	685	9	AQ419762	AQ419762
C 866	19	0.6	652	6	CF808984	CF808984 P8B041X1	C 939	19	0.6	686	3	B0380503	B0380503
C 867	19	0.6	652	7	CM074357	CM074357 EC0CBA005	C 940	19	0.6	686	6	CB833984	CB833984
C 868	19	0.6	652	10	CE441108	CE441108 t1gr-g88-	C 941	19	0.6	686	9	CE106835	CE106835
C 869	19	0.6	653	1	AL868283	AL868283 AL868283	C 942	19	0.6	687	8	DR549055	DR549055
C 870	19	0.6	653	2	BE795889	BE795889 601591238	C 943	19	0.6	687	9	CE046764	CE046764
C 871	19	0.6	655	3	BF298808	BF298808 021PDD05	C 944	19	0.6	689	2	BE794870	BE794870
C 872	19	0.6	655	3	B0373645	B0373645 B0373645	C 945	19	0.6	689	5	B0342534	B0342534
C 873	19	0.6	655	10	CM356722	CM356722 feb001f0	C 946	19	0.6	689	9	BH067015	BH067015
C 874	19	0.6	655	10	AG111895	AG111895 Pan t1gr01	C 947	19	0.6	690	6	CA384098	CA384098
C 875	19	0.6	655	10	CL919527	CL919527 CA_Aba002	C 948	19	0.6	690	11	CR882501	CR882501
C 876	19	0.6	656	5	B0708132	B0708132 UI-M_FCO-	C 949	19	0.6	691	9	BZ012158	BZ012158
C 877	19	0.6	656	10	CM296077	CM296077 104_777_1	C 950	19	0.6	691	9	CC408042	CC408042
C 878	19	0.6	657	3	B0378935	B0378935 B0378935	C 951	19	0.6	693	9	AZ337730	AZ337730
C 879	19	0.6	657	3	B0383584	B0383584 B0383584	C 952	19	0.6	693	3	B0383155	B0383155
C 880	19	0.6	657	8	CK690110	CK690110 ydc77h05.	C 953	19	0.6	695	3	B0385722	B0385722
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DEFINITION Homo sapiens mRNA; cDNA DKFPZ686K087 (from clone DKFPZ686K087).  
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VERSION CR749572.1 GI:51476810  
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1 (bases 1 to 5829)  
Pousette, A., Albert, R., Moosmayer, P., Schnupp, I., Wellenreuther, R.,  
Menes, H.W., Weil, B., Amid, C., Osanger, A., Fodor, G., Han, M. and  
Wiemann, S.  
The German cDNA Consortium  
Direct Submission  
Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuharberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFPZ686K087) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering:  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFPZ686K087>  
Further information about the clone and the sequencing project is  
available at <http://mips.gsf.de/projects/cdna/>.

## FEATURES

## SOURCE

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Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarwal,A.,  
Todd,M.A., Tanendau,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Perliera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.D.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PubMed 14671302

REFERENCE 2 (bases 1 to 1665)  
 AUTHORS Clark, A.G., Glanowski, S., Nijelson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeleo, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smirsky, J.O.,  
 Adams, M.D. and Cargill, M.  
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 Rockville, MD 20850, USA  
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 QY 1380 CACATCTTTGCTGATTAATACAGAGAGTCTACTTTAGTCCAGAACTTCCCTCTGTTGA 1439  
 DB 459 CACATCTTTGCTGATTAATACAGAGAGTCTACTTTAGTCCAGAACTTCCCTCTGTTGA 518  
 QY 1440 ACCCCAGCTTGAAGAGTGAAGGAGCAGAGCATGGTCTACTGACACTTCTTGGTCTCC 1499  
 DB 519 ACCCCAGCTTGAAGAGTGAAGGAGCAGAGCATGGTCTACTGACACTTCTTGGTCTCC 578  
 QY 1500 ACCTGCTATGAGCTCTACTCTCTCTGTGAGAGCTTCCACTTTCTTTATGCAATCAAGCAT 1559  
 DB 579 ACCTGCTATGAGCTCTACTCTCTCTGTGAGAGCTTCCACTTTCTTTATGCAATCAAGCAT 638  
 QY 1560 CTTCCTGCTGACTGATCAAGGACCAAGATACAAATGACATGACGACCAAGAAATGCTAGT 1619  
 DB 639 CTTCCTGCTGACTGATCAAGGACCAAGATACAAATGACATGACGACCAAGAAATGCTAGT 698  
 QY 1620 ACCAGAGCTTCAACATCCCAACCAAGTATTTCTGCAATCAGCCAACTGGCTCTGGAGAT 1679  
 DB 699 ACCAGAGCTTCAACATCCCAACCAAGTATTTCTGCAATCAGCCAACTGGCTCTGGAGAT 758  
 QY 1680 TTCAATCCACTGATCTTTCAGATGACAGCCGATCAAGTGAAGTGGCGAAAGATATGAT 1739  
 DB 759 TTCAATCCACTGATCTTTCAGATGACAGCCGATCAAGTGAAGTGGCGAAAGATATGAT 818  
 QY 1740 CAGACACCTAGATGAATGATCTGTGACACTCTGCGCCATCTGAGGTACCGAGACT 1799  
 DB 819 CAGACACCTAGATGAATGATCTGTGACACTCTGCGCCATCTGAGGTACCGAGACT 878  
 QY 1800 CAGCAATATGTTTCTGTCCAGATCAATTTCTTGAGAGATACCACTCTGTCTCAGCTTT 1859

DB 879 CAGCAATATGTTTCTGTCCAGATCAATTTCTTGAGAGATACCACTCTGTCTCAGCTTT 938  
 QY 1860 ACGATATATCACCACTAGTCTTATGACCATTTGCCCGGAGGCGAGAGCTGTATGTTT 1919  
 DB 939 ACGATATATCACCACTAGTCTTATGACCATTTGCCCGGAGGCGAGAGCTGTATGTTT 998  
 QY 1920 CTTGAGTGGGTGTGTTGCTACATAGCGCTTCCAGAGAGCTGTTCACAGAGCTCTCT 1979  
 DB 999 CTTGAGTGGGTGTGTTGCTACATAGCGCTTCCAGAGAGCTGTTCACAGAGCTCTCT 1058  
 QY 1980 GAGATACCGAGCTGTGAGCAACAATTCACACAGCTGTGTTCCATATCTACATCCAA 2039  
 DB 1059 GAGATACCGAGCTGTGAGCAACAATTCACACAGCTGTGTTCCATATCTACATCCAA 1118  
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 QY 2100 TAGCAAAATGAAAGTTTGCTAGTCTGTGCGGATATTAACCTCAAGAGCTGTGCAAGGGGT 2159  
 DB 1179 TAGCAAAATGAAAGTTTGCTAGTCTGTGCGGATATTAACCTCAAGAGCTGTGCAAGGGGT 1238  
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 QY 2220 TCTCAACATTGAACCACTGATATCAAGCAGATCCCTGTGCAAGTTCTGTGCGCGGAAAT 2279  
 DB 1299 TCTCAACATTGAACCACTGATATCAAGCAGATCCCTGTGCAAGTTCTGTGCGCGGAAAT 1358  
 QY 2280 TGCCCAATGTGTAAGAACGAAACGAACTGAGAAAGCGAGTGTGCTGCAAAACAGATA 2339  
 DB 1359 TGCCCAATGTGTAAGAACGAAACGAACTGAGAAAGCGAGTGTGCTGCAAAACAGATA 1418  
 QY 2340 TGACAGCCAGGAGAGCTGTGACGCTGTGAAACAGGCTCTGTGAGCCTGTGCAACAAAG 2399  
 DB 1419 TGACAGCCAGGAGAGCTGTGACGCTGTGAAACAGGCTCTGTGAGCCTGTGCAACAAAG 1478  
 QY 2400 ATGGAAGTCTCTCCAGGAAAGGAGCTCCATGCAAGTTGCGCAATCTCTGAAATCA 2459  
 DB 1479 ATGGAAGTCTCTCCAGGAAAGGAGCTCCATGCAAGTTGCGCAATCTCTGAAATCA 1538  
 QY 2460 AGCATACAAACTAGTGTAAAGTTCCAAATCAACAAATTAACAAGATATCAGTAA 2519  
 DB 1539 AGCATACAAACTAGTGTAAAGTTCCAAATCAACAAATTAACAAGATATCAGTAA 1598  
 QY 2520 AAGAAATTCGAATTTACTGACCGTGAATATGAAGAAATTTAAGCATCAAGATTGGAAAG 2579  
 DB 1599 AAGAAATTCGAATTTACTGACCGTGAATATGAAGAAATTTAAGCATCAAGATTGGAAAG 1658  
 QY 2580 AAATTTAA 2586  
 DB 1659 AAATTTAA 1665  
 RESULT 3  
 EXS10244  
 LOCUS  
 DEFINITION DKF2P686P2496.t1 686 (synonym: h1cc3) Homo sapiens cDNA clone  
 ACCESSION BX510244  
 VERSION BX510244.1 GI:32050551  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo  
 REFERENCE 1 (bases 1 to 690)  
 AUTHORS Poulet, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
 Mewes, H.W., Well, B., Amlid, C., Oesanger, A., Fobo, G., Han, M. and  
 Wiemann, S.

TITLE EST (Pouska, A., Albert, R., Moosmayer, P., Schupp, I.,  
Wellenreuther, R., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MTPS

MTPS  
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.  
No at sequence available.  
This clone (DKFZ686P2496) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

## FEATURES

source  
1. 690  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZ686P2496"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlc3)"  
/note="Vector: pTriplEx2; Site\_1: SfiI; Site\_2: SfiI; B;  
cDNA-collection"

## ORIGIN

Query Match 19.0%; Score 634; DB 5; Length 690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TAAACCAAGAGGTATCTCTCAATCATCTGTGATCATATATATATTTTTCACATTC 60  
DB 57 TAAACCAAGAGGTATCTCTCAATCATCTGTGATCATATATATATTTTTCACATTC 116  
QY 61 TGTACTTTTATATGAGATTGAGGTTGCTGCTGATTTGATACAAATTAACCAATGC 120  
DB 117 TGTACTTTTATATGAGATTGAGGTTGCTGCTGATTTGATACAAATTAACCAATGC 176  
QY 121 AAAAGCCAGATGTATTTGAACTGAAAGAGCTATTTTGTGTTTGTGATTTTTCCTCA 180  
DB 177 AAAAGCCAGATGTATTTGAACTGAAAGAGCTATTTTGTGTTTGTGATTTTTCCTCA 236  
QY 181 AGTTCAAGAACCAAGATATCTCCATTAACATATACATTTGAAACTTAAGACATAGA 240  
DB 237 AGTTCAAGAACCAAGATATCTCCATTAACATATACATTTGAAACTTAAGACATAGA 296  
QY 241 CAATCCCCCAAGAAATGAAACCACTGAAAGTACTGAAAAATGTACAAATGTCAACTAT 300  
DB 297 CAATCCCCCAAGAAATGAAACCACTGAAAGTACTGAAAAATGTACAAATGTCAACTAT 356  
QY 301 GAGAGCAATATTTGATTTGGCAAGATGGAACAAAAGATCCGCAATTTTCCCAAGGG 360  
DB 357 GAGAGCAATATTTGATTTGGCAAGATGGAACAAAAGATCCGCAATTTTCCCAAGGG 416  
QY 361 GGTAAAGTCTGTCCACAGAAATCATGAAACAGATTTTGAACAGTCTTCAAGCTATTA 420  
DB 417 GGTAAAGTCTGTCCACAGAAATCATGAAACAGATTTTGAACAGTCTTCAAGCTATTA 476  
QY 421 TAGATTGAGAGTGTCTCAGAGCAATATGGAAGCAATATCGGATCTTTCTGGATGGCAT 480  
DB 477 TAGATTGAGAGTGTCTCAGAGCAATATGGAAGCAATATCGGATCTTTCTGGATGGCAT 536  
QY 481 CCTGACACAGGGGATATCAGAGCTGGGTCAAGCATCTGCACAGAGACCTTCTGCTT 540  
DB 537 CCTGACACAGGGGATATCAGAGCTGGGTCAAGCATCTGCACAGAGACCTTCTGCTT 596  
QY 541 CTTTGACATTTGAAAAAATCTTCAAGATTTCCAGAGCACTTGATCTTCTCCAGAGAG 600  
DB 597 CTTTGACATTTGAAAAAATCTTCAAGATTTCCAGAGCACTTGATCTTCTCCAGAGAG 656

QY 601 AATAAACAGAGAGTTCCTGACAGAAAGAT 634  
DB 657 AATAAACAGAGAGTTCCTGACAGAAAGAT 690

RESULT 4  
B0639265  
DEFINITION  
LOCUS  
B0639265  
hd33d04.y1 Human Retina cDNA (un-normalized, unamplified): hd/he  
Homo sapiens CDNA clone hd33d04 5', mRNA sequence.  
B0639265  
ACCESSION  
B0639265  
KEYWORDS  
SOURCE  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT  
1 (bases 1 to 626)  
Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behl, A.,  
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
Expressed sequence tag analysis of human retina for the NEIBank  
Project: Retbindin, an abundant, novel retinal CDNA and alternative  
splicing of other retina-preferred gene transcripts  
Mol. Vis. 8 (4), 196-204 (2002)  
12107411  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: gwaem@helix.nih.gov  
Plate: 33 row: d column: 04  
Seq primer: M13P1 reverse primer (ABI).  
Location/Qualifiers

## FEATURES

source  
1. 626  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="hd33d04"  
/tissue="Retina"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retina cDNA (un-normalized,  
unamplified): hd/he"  
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGATGAGTTCAGATCCGACGGCCGCTT]5-3'. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 18.8%; Score 626; DB 5; Length 626;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 968 ACCAGAGCTGACAGAAAGTCCCACTTCAGATGCAAAAGTATTTAAGAACTTCGAG 1027  
DB 1 ACCAGAGCTGACAGAAAGTCCCACTTCAGATGCAAAAGTATTTAAGAACTTCGAG 60  
QY 1028 GATTCAAAAAATTCATGTGTAGATTAGCAAGAAAGAAAGATGAGCTCAAGCT 1087  
DB 61 GATTCAAAAAATTCATGTGTAGATTAGCAAGAAAGAAAGATGAGCTCAAGCT 120

QY 1088 CCAGAGATGCACTTACGGCCATCTTTAAGAGACAGTGCAGAGCAAAAAGCCCTG 1147  
DB 121 CCAGAGATGCACTTACGGCCATCTTTAAGAGACAGTGCAGAGCAAAAAGCCCTG 180  
QY 1148 CAAGTACCTCTGCTCTTTTGTTCACAAATTTGAAGTGAAGTCTATCATGAA 1207  
DB 181 CAAGTACCTCTGCTCTTTTGTTCACAAATTTGAAGTGAAGTCTATCATGAA 240  
QY 1208 CCATGAGAGAGAGACAGCAACCAAAATCTATCTACAGCTACAGCTCCAAAAGCTGA 1267  
DB 241 CCATGAGAGAGAGACAGCAACCAAAATCTATCTACAGCTACAGCTCCAAAAGCTGA 300  
QY 1268 TCAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGAGCAATTCAGTCACTGATG 1327  
DB 301 TCAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGAGCAATTCAGTCACTGATG 360  
QY 1338 AAATGCTGATCACTGCGCAGCTTTGTCTGACAGCCCAATCAGAGCTGCCACATCTT 1387  
DB 361 AAATGCTGATCACTGCGCAGCTTTGTCTGACAGCCCAATCAGAGCTGCCACATCTT 420  
QY 1388 TTGCTGTTATACAGAGATGCTACTTTGATGTCAGAACTTCTCTGTTGAACCCAGC 1447  
DB 421 TTGCTGTTATACAGAGATGCTACTTTGATGTCAGAACTTCTCTGTTGAACCCAGC 480  
QY 1448 TTGAGACAGTGAAGAGAGAGAGATGCTACTGACACCTTTGTCTCCAGCTGCTA 1507  
DB 481 TTGAGACAGTGAAGAGAGAGATGCTACTGACACCTTTGTCTCCAGCTGCTA 540  
QY 1508 TGGCTCTACCTCCCTGTGACAGAGCTCCACCTTTTATGAGCATCAAGCATCTTCTGTC 1567  
DB 541 TGGCTCTACCTCCCTGTGACAGAGCTCCACCTTTTATGAGCATCAAGCATCTTCTGTC 600  
QY 1568 TGACTGATTAAGGACACACAGATACA 1593  
DB 601 TGACTGATTAAGGACACACAGATACA 626

RESULT 5  
BM690735 675 bp mRNA linear EST 28-FEB-2002  
LOCUS UI-E-CK0-sav-c-12-0-UI.r1 UI-E-CK0 Homo sapiens cDNA clone  
DEFINITION UI-E-CK0-sav-c-12-0-UI 5', mRNA sequence.  
ACCESSION BM690735  
VERSION BM690735.1 GI:19003993  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 675)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
JOURNAL discovery  
PUBMED Genome Res. 6 (9), 791-806 (1996)  
COMMENT 8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: benito-soares@iowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resegen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..675

FEATURES  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-CK0-sav-c-12-0-UI"  
/tissue\_type="Retina Foveal and Macular"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CK0"  
/note="Organ: eye; Vector: pTR73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-CK0 is a cDNA library containing the following  
tissue(s): Retina Foveal and Macular. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pTR73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is CTCG.  
This library was created for the program, Gene Discovery  
in the Visual System, supported by National Eye Institute  
(NEI)."

## ORIGIN

Query Match 16.8%; Score 558; DB 3; Length 675;  
Best Local Similarity 100.0%; Pred. No. 2.0e-287;  
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2773 AAAAAGACCTTACTTATTTAAACCCCAATGCAATCAGCGAAATATTTTACTA 2832  
DB 52 AAAAAGACCTTACTTATTTAAACCCCAATGCAATCAGCGAAATATTTTACTA 111  
QY 2833 TTTTGAATGATGATCAAAATGATCATAGCCAGGTTTGTCTTCCACTTCCCTGAAAAT 2892  
DB 112 TTTTGAATGATGATCAAAATGATCATAGCCAGGTTTGTCTTCCACTTCCCTGAAAAT 171  
QY 2893 TTACTCAGATCACTTTTGAACAAGCAATGCTTCTTATGAGGACGAAACAATTT 2952  
DB 172 TTACTCAGATCACTTTTGAACAAGCAATGCTTCTTATGTTTGAAGGACGAAACAATTT 231  
QY 2953 ATTGGGAAGCAAACTCTTTATGCTAGAAAGTCACTTTAAAGATGACTCTTACGAG 3012  
DB 232 ATTGGGAAGCAAACTCTTTATGCTAGAAAGTCACTTTAAAGATGACTCTTACGAG 291  
QY 3013 GGAAGATGCAAGTCTCTTAAACGATGATGATGATGATGATGATGATGATGATGATG 3072  
DB 292 GGAAGATGCAAGTCTCTTAAACGATGATGATGATGATGATGATGATGATGATGATGATG 351  
QY 3073 TATATAGCTCAGACGTCGATTAACCAAACTCAGATTAAGTATTAAGGACA 3132  
DB 352 TATATAGCTCAGACGTCGATTAACCAAACTCAGATTAAGTATTAAGGACA 411  
QY 3133 CTAGTTTATAGCAACTACTGCTTACATAGTACTGTTTGTGCGCAATATCTTTGA 3192  
DB 412 CTAGTTTATAGCAACTACTGCTTACATAGTACTGTTTGTGCGCAATATCTTTGA 471  
QY 3193 ATTGTTCTTTAAAGAACTGAGGTTCCAGATACATACATGAAATATCTTACTTTTC 3252  
DB 472 ATTGTTCTTTAAAGAACTGAGGTTCCAGATACATACATGAAATATCTTACTTTTC 531  
QY 3253 TTGTTACTACCAAAAGCTATTTTAAAGAGATGCTATGTTGGAGAAAGGGAAGTTGTA 3312  
DB 532 TTGTTACTACCAAAAGCTATTTTAAAGAGATGCTATGTTGGAGAAAGGGAAGTTGTA 591  
QY 3313 CTATATGACATATCAAT 3330  
DB 592 CTATATGACATATCAAT 609

RESULT 6  
BM695987

LOCUS BM695987 633 bp mRNA 1linear EST 28-FEB-2002  
 DEFINITION UI-E-CL1-afa-m-11-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone  
 ACCESSION UI-E-CL1-afa-m-11-0-UI.5, mRNA sequence.  
 VERSION BM695987  
 KEYWORDS EST.  
 SOURCE GI:19009245  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 633)  
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 PUBMED 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@iowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse  
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 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
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 /dev\_stage="adult"  
 /lab\_host="PH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_1ib="UI-E-CL1"  
 /note="Organ: eye; Vector: pRT3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-E-CL1 is a normalized cDNA library containing the  
 following tissue(s): retina. The library was constructed  
 according to Ronaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pRT3-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is CCGCG. This library was  
 created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 14.4%; Score 480; DB 3; Length 633;  
 Best Local Similarity 99.5%; Pred. No. 2,1e-245;  
 Matches 630; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2529 TGAATTACTGACCGTGAATATGAGAAATTTAAACATCAAGATTGGAGGAATTTAAA 2588  
 DB 1 TGAATTACTGACCGTGAATATGAGAAATTTAAACATCAAGATTGGAGGAATTTAAA 60  
 QY 2589 ACTGAAAAGTATACATTAATCACTTAGGCTATCGAAGAGATGATTTGCCCTTCTCAAG 2648  
 DB 61 ACTGAAAAGTATCAATTAATCACTTAGGCTATCGAAGAGATGATTTGCCCTTCTCAAG 120  
 QY 2649 AAAATGAGACAGCATATTCATGGGTCAATCAAAATCCAGACATACAGTCAACACTGAGA 2708  
 DB 121 AAAATGAGACAGCATATTCATGGGTCAATCAAAATCCAGACATACAGTCAACACTGAGA 180

QY 2709 ATCAGACACACCATATTTTCAATATAGAGAGCTAGTACTTGGCAACCGAATATTC 2768  
 DB 181 ATCAGACACACCATATTTTCAATATAGAGAGCTAGTACTTGGCAACCGAATATTC 240  
 QY 2769 GAAAAAAGACATCTTATTTAAAGCCCAATGCAATCCAGCGCAACATATTTT 2828  
 DB 241 GAAAAAAGACATCTTATTTAAAGCCCAATGCAATCCAGCGCAACATATTTT 300  
 QY 2829 ACTATCTTGGATGATGATCAAAATGATCATAGACAGGTTGCTTCCACTCCCTGAA 2888  
 DB 301 ACTATCTTGGATGATGATCAAAATGATCATAGACAGGTTGCTTCCACTCCCTGAA 360  
 QY 2889 AATTTTACTCAGACATCATTTGCAACAGACATAGCTTACTTATTTTGGAGCTGAAC 2948  
 DB 361 AATTTTACTCAGACATCATTTGCAACAGACATAGCTTACTTATTTTGGAGCTGAAC 420  
 QY 2949 AATTTATGGGAGCAAACTTTATATGCTAGAAAGTACATTTAAAGTACTCTTAC 3008  
 DB 421 AATTTATGGGAGCAAACTTTATATGCTAGAAAGTACATTTAAAGTACTCTTAC 480  
 QY 3009 GCAGGAGATGACAGGCTCTCTTAAACGATGATGATGATGATGATGATGATGATG 3068  
 DB 481 GCAGGAGATGACAGGCTCTCTTAAACGATGATGATGATGATGATGATGATGATG 540  
 QY 3069 AGTGTATATATGCTTCAACATGCTGTGATTAACCAAACTCAGTATTCAGTTATAG 3128  
 DB 541 AGTGTATATATGCTTCAACATGCTGTGATTAACCAAACTCAGTATTCAGTTATAG 600  
 QY 3129 CACTAGTTTATATGCAACATCAGCTTACT 3161  
 DB 601 CACTAGTTTATATGCAACATCAGCTTACT 633

RESULT 7  
 BX097138 472 bp mRNA 1linear EST 04-FEB-2003  
 LOCUS BX097138  
 DEFINITION BX097138 Soares retina N2b4HR Homo sapiens cDNA clone  
 ACCESSION IMAGP998N11359 ; IMAGE:190666, mRNA sequence.  
 VERSION BX097138  
 KEYWORDS EST.  
 SOURCE BX097138.1 GI:27843098  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 472)  
 Ebert,L., Hell,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
 Radelof,U., Schneider,D. and Korn,B.  
 TITLE Human Unigeneset - RZPD3  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGP998N11359.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD.  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, primer sequence: TTTCACACAGGAAACACTATGAC.  
 FEATURES  
 source  
 1..472  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"



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/clone="IMAGP998N11359 ; IMAGE:190666"  
/sex="male"  
/tissue_type="retina"  
/dev_stage="55 year old"  
/lab_host="DH10B (ampicillin resistant)"  
/clone_lib="Soares retina N2b4HR"  
/note="Organ: eye; Vector: pT73D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TCTTACATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). The retinas were obtained from a 55 year old  
Caucasian and total cellular poly(A)+ RNA was extracted 6  
hrs after their removal. The retina RNA was kindly  
provided by Roderick R. McInnes M.D. Ph.D. from the  
University of Toronto. Library constructed by Bento  
Soares and M.Fatima Bonaldo."
```

## ORIGIN

```
Query Match 14.2%; Score 472; DB 5; Length 472;  
Best Local Similarity 100.0%; Pred. No. 4.1e-241;  
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1307 GGACATTCAGTTCAGTGAATGCTGATCACTGCGACGCTTGGTCTGACACCC 1366  
DB 1 GGACATTCAGTTCAGTGAATGCTGATCACTGCGACGCTTGGTCTGACACCC 60  
QY 1367 AATCAGAGCTGCCACATCTTTTGTGTATTAACAGAGATGCTACTTGTAGTCCAGAAC 1426  
DB 61 AATCAGAGCTGCCACATCTTTTGTGTATTAACAGAGATGCTACTTGTAGTCCAGAAC 120  
QY 1427 TTCCTCTGTGAACCCGAGCTTGAAGAGTGAACGAGACAGATGCTTAACTGACA 1486  
DB 121 TTCCTCTGTGAACCCGAGCTTGAAGAGTGAACGAGACAGATGCTTAACTGACA 180  
QY 1487 CTCTCTGTGCTCCAGCTGCTATGAGCTTACCTCCCTGTCAAGAGCTCCACCTTTCTTA 1546  
DB 181 CTCTCTGTGCTCCAGCTGCTATGAGCTTACCTCCCTGTCAAGAGCTCCACCTTTCTTA 240  
QY 1547 TGGCATCAAGCATCTTCTCTGACTGATCAAGGACCAAGATCAATGAGCCACTGACC 1606  
DB 241 TGGCATCAAGCATCTTCTCTGACTGATCAAGGACCAAGATCAATGAGCCACTGACC 300  
QY 1607 AAGCAATGCTAAGTACCAAGGGCTCACATCCCAAGGATTAATTGTGAATCAAGCAAC 1666  
DB 301 AAGCAATGCTAAGTACCAAGGGCTCACATCCCAAGGATTAATTGTGAATCAAGCAAC 360  
QY 1667 TGGCTCTGGGAATTTTCAATCCACCTGACCTTTCAGATGACAGCCGATCAAGTGCAGTG 1726  
DB 361 TGGCTCTGGGAATTTTCAATCCACCTGACCTTTCAGATGACAGCCGATCAAGTGCAGTG 420  
QY 1727 GCGAAGATATGCTGACAGACCTTGAATGAATGATCTGTCTGACACTCTCTGC 1778  
DB 421 GCGAAGATATGCTGACAGACCTTGAATGAATGATCTGTCTGACACTCTCTGC 472
```

```
RESULT 8  
LOCUS B0638902 622 bp mRNA linear EST 15-JUL-2002  
DEFINITION hd29a06.y1 Human Retina cDNA (Un-normalized, unamblyfied): hd/he  
ACCESSION B0638902  
VERSION B0638902.1 GI:21763361  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 622)  
Wistow,G., Bernstein,S.T., Wyatt,M.K., Ray,S., Behal,A.,
```

```
TITLE  
Expressed sequence tag analysis of human retina for the NEIRank  
Project: Retindin, an abundant, novel retinal cDNA and alternative  
splicing of other retina-preferred gene transcripts  
JOURNAL  
PUBMED  
COMMENT  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 402 0078  
Email: giseme@helix.nih.gov  
Plate: 29 row: a column: 06  
Seq primer: M13Rpl reverse primer (ABI).  
Location/Qualifiers  
1. 622  
/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="hd29a06"  
/tissue_type="Retina"  
/dev_stage="Adult"  
/lab_host="EMDH10B"  
/clone_lib="Human Retina cDNA (Un-normalized,  
unamblyfied): hd/he"
```

## FEATURES

source

was dissected from two 80 year old donors with no observed eye disease. 100ng of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioerive Biotechnology (Laurel MD) essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTAGTTCAGATGCGAGCGCGCC(T)15-3'). EST analysis was performed on the unamblyfied library at the NIH Intramural Sequencing Center (NISC)."

## ORIGIN

```
Query Match 14.1%; Score 469; DB 5; Length 622;  
Best Local Similarity 99.5%; Pred. No. 1.7e-239;  
Matches 619; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2480 AAAAGTCCAAATCAACAAATAAACAAGTATCATGTAAGAAATTCGAAATTACTGA 2539  
DB 1 AAAAGTCCAAATCAACAAATAAACAAGTATCATGTAAGAAATTCGAAATTACTGA 60  
QY 2540 CCGTGAATATGAAGAAATTTTAAACATCAAGATTGGGAAGAAATTTAAACCTGAATGCT 2599  
DB 61 CCGTGAATATGAAGAAATTTTAAACATCAAGATTGGGAAGAAATTTAAACCTGAATGCT 120  
QY 2600 ACAATTATCACTTACGCTATCTCAAGAGATGATTTTCTTCTCAAGAAATGAGAC 2659  
DB 121 ACAATTATCACTTACGCTATCTCAAGAGATGATTTTCTTCTCAAGAAATGAGAC 180  
QY 2660 AGGCATATTCATGGTCAATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGACACA 2719  
DB 181 AGGCATATTCATGGTCAATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGACACA 240  
QY 2720 CCATTTTCAAAATATGAGAGGCTCATGTAATTTGGCAACAGTAATTTCTGAAAAAAGA 2779  
DB 241 CCATTTTCAAAATATGAGAGGCTCATGTAATTTGGCAACAGTAATTTCTGAAAAAAGA 300  
QY 2780 CACTTACTTATTTAAACCCCAATGCAATGACGAGAAATATTTTACTATTTCTGG 2839  
DB 301 CACTTACTTATTTAAACCCCAATGCAATGACGAGAAATATTTTACTATTTCTGG 360  
QY 2840 ATGATATGCAAAATGATCATAGCCAGGTTGCTTCCACTTCCCTGAAAAATTTTACTCA 2899  
DB 361 ATGATATGCAAAATGATCATAGCCAGGTTGCTTCCACTTCCCTGAAAAATTTTACTCA 420
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QY 2900 CAGATCATTTGCAAGAGATAGCTTACTTATTTAGGAGTGAACAATTTATTTGGGA 2959  
 |||||||  
 Db 421 CAGATCATTTGCAAGAGATAGCTTACTTATTTAGGAGTGAACAATTTATTTGGGA 480  
 |||||||  
 QY 2960 AGCAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTTACGACGAGAGATG 3019  
 |||||||  
 Db 481 AGCAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTTACGACGAGAGATG 540  
 |||||||  
 QY 3020 CAGGCTCTCTTAAGCAGATGATGATGATGATGATGATGATGATGATGATGAT 3079  
 |||||||  
 Db 541 CAGGCTCTCTTAAGCAGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 |||||||  
 QY 3080 GCTCCACACTAGCTCTGATATA 3101  
 |||||||  
 Db 601 GCTCCACACTAGCTCTGATATA 622  
 |||||||

RESULT 9  
 BM685921 653 bp mRNA linear EST 27-FEB-2002  
 LOCUS UI-E-CKO-aas-h-07-0-UI-x1 UI-E-CKO Homo sapiens cDNA clone  
 DEFINITION UI-E-CKO-aas-h-07-0-UI-x1, mRNA sequence.  
 ACCESSION BM685921  
 VERSION BM685921.1 GI:18995817  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 653)  
 REFERENCE  
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 PUID 8889548

COMMENT  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.reagen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1. 653

FEATURES  
 source

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-CKO-aas-h-07-0-UI"  
 /cissue\_type="Retina Foveal and Macular"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-CKO"  
 /notes="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 UI-E-CKO is a cDNA library containing the following  
 tissue(s): Retina Foveal and Macular. The library was  
 constructed according to Ronaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the

## ORIGIN

(db) 18 tail. The sequence tag for this library is GACC.  
 This library was created for the program, Gene Discovery  
 in the Visual System, supported by National Eye Institute  
 (NEI). "

Query Match 14.0%; Score 467; DB 3; Length 653;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-238;  
 Matches 617; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2711 CAGCACACCATATTTCAATATATAGAGATGATGATGATGATGATGATGATGATGAT 2770  
 |||||||  
 Db 12 CAGCACACCATATTTCAATATATAGAGATGATGATGATGATGATGATGATGATGAT 71  
 |||||||  
 QY 2771 AAAAAAGACCTTAT 2830  
 |||||||  
 Db 72 AAAAAAGACCTTAT 131  
 |||||||  
 QY 2831 TATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2890  
 |||||||  
 Db 132 TATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191  
 |||||||  
 QY 2891 TTTTACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2950  
 |||||||  
 Db 192 TTTTACTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251  
 |||||||  
 QY 2951 TTTTGGGAGCAACTCTTTATATGCTAGAAAGTACATTTAAAGATGATGATGATGAT 3010  
 |||||||  
 Db 252 TTTTGGGAGCAACTCTTTATATGCTAGAAAGTACATTTAAAGATGATGATGATGAT 311  
 |||||||  
 QY 3011 AGGAGATGAGAGCTCTCTTAAAGCAGATGATGATGATGATGATGATGATGATGAT 3070  
 |||||||  
 Db 312 AGGAGATGAGAGCTCTCTTAAAGCAGATGATGATGATGATGATGATGATGATGAT 371  
 |||||||  
 QY 3071 TGTATATATGCTCCACACTAGCTGATATATATATATATATATATATATATATAT 3130  
 |||||||  
 Db 372 TGTATATATGCTCCACACTAGCTGATATATATATATATATATATATATATATAT 431  
 |||||||  
 QY 3131 CACTAGTTTATATAGCAACTAGCTGCTTACATATATATATATATATATATATATAT 3190  
 |||||||  
 Db 432 CACTAGTTTATATAGCAACTAGCTGCTTACATATATATATATATATATATATATAT 491  
 |||||||  
 QY 3191 GAATGTTCTTTAAAGAACTGAGGTTCAATATATATATATATATATATATATATAT 3250  
 |||||||  
 Db 492 GAATGTTCTTTAAAGAACTGAGGTTCAATATATATATATATATATATATATATAT 551  
 |||||||  
 QY 3251 TCTTGTCTACACAAAGCTATTTAAAGAGATGCTATGTTGGAGAAAGGCGAAGTTG 3310  
 |||||||  
 Db 552 TCTTGTCTACACAAAGCTATTTAAAGAGATGCTATGTTGGAGAAAGGCGAAGTTG 611  
 |||||||  
 QY 3311 TACTATATGACATATATCAAT 3330  
 |||||||  
 Db 612 TACTATATGACATATATCAAT 631  
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RESULT 10  
 B1752112 836 bp mRNA linear EST 25-SEP-2001  
 LOCUS B1752112  
 DEFINITION 603022362P1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5192991 5',  
 mRNA sequence.  
 ACCESSION B1752112 GI:15743690  
 VERSION B1752112.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 836)  
 REFERENCE  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNLT at:  
<http://image.llnl.gov>  
 Plate: L14M11482 row: 1 column: 16  
 High quality sequence stop: 822.  
 Location/Qualifiers

## FEATURES

source

1..836  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5192991"  
 /lab\_host="DH10B"  
 /clone\_1lb="NIH\_MGC\_114"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: BclRV (destroyed); RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT  
 primed and directionally cloned (BclRV site is destroyed  
 upon cloning). Average insert size 1.5 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 019. Note:  
 this is a NIH\_MGC Library."

## ORIGIN

Query Match

Best Local Similarity 13.0%; Score 433; DB 3; Length 836;

Matches 533; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2237 CTGATCAACGACATCCCTGCAAGTCTCTGGCTGGGGGCAATTTGGCCCAATGTGTAAGA 2296
DB 127 CTGATCAACGACATCCCTGCAAGTCTCTGGCTGGGGGCAATTTGGCCCAATGTGTAAGA 186
QY 2297 AGGAACGAGCTGAGGAAGGAGTGTGCTGCAACACGAGATATGACAGCGAGGAGCC 2356
DB 187 AGGAACGAGCTGAGGAAGGAGTGTGCTGCAACACGAGATATGACAGCGAGGAGCC 246
QY 2357 TGGACGCTGTGAAACGAGGCTCTGTGCTGTGGCAAAAGAAATGCAAGTCTTCACAG 2416
DB 247 TGGACGCTGTGAAACGAGGCTCTGTGCTGTGGCAAAAGAAATGCAAGTCTTCACAG 306
QY 2417 GAAAGGAGCTCCATGCAAGTGTGCGGATGATCTGTGAAATCAAGATCAAACTAGTG 2476
DB 307 GAAAGGAGCTCCATGCAAGTGTGCGGATGATCTGTGAAATCAAGATCAAACTAGTG 366
QY 2477 TTAATAAGTCCAAATCAACAAATATACAGATATGTAAGAAATTCGATTTAC 2536
DB 367 TTAATAAGTCCAAATCAACAAATATACAGATATGTAAGAAATTCGATTTAC 426
QY 2537 TACCGTAGAATATGAAAGATTTTAAACCATCAAGATTTGGAGAGAAATTTAAACTGAAA 2596
DB 427 TACCGTAGAATATGAAAGATTTTAAACCATCAAGATTTGGAGAGAAATTTAAACTGAAA 486
QY 2597 TGTACCAATATCACTTAGGCTATCTCAAGAGATGATTTGGCTTCAAGAGAAATGGA 2656
DB 487 TGTACCAATATCACTTAGGCTATCTCAAGAGATGATTTGGCTTCAAGAGAAATGGA 546
QY 2657 GACAGGATATTCATGGGTCAATCAAAATCAAGATCAATGATCAAGATCAAGATCAAGC 2716
DB 547 GACAGGATATTCATGGGTCAATCAAAATCAAGATCAATGATCAAGATCAAGATCAAGC 606
QY 2717 ACACCATATTTCAAAATATGAAAGATCATGTACTTGGCAACAGTAATTTGAA 2771
DB 607 ACACCATATTTCAAAATATGAAAGATCATGTACTTGGCAACAGTAATTTGAA 661

```

RESULT 11  
 BM726533  
 LOCUS

BM726533 422 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-EJ0-ai1-e-04-0-UI-r1 UI-E-EJ0 Homo sapiens cDNA clone  
 UI-E-EJ0-ai1-e-04-0-UI 5', mRNA sequence.  
 ACCSSION BM726533  
 VERSION BM726533.1 GI:19047866  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 422)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL PUBLISHED  
 8889548  
 Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu

## COMMENT

Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

## FEATURES

source

1..422  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-EJ0-ai1-e-04-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina Foveal and Macular, RPS and  
 Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_1lb="UI-E-EJ0"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site 1: BclRV; Site 2: Not I;  
 UI-E-EJ0 is a subcloned cDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an BclRV adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are: fetal eyes,  
 AGATTCAGAG; lens, CGATTCAGAG; eye anterior segment,  
 AATGCGCAT; optic nerve, CCGTTCAGAG; retina, CCGCG;  
 Foveal and Macular, GTCC; RPS and Choroid, ACGTA. This  
 library was created for the program, Gene Discovery in the  
 Visual System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match

Best Local Similarity 12.3%; Score 409; DB 3; Length 422;

Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1566 TCTGACTGATCAAGGACCAAGATACATGAGCCACTGACCAAGCAATGCTAGTACAGG 1625
DB 1 TCTGACTGATCAAGGACCAAGATACATGAGCCACTGACCAAGCAATGCTAGTACAGG 60
QY 1626 GCTACCAATCCCAACCAAGTATTTCTGCAATCAGCAATGCTGAGGAATTTCA 1685
DB 61 GCTACCAATCCCAACCAAGTATTTCTGCAATCAGCAATGCTGAGGAATTTCA 120

```

QY 1686 TCACCTGCATCTTCAGATGACGCCGATCAAGTGCAGTGGGAGATATGCTCAGACA 1745  
 |||  
 DB 121 TCACCTGCATCTTCAGATGACGCCGATCAAGTGCAGTGGGAGATATGCTCAGACA 180  
 |||  
 QY 1746 CCTAGATGAATGATCTCTGACACTCTCGCCCATCTGAGATACAGAGCTCAGCA 1805  
 |||  
 DB 181 CCTAGATGAATGATCTCTGACACTCTCGCCCATCTGAGATACAGAGCTCAGCA 240  
 |||  
 QY 1806 ATATGTTTCTGCTCCGATCATTTCTTGAGAGATACACTCTCTGCTCAGCTTACAGTA 1865  
 |||  
 DB 241 ATATGTTTCTGCTCCGATCATTTCTTGAGAGATACACTCTCTGCTCAGCTTACAGTA 300  
 |||  
 QY 1866 TATCACCACATGTTCTATGACATTCGCCCCCAGAGGCGGAGAGCTGTGTCTTCAG 1925  
 |||  
 DB 301 TATCACCACATGTTCTATGACATTCGCCCCCAGAGGCGGAGAGCTGTGTCTTCAG 360  
 |||  
 QY 1926 TCTGCTGTGCTATACATGAGCTTCTCAACGACGCTGTTCAACAGC 1974  
 |||  
 DB 361 TCTGCTGTGCTATACATGAGCTTCTCAACGACGCTGTTCAACAGC 409  
 |||

RESULT 12  
 CA393958 508 bp mRNA linear EST 06-NOV-2002  
 LOCUS cs44g04.y1 Human Retinal pigment epithelium/choroid cDNA  
 DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs44g04  
 5', mRNA sequence.

ACCESSION CA393958  
 VERSION CA393958  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 508)  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
 Tissue-specific expression of human RPE/choroid for the  
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL 12107410  
 PUBMED  
 COMMENT Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: gwaem@helix.nih.gov  
 Plate: 44 row: 9 column: 04  
 Seg primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers

FEATURES  
 source  
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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="cs44g04"  
 /issue\_type="RPE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the Superscript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>". The library code  
 designation was cs. For this library, cDNA inserts were

cloned into the NotI/Mlu sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 12.1%; Score 402; DB 6; Length 508;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-203;  
 Matches 452; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1442 CCCAGCTTGAGACAGTGGACGAGACAGATGCTTACCTGACACTTCTGTCTCCAC 1501  
 |||  
 DB 1 CCCAGCTTGAGACAGTGGACGAGACAGATGCTTACCTGACACTTCTGTCTCCAC 60  
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 QY 1502 CTGCTATGAGCTCTTCACTCTCCCTGTGCAAGAGCTCCACCTTTCTTATGAGCATCAAGCATCT 1561  
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 DB 61 CTGCTATGAGCTCTTCACTCTCCCTGTGCAAGAGCTCCACCTTTCTTATGAGCATCAAGCATCT 120  
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 QY 1562 TCTCTCTGACATGATCAAGGACACAGATATGAGGCGCATGACGAGATGCTATGAC 1621  
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 DB 121 TCTCTCTGACATGATCAAGGACACAGATATGAGGCGCATGACGAGATGCTATGAC 180  
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 QY 1622 CAGGCTCAGCATCCCAACAGTGAATTTCTGCAATCAGCAACTGCTCTGGAAATTT 1681  
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 DB 181 CAGGCTCAGCATCCCAACAGTGAATTTCTGCAATCAGCAACTGCTCTGGAAATTT 240  
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 QY 1802 GGAATATGTTCTGTCCAGATCACTTCTTGAAGATGACACTCTGCTCAGCTTTTAC 1861  
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 DB 361 TCGAATATGTTCTGTCCAGATCACTTCTTGAAGATGACACTCTGCTCAGCTTTTAC 420  
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 QY 1862 AGTATATACACACTAGTTCTATGACATTGCCC 1894  
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 DB 421 AGTATATACACACTAGTTCTATGACATTGCCC 453  
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RESULT 13  
 BG196799 801 bp mRNA linear EST 21-APR-2001  
 LOCUS RST16026 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BG196799  
 ACCESSION BG196799  
 VERSION BG196799.1 GI:13718486  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 801)  
 Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,  
 Whitington, J., Lerner, L., Costanzo, D., McBilligott, K., Booser, S.,  
 May, R., Smith, E., Veloso, N., Kliska, A., Hess, J., Cothran, K., Lo, K.,  
 Ofendacher, J., Danzig, J. and Ducar, M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL 11329013  
 PUBMED  
 COMMENT Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@athersys.com  
 High quality sequence accp: 474.  
 Location/Qualifiers

FEATURES  
 source  
 1..801

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HT1080"
/note="See 'Atherlys RAGE Library'
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

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## ORIGIN

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Query Match      11.9%; Score 395; DB 2; Length 801;
Best Local Similarity 99.5%; Pred. No. 1.1e-199;
Matches 545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2558 TTACCATCAAGATTGGAGAGAAATTAACTGAAATGTACATTATCACTTAGGCT 2617
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DB 131 TTACCATCAAGATTGGAGAGAAATTAACTGAAATGTACATTATCACTTAGGCT 190
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QY 2618 ATCTCAAGAGATGATTGGCTTCTCAAGAGAAATGAGACAGGATTTCAAGGCTCA 2677
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DB 191 ATCTCAAGAGATGATTGGCTTCTCAAGAGAAATGAGACAGGATTTCAAGGCTCA 250
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QY 2678 TCAAAATCCAGACATACAGTCAACAGTGAATTCGAAAAAAGACACTTATTATTA 2737
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DB 251 TCAAAATCCAGACATACAGTCAACAGTGAATTCGAAAAAAGACACTTATTATTA 310
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DB 311 AGAGTCATGTACTTGGCAACAGTAATTTCTGAAAAAAGACACTTATTATTA 370
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DB 431 ATTAAGCAGGTTGGCTTCCACCTTCCCTGAAAAATTTTACTCAAGATCATTGCAACA 490
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DB 551 TAGAAAGTACATTTAAAGATGACTTACGACAGGAGATGCAAGTCTCTCTAAACGA 610
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QY 3098 TAAACACA 3105
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DB 671 TAAACACA 678
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RESULT 14
BO636596      598 bp      mRNA      linear      EST 15-JUL-2002
LOCUS        hd11h02.v1 Human Retina cDNA (Un-normalized, unamblyfied): hd/he
DEFINITION   Homo sapiens cDNA clone hd11h02 5', mRNA sequence.
ACCESSION    BO636596
VERSION      BO636596.1 GI:21761055
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

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REFERENCE
1 (bases 1 to 598)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,

```

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TITLE
JOURNAL
PUBMED
COMMENT
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gwaen@helix.nih.gov
Plate: 11 row: h column: 02
Seq primer: M13RPL reverse primer (ABI).
Location/Qualifiers

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## FEATURES

source

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1..598
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/db_xref="taxon:9606"
/clone="hd11h02"
/clone_lib="Retina"
/dev_stage="Adult"
/lab_host="EMD10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ng of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the Superscript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTGCTTCGATGTCGAGCGCGCC(7)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
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## ORIGIN

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Query Match      11.4%; Score 380; DB 5; Length 598;
Best Local Similarity 99.3%; Pred. No. 1.2e-191;
Matches 580; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1550 CATCAAGATCTTCTCTGCTGATGATCAAGCAGACAGATCAATGGCCACTGACGA 1609
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DB 75 CATCAAGATCTTCTCTGCTGATGATCAAGCAGACAGATCAATGGCCACTGACGA 134
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QY 1610 CAATGCTAGTACAGGGCTCAACATCCCAAGATGATTTATTTGCAATGACCAACTG 1669
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DB 135 CAATGCTAGTACAGGGCTCAACATCCCAAGATGATTTATTTGCAATGACCAACTG 194
    |||||
QY 1670 CTCTGGAAATTTACATCCACTGATCTTCAAGATGACAGCCGATCAAGTGAAGTGG 1729
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DB 195 CTCTGGAAATTTACATCCACTGATCTTCAAGATGACAGCCGATCAAGTGAAGTGG 254
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QY 1730 AAGATATGTCAGACACTAGATGAAGAATGCTGTGACATCTCTGCCCATCTGAGG 1789
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DB 255 AAGATATGTCAGACACTAGATGAAGAATGCTGTGACATCTCTGCCCATCTGAGG 314
    |||||
QY 1790 TACAGAGCTCAGCAATATGTTTCTGCCAGATCATTTCTTGGAGATACCACTCTG 1849
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DB 315 TACAGAGCTCAGCAATATGTTTCTGCCAGATCATTTCTTGGAGATACCACTCTG 374
    |||||
QY 1850 TCTCAGCTTTACAGTATATCAACCACTAGTTCTATGACCATTTGCCCAAGGCGAGAG 1909
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DB 375 TCTCAGCTTTACAGTATATCAACCACTAGTTCTATGACCATTTGCCCAAGGCGAGAG 434
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QY 1910 TGGTAGGTTCTTCAGTGGCGGTTGCTTAACATGGCTTCCCAAGACCTTTCAACA 1969  
 DB 435 TGGTAGGTTCTTCACATCTGCGTGTGTCAACATGGCTTCCCAAGACCTTTCAACA 494  
 QY 1970 AGAGCTCTCTGAGTACCGAGCTCTGGAGCAACATTCACACAGCTGTGCTTCATATC 2029  
 DB 495 AGAGCTCTCTGAGTACCGAGCTCTGGAGCAACATTCACACAGCTGTGCTTCATATC 554  
 QY 2030 TACGATCCAACTTTACAGATTTAAGCACTTGAATTAATTAC 2073  
 DB 555 TACGATCCAACTTTACAGATTTAAGCACTTGAATTAATTAC 598

RESULT 15  
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 LOCUS BU732814 UI-E-COI-afz-1-04-0-UI.s1 UI-E-COI Homo sapiens cDNA clone  
 DEFINITION UI-E-COI-afz-1-04-0-UI 3', mRNA sequence.  
 ACCESSION BU732814  
 VERSION BU732814.1 GI:23659091  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Bularhota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 683)  
 Bernaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery

JOURNAL  
 PUBMED Genome Res. 6 (9), 791-806 (1996)  
 COMMENT 8889548

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@iowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 FORWARD  
 POLYA=yes.

FEATURES  
 source Location/Qualifiers

1..683  
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 /db\_xref="taxon:9606"  
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 /dev\_stage="adult"  
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 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
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 UI-E-COI is a normalized cDNA library containing the  
 following tissue(s): optic nerve. The library was  
 constructed according to Bernaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 CCAATTAAGTC. This library was created for the program, Gene  
 Discovery in the Visual System, supported by National Eye

INSTITUTE (NEI).  
 TAG\_TISSUE=human optic nerve  
 TAG\_LIB=UI-E-COI  
 TAG\_SEQ=CCATTAAGTC"

Query Match 11.2%; Score 373; DB 5; Length 683;  
 Best Local Similarity 100.0%; Pred. No. 7e-188;  
 Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2958 GAAGCAAACTTTTAAAGCTAGAAAGTACATTTAAAGATGACTTACGAGGAGG 3017  
 DB 620 GAGCAAACTTTTATATATCTAGAAAGTACATTTAAAGATGACTTACGAGGAGG 561  
 QY 3018 TCGAGGTCTCTTAAACGATGATGATGATGATGATGATGATGATGATGATGAT 3077  
 DB 560 TCGAGGTCTCTTAAACGATGATGATGATGATGATGATGATGATGATGATGAT 501  
 QY 3078 ATGCTCCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3137  
 DB 500 ATGCTCCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441  
 QY 3138 TTTATACGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3197  
 DB 440 TTTATACGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 381  
 QY 3198 TCTTTAAAGAACTGAGGTTGATGATGATGATGATGATGATGATGATGATGAT 3257  
 DB 380 TCTTTAAAGAACTGAGGTTGATGATGATGATGATGATGATGATGATGATGAT 321  
 QY 3258 ACTACCAAAAGCTATTTTAAAGATGATGATGATGATGATGATGATGATGATGAT 3317  
 DB 320 ACTACCAAAAGCTATTTTAAAGATGATGATGATGATGATGATGATGATGATGAT 261  
 QY 3318 TGACATTAATCAAT 3330  
 DB 260 TGACATTAATCAAT 248

Search completed: January 13, 2006, 23:42:51  
 Job time : 12744 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2006, 23:42:54 ; Search time 526 Seconds  
(without alignments)  
5123.821 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 ttaaccagaaggtatcct.....tactatagacataatcaat 3330

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 6038814 seqs, 404674181 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 1000 summaries

Database : Published Applications NA.New.\*

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Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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17	23	0.7	23	6	US-10-310-914A-213683
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19	23	0.7	23	6	US-10-310-914A-213671
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C 91	19	0.6	19	8	US-11-101-244-256292	Sequence 256292,
C 92	19	0.6	19	8	US-11-101-244-256293	Sequence 256293,
C 93	19	0.6	19	8	US-11-101-244-256294	Sequence 256294,
C 94	19	0.6	19	8	US-11-101-244-256295	Sequence 256295,
C 95	19	0.6	19	8	US-11-101-244-256296	Sequence 256296,
C 96	19	0.6	19	8	US-11-101-244-256297	Sequence 256297,

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98	19	0	6	19	8	US-11-101-244-256299	Sequence	256299		171	19	0	6	19	9	US-11-083-784-256272	Sequence	256272
99	19	0	6	19	8	US-11-101-244-256300	Sequence	256300		172	19	0	6	19	9	US-11-083-784-256273	Sequence	256273
100	19	0	6	19	8	US-11-101-244-256301	Sequence	256301		173	19	0	6	19	9	US-11-083-784-256274	Sequence	256274
101	19	0	6	19	8	US-11-101-244-256302	Sequence	256302		174	19	0	6	19	9	US-11-083-784-256275	Sequence	256275
102	19	0	6	19	8	US-11-101-244-256303	Sequence	256303		175	19	0	6	19	9	US-11-083-784-256276	Sequence	256276
103	19	0	6	19	8	US-11-101-244-256304	Sequence	256304		176	19	0	6	19	9	US-11-083-784-256277	Sequence	256277
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244	19	0.6	19	9	US-11-083-784-256345	Sequence 256345,	317	18	0.5	1080000	6	US-10-928-446A-191	Sequence 191, App
245	19	0.6	19	9	US-11-083-784-256346	Sequence 256346,	318	18	0.5	1080000	6	US-10-928-446A-193	Sequence 193, App
246	19	0.6	19	9	US-11-083-784-256347	Sequence 256347,	319	18	0.5	1080000	6	US-10-928-446A-195	Sequence 195, App
247	19	0.6	1031	6	US-10-750-185-55729	Sequence 55729, A	320	18	0.5	1080000	6	US-10-928-446A-197	Sequence 197, App
248	19	0.6	1290	6	US-10-750-185-55729	Sequence 55729, A	321	18	0.5	1080000	6	US-10-928-446A-199	Sequence 199, App
249	19	0.6	1290	6	US-10-750-185-55729	Sequence 55729, A	322	18	0.5	1080000	6	US-10-928-446A-201	Sequence 201, App
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251	19	0.6	2107	6	US-10-750-185-44725	Sequence 44725, A	324	17	0.5	19	8	US-11-101-244-252134	Sequence 252134, A
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253	19	0.6	2259	6	US-10-750-185-59838	Sequence 59838, A	326	17	0.5	19	8	US-11-101-244-252134	Sequence 252134, A
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255	19	0.6	6257	7	US-11-136-527-272	Sequence 59838, A	328	17	0.5	19	8	US-11-101-244-252134	Sequence 252134, A
256	19	0.6	95050	6	US-10-857-780-7	Sequence 272, App	329	17	0.5	19	9	US-11-083-784-252134	Sequence 252134, A
257	19	0.6	170837	6	US-11-121-086-97	Sequence 97, App1	330	17	0.5	19	9	US-11-083-784-252134	Sequence 252134, A
258	19	0.6	244196	6	US-10-995-561-13327	Sequence 13327, A	331	17	0.5	19	9	US-11-083-784-252134	Sequence 252134, A
259	18	0.5	18	6	US-10-310-914A-213674	Sequence 213674,	332	17	0.5	19	9	US-11-083-784-252134	Sequence 252134, A
260	18	0.5	18	6	US-10-310-914A-213680	Sequence 213680,	333	17	0.5	19	9	US-11-083-784-252134	Sequence 252134, A
261	18	0.5	18	6	US-10-310-914A-213682	Sequence 213682,	334	17	0.5	21	6	US-10-310-914A-1030853	Sequence 1030853, A
262	18	0.5	18	6	US-10-310-914A-213684	Sequence 213684,	335	17	0.5	23	6	US-10-310-914A-189445	Sequence 189445, A
263	18	0.5	18	6	US-10-310-914A-213688	Sequence 213688,	336	17	0.5	24	6	US-10-310-914A-1030859	Sequence 1030859, A
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266	18	0.5	20	6	US-10-310-914A-796612	Sequence 796612,	339	17	0.5	30	6	US-11-121-849-14731	Sequence 14731, A
267	18	0.5	22	6	US-10-310-914A-796613	Sequence 796613,	340	17	0.5	201	6	US-10-995-561-33530	Sequence 249, App
268	18	0.5	26	6	US-10-310-914A-796611	Sequence 796611,	341	17	0.5	201	6	US-10-995-561-33530	Sequence 249, App
269	18	0.5	201	6	US-10-995-561-42405	Sequence 42405, A	342	17	0.5	201	6	US-10-995-561-42405	Sequence 42405, A
270	18	0.5	201	6	US-10-995-561-52687	Sequence 52687, A	343	17	0.5	201	6	US-10-995-561-52687	Sequence 52687, A
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272	18	0.5	201	7	US-11-124-368A-18834	Sequence 18834, A	345	17	0.5	201	7	US-11-124-368A-18834	Sequence 18834, A
273	18	0.5	600	6	US-10-750-185-3609	Sequence 3609, App	346	17	0.5	201	7	US-11-124-368A-18834	Sequence 18834, A
274	18	0.5	600	6	US-10-750-185-3609	Sequence 3609, App	347	17	0.5	201	7	US-11-124-368A-18834	Sequence 18834, A
275	18	0.5	603	6	US-10-524-198-1	Sequence 1, App1	348	17	0.5	449	7	US-11-128-061-90	Sequence 90, App1
276	18	0.5	1069	6	US-10-750-185-46512	Sequence 46512, A	349	17	0.5	499	7	US-11-128-061-90	Sequence 90, App1
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278	18	0.5	1137	6	US-10-750-185-29661	Sequence 29661, A	351	17	0.5	600	6	US-10-750-185-3376	Sequence 3376, App
279	18	0.5	1137	6	US-10-750-185-29661	Sequence 29661, A	352	17	0.5	600	6	US-10-750-185-3376	Sequence 3376, App
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282	18	0.5	1283	6	US-10-750-185-38249	Sequence 38249, A	355	17	0.5	600	6	US-10-750-185-3376	Sequence 3376, App
283	18	0.5	1293	6	US-10-750-185-38249	Sequence 38249, A	356	17	0.5	600	6	US-10-750-185-3376	Sequence 3376, App
284	18	0.5	1400	7	US-11-136-527-6474	Sequence 6474, App	357	17	0.5	600	7	US-11-136-527-6474	Sequence 6474, App
285	18	0.5	1476	6	US-10-750-185-48316	Sequence 48316, A	358	17	0.5	600	7	US-11-136-527-6474	Sequence 6474, App
286	18	0.5	1476	6	US-10-750-185-48316	Sequence 48316, A	359	17	0.5	851	6	US-10-750-185-53468	Sequence 53468, A
287	18	0.5	1571	6	US-10-750-185-64078	Sequence 64078, A	360	17	0.5	851	6	US-10-750-185-53468	Sequence 53468, A
288	18	0.5	1571	6	US-10-750-185-64078	Sequence 64078, A	361	17	0.5	953	6	US-10-750-185-60943	Sequence 60943, A
289	18	0.5	1758	6	US-10-750-185-39829	Sequence 39829, A	362	17	0.5	953	6	US-10-750-185-60943	Sequence 60943, A
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292	18	0.5	2768	7	US-11-136-527-2378	Sequence 2378, App	365	17	0.5	953	6	US-10-750-185-60943	Sequence 60943, A
293	18	0.5	2919	6	US-10-821-234-735	Sequence 735, App	366	17	0.5	953	6	US-10-750-185-60943	Sequence 60943, A
294	18	0.5	3249	6	US-10-793-626-3476	Sequence 3476, App	367	17	0.5	953	6	US-10-750-185-60943	Sequence 60943, A
295	18	0.5	3249	6	US-10-793-626-3476	Sequence 3476, App	368	17	0.5	953	6	US-10-750-185-60943	Sequence 60943, A
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297	18	0.5	7402	6	US-10-750-185-2713	Sequence 2713, A	370	17	0.5	1083	6	US-10-750-185-48783	Sequence 48783, A
298	18	0.5	7402	6	US-10-750-185-2713	Sequence 2713, A	371	17	0.5	1120	6	US-10-750-185-48783	Sequence 48783, A
299	18	0.5	7664	6	US-10-240-708-84	Sequence 7433, A	372	17	0.5	1120	6	US-10-750-185-48783	Sequence 48783, A
300	18	0.5	26772	6	US-10-995-561-13313	Sequence 13313, A	373	17	0.5	1129	6	US-10-750-185-48783	Sequence 48783, A
301	18	0.5	54946	6	US-10-995-561-13379	Sequence 13379, A	374	17	0.5	1129	6	US-10-750-185-48783	Sequence 48783, A
302	18	0.5	59110	6	US-10-995-561-13324	Sequence 13324, A	375	17	0.5	1217	6	US-10-750-185-51885	Sequence 51885, A
303	18	0.5	87672	6	US-10-995-561-13337	Sequence 13337, A	376	17	0.5	1217	6	US-10-750-185-51885	Sequence 51885, A
304	18	0.5	147700	6	US-10-857-780-3	Sequence 13237, A	377	17	0.5	1217	6	US-10-750-185-51885	Sequence 51885, A
305	18	0.5	151628	7	US-11-117-187-197	Sequence 87, App1	378	17	0.5	1263	6	US-10-750-185-46919	Sequence 46919, A
306	18	0.5	156260	7	US-11-121-086-87	Sequence 87, App1	379	17	0.5	1334	6	US-10-750-185-46919	Sequence 46919, A
307	18	0.5	166339	7	US-11-121-086-52	Sequence 28, App1	380	17	0.5	1334	6	US-10-750-185-46919	Sequence 46919, A
308	18	0.5	172311	7	US-11-121-086-28	Sequence 25, App1	381	17	0.5	1366	6	US-10-750-185-31419	Sequence 31419, A
309	18	0.5	172781	7	US-11-112-908-25	Sequence 107, App	382	17	0.5	1414	6	US-10-750-185-63931	Sequence 63931, A
310	18	0.5	197096	7	US-11-121-086-107	Sequence 181, App	383	17	0.5	1414	6	US-10-750-185-63931	Sequence 63931, A
311	18	0.5	1080000	6	US-10-928-446A-181	Sequence 181, App	384	17	0.5	1432	6	US-10-750-185-63931	Sequence 63931, A
312	18	0.5	1080000	6	US-10-928-446A-183	Sequence 183, App	385	17	0.5	1432	6	US-10-750-185-63931	Sequence 63931, A
313	18	0.5	1080000	6	US-10-928-446A-185	Sequence 185, App	386	17	0.5	1456	6	US-10-750-185-32767	Sequence 32767, A
314	18	0.5	1080000	6	US-10-928-446A-185	Sequence 185, App	387	17	0.5	1456	6	US-10-750-185-32767	Sequence 32767, A
315	18	0.5	1080000	6	US-10-928-446A-187	Sequence 187, App	388	17	0.5	1456	6	US-10-750-185-32767	Sequence 32767, A

389	17	0.5	1472	6	US-10-750-185-50008	Sequence 50008, A	C 462	17	0.5	4282	7	US-11-128-061-452	Sequence 452, App
390	17	0.5	1472	6	US-10-750-623-50008	Sequence 50008, A	C 463	17	0.5	4301	7	US-11-136-527-8816	Sequence 3816, Ap
391	17	0.5	1492	6	US-10-750-185-47603	Sequence 47603, A	C 464	17	0.5	4343	7	US-11-113-557-7694	Sequence 2694, Ap
392	17	0.5	1492	6	US-10-750-623-47603	Sequence 47603, A	C 465	17	0.5	4552	6	US-10-750-185-33133	Sequence 33133, A
393	17	0.5	1497	6	US-10-750-185-55977	Sequence 55977, A	C 466	17	0.5	4552	6	US-10-750-623-33133	Sequence 33133, A
394	17	0.5	1497	6	US-10-750-623-55977	Sequence 55977, A	C 467	17	0.5	5039	6	US-10-750-185-33133	Sequence 33133, A
395	17	0.5	1515	6	US-10-750-185-35828	Sequence 35828, A	C 468	17	0.5	5039	6	US-10-750-185-33133	Sequence 33133, A
396	17	0.5	1515	6	US-10-750-623-35828	Sequence 35828, A	C 469	17	0.5	6639	6	US-10-750-623-31557	Sequence 31557, A
397	17	0.5	1535	6	US-10-750-185-34363	Sequence 34363, A	C 470	17	0.5	6702	6	US-10-240-708-6	Sequence 6, App1
398	17	0.5	1535	6	US-10-750-623-34363	Sequence 34363, A	C 471	17	0.5	6702	6	US-10-873-528-109	Sequence 209, App
399	17	0.5	1540	6	US-10-750-185-53125	Sequence 53125, A	C 472	17	0.5	22455	6	US-10-995-561-13390	Sequence 13390, A
400	17	0.5	1540	6	US-10-750-623-53125	Sequence 53125, A	C 473	17	0.5	22959	6	US-10-995-561-13390	Sequence 13390, A
401	17	0.5	1551	6	US-10-750-185-25455	Sequence 25455, A	C 474	17	0.5	30192	7	US-10-995-561-13306	Sequence 13306, A
402	17	0.5	1551	6	US-10-750-623-25455	Sequence 25455, A	C 475	17	0.5	31936	6	US-11-124-368A-2891	Sequence 2891, Ap
403	17	0.5	1621	6	US-10-750-185-62666	Sequence 62666, A	C 476	17	0.5	40439	6	US-10-995-561-13359	Sequence 13359, A
404	17	0.5	1621	6	US-10-750-623-62666	Sequence 62666, A	C 477	17	0.5	60844	6	US-10-995-561-13359	Sequence 13359, A
405	17	0.5	1627	6	US-10-750-185-46094	Sequence 46094, A	C 478	17	0.5	64555	7	US-11-124-368A-2884	Sequence 2884, Ap
406	17	0.5	1627	6	US-10-750-623-46094	Sequence 46094, A	C 479	17	0.5	75589	6	US-10-995-561-13322	Sequence 13322, A
407	17	0.5	1636	6	US-10-750-185-53953	Sequence 53953, A	C 480	17	0.5	75589	6	US-10-995-561-13322	Sequence 13322, A
408	17	0.5	1636	6	US-10-750-623-53953	Sequence 53953, A	C 481	17	0.5	98309	7	US-11-124-368A-2921	Sequence 2921, Ap
409	17	0.5	1699	6	US-10-750-185-59477	Sequence 59477, A	C 482	17	0.5	110847	7	US-11-121-086-11	Sequence 11, App1
410	17	0.5	1699	6	US-10-750-623-59477	Sequence 59477, A	C 483	17	0.5	114801	7	US-11-121-086-22	Sequence 22, App1
411	17	0.5	1792	6	US-10-750-185-40231	Sequence 40231, A	C 484	17	0.5	118996	7	US-11-121-086-84	Sequence 84, App1
412	17	0.5	1792	6	US-10-750-623-40231	Sequence 40231, A	C 485	17	0.5	128021	7	US-11-117-187-202	Sequence 202, App
413	17	0.5	1809	6	US-10-750-185-38041	Sequence 38041, A	C 486	17	0.5	130472	6	US-10-995-561-13312	Sequence 13312, A
414	17	0.5	1809	6	US-10-750-623-38041	Sequence 38041, A	C 487	17	0.5	137671	7	US-11-121-086-47	Sequence 47, App1
415	17	0.5	1831	6	US-10-750-185-43691	Sequence 43691, A	C 488	17	0.5	146556	7	US-11-121-086-68	Sequence 68, App1
416	17	0.5	1831	6	US-10-750-623-43691	Sequence 43691, A	C 489	17	0.5	158410	7	US-11-121-086-46	Sequence 46, App1
417	17	0.5	1856	6	US-10-750-185-60696	Sequence 60696, A	C 490	17	0.5	157878	7	US-11-121-086-92	Sequence 92, App1
418	17	0.5	1856	6	US-10-750-623-60696	Sequence 60696, A	C 491	17	0.5	160282	7	US-11-121-086-29	Sequence 29, App1
419	17	0.5	1874	7	US-11-150-533-13	Sequence 13, App1	C 492	17	0.5	165317	7	US-11-117-187-212	Sequence 212, App
420	17	0.5	1922	6	US-10-750-185-25924	Sequence 25924, A	C 493	17	0.5	175503	7	US-11-121-086-53	Sequence 53, App1
421	17	0.5	1922	6	US-10-750-623-25924	Sequence 25924, A	C 494	17	0.5	178877	7	US-11-121-086-17	Sequence 17, App1
422	17	0.5	1951	6	US-10-750-185-32751	Sequence 32751, A	C 495	17	0.5	181172	7	US-11-121-086-41	Sequence 41, App1
423	17	0.5	1951	6	US-10-750-623-32751	Sequence 32751, A	C 496	17	0.5	181172	7	US-11-121-086-41	Sequence 41, App1
424	17	0.5	2030	6	US-10-750-185-31356	Sequence 31356, A	C 497	17	0.5	196276	6	US-10-661-966-1	Sequence 1, App1
425	17	0.5	2030	6	US-10-750-623-31356	Sequence 31356, A	C 498	17	0.5	199331	7	US-11-112-908-20	Sequence 20, App1
426	17	0.5	2116	6	US-10-750-185-55368	Sequence 55368, A	C 499	17	0.5	324000	6	US-11-112-908-53	Sequence 53, App1
427	17	0.5	2116	6	US-10-750-623-55368	Sequence 55368, A	C 500	17	0.5	394468	6	US-10-775-169-52	Sequence 52, App1
428	17	0.5	2120	6	US-10-750-185-58147	Sequence 58147, A	C 501	17	0.5	199161	6	US-10-775-169-52	Sequence 52, App1
429	17	0.5	2120	6	US-10-750-623-58147	Sequence 58147, A	C 502	17	0.5	199161	6	US-10-775-169-52	Sequence 52, App1
430	17	0.5	2203	6	US-10-750-185-64144	Sequence 64144, A	C 503	17	0.5	249860	7	US-11-121-086-8	Sequence 8, App1
431	17	0.5	2203	6	US-10-750-623-64144	Sequence 64144, A	C 504	17	0.5	324000	6	US-10-995-561-13204	Sequence 13204, A
432	17	0.5	2264	6	US-10-750-185-51613	Sequence 51613, A	C 505	17	0.5	340009	7	US-11-102-978-3	Sequence 3, App1
433	17	0.5	2264	6	US-10-750-623-51613	Sequence 51613, A	C 506	17	0.5	394468	6	US-10-995-561-13473	Sequence 13473, A
434	17	0.5	2424	6	US-10-750-185-34345	Sequence 34345, A	C 507	17	0.5	643170	6	US-10-995-561-13293	Sequence 13293, A
435	17	0.5	2424	6	US-10-750-623-34345	Sequence 34345, A	C 508	17	0.5	1125000	6	US-10-995-561-13286	Sequence 13286, A
436	17	0.5	2453	6	US-10-750-185-46634	Sequence 46634, A	C 509	17	0.5	18	6	US-11-101-244-108221	Sequence 108221, A
437	17	0.5	2453	6	US-10-750-185-57978	Sequence 57978, A	C 510	16	0.5	19	8	US-11-101-244-108317	Sequence 108317, A
438	17	0.5	2453	6	US-10-750-623-46634	Sequence 46634, A	C 511	16	0.5	19	8	US-11-101-244-108317	Sequence 108317, A
439	17	0.5	2453	6	US-10-750-623-57978	Sequence 57978, A	C 512	16	0.5	19	8	US-11-101-244-108470	Sequence 108470, A
440	17	0.5	2453	6	US-10-750-185-43843	Sequence 43843, A	C 513	16	0.5	19	8	US-11-101-244-108520	Sequence 108520, A
441	17	0.5	2645	6	US-10-750-623-43843	Sequence 43843, A	C 514	16	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
442	17	0.5	2645	6	US-10-750-185-25629	Sequence 25629, A	C 515	16	0.5	19	8	US-11-101-244-240635	Sequence 240635, A
443	17	0.5	2675	6	US-10-750-623-25629	Sequence 25629, A	C 516	16	0.5	19	8	US-11-101-244-461118	Sequence 461118, A
444	17	0.5	2797	6	US-10-750-185-59963	Sequence 59963, A	C 517	16	0.5	19	8	US-11-101-244-508525	Sequence 508525, A
445	17	0.5	2797	6	US-10-750-623-59963	Sequence 59963, A	C 518	16	0.5	19	8	US-11-101-244-545859	Sequence 545859, A
446	17	0.5	3012	6	US-10-750-185-31651	Sequence 31651, A	C 519	16	0.5	19	8	US-11-101-244-651882	Sequence 651882, A
447	17	0.5	3012	6	US-10-750-623-31651	Sequence 31651, A	C 520	16	0.5	19	8	US-11-101-244-859507	Sequence 859507, A
448	17	0.5	3236	6	US-10-750-185-38585	Sequence 38585, A	C 521	16	0.5	19	8	US-11-101-244-1069317	Sequence 1069317, A
449	17	0.5	3236	6	US-10-750-623-38585	Sequence 38585, A	C 522	16	0.5	19	8	US-11-101-244-1173681	Sequence 1173681, A
450	17	0.5	3249	7	US-11-128-061-3436	Sequence 3436, Ap	C 523	16	0.5	19	8	US-11-101-244-1271654	Sequence 1271654, A
451	17	0.5	3301	6	US-10-750-185-35555	Sequence 35555, A	C 524	16	0.5	19	8	US-11-101-244-1271701	Sequence 1271701, A
452	17	0.5	3301	6	US-10-750-623-35555	Sequence 35555, A	C 525	16	0.5	19	8	US-11-101-244-166625	Sequence 1466025, A
453	17	0.5	3607	6	US-10-750-185-41921	Sequence 41921, A	C 526	16	0.5	19	8	US-11-101-244-168839	Sequence 1468839, A
454	17	0.5	3607	6	US-10-750-623-41921	Sequence 41921, A	C 527	16	0.5	19	8	US-11-101-244-189779	Sequence 1489779, A
455	17	0.5	3741	7	US-11-044-899-1	Sequence 1, App1	C 528	16	0.5	19	8	US-11-101-244-189789	Sequence 1489789, A
456	17	0.5	3874	6	US-10-750-185-34427	Sequence 34427, A	C 529	16	0.5	19	8	US-11-101-244-1503894	Sequence 1503894, A
457	17	0.5	3874	6	US-10-750-623-34427	Sequence 34427, A	C 530	16	0.5	19	8	US-11-101-244-1503931	Sequence 1503931, A
458	17	0.5	4049	6	US-10-750-185-46291	Sequence 46291, A	C 531	16	0.5	19	8	US-11-101-244-1527897	Sequence 1527897, A
459	17	0.5	4049	6	US-10-750-623-46291	Sequence 46291, A	C 532	16	0.5	19	8	US-11-101-244-1527897	Sequence 1527897, A
460	17	0.5	4162	6	US-10-750-185-63977	Sequence 63977, A	C 533	16	0.5	19	9	US-11-083-784-108221	Sequence 108221, A
461	17	0.5	4162	6	US-10-750-623-63977	Sequence 63977, A	C 534	16	0.5	19	9	US-11-083-784-108317	Sequence 108317, A

C 535	16	0.5	19	9	US-11-083-784-108420	Sequence 108420,	608	16	0.5	201	6	US-10-995-561-33533	Sequence 33533, A
C 536	16	0.5	19	9	US-11-083-784-108520	Sequence 108520,	609	16	0.5	201	6	US-10-995-561-33802	Sequence 33802, A
C 537	16	0.5	19	9	US-11-083-784-108619	Sequence 108619,	610	16	0.5	201	6	US-10-995-561-33803	Sequence 33803, A
C 538	16	0.5	19	9	US-11-083-784-240695	Sequence 240695,	611	16	0.5	201	6	US-10-995-561-34281	Sequence 34281, A
C 539	16	0.5	19	9	US-11-083-784-461118	Sequence 461118,	612	16	0.5	201	6	US-10-995-561-36309	Sequence 36309, A
C 540	16	0.5	19	9	US-11-083-784-508525	Sequence 508525,	613	16	0.5	201	6	US-10-995-561-36365	Sequence 36365, A
C 541	16	0.5	19	9	US-11-083-784-545859	Sequence 545859,	614	16	0.5	201	6	US-10-995-561-36872	Sequence 36872, A
C 542	16	0.5	19	9	US-11-083-784-661892	Sequence 661892,	615	16	0.5	201	6	US-10-995-561-50343	Sequence 50343, A
C 543	16	0.5	19	9	US-11-083-784-859507	Sequence 859507,	616	16	0.5	201	6	US-10-995-561-51569	Sequence 51569, A
C 544	16	0.5	19	9	US-11-083-784-1069137	Sequence 1069137,	617	16	0.5	201	6	US-10-995-561-63600	Sequence 63600, A
C 545	16	0.5	19	9	US-11-083-784-1173681	Sequence 1173681,	618	16	0.5	201	6	US-10-995-561-63601	Sequence 63601, A
C 546	16	0.5	19	9	US-11-083-784-1271654	Sequence 1271654,	619	16	0.5	201	6	US-10-995-561-67283	Sequence 67283, A
C 547	16	0.5	19	9	US-11-083-784-1271701	Sequence 1271701,	620	16	0.5	201	6	US-10-995-561-74357	Sequence 74357, A
C 548	16	0.5	19	9	US-11-083-784-1466025	Sequence 1466025,	621	16	0.5	201	6	US-10-995-561-74566	Sequence 74566, A
C 549	16	0.5	19	9	US-11-083-784-1468839	Sequence 1468839,	622	16	0.5	201	6	US-10-995-561-74570	Sequence 74570, A
C 550	16	0.5	19	9	US-11-083-784-1489779	Sequence 1489779,	623	16	0.5	201	6	US-10-995-561-74970	Sequence 74970, A
C 551	16	0.5	19	9	US-11-083-784-1489789	Sequence 1489789,	624	16	0.5	201	6	US-10-995-561-74984	Sequence 74984, A
C 552	16	0.5	19	9	US-11-083-784-1489806	Sequence 1489806,	625	16	0.5	201	6	US-10-995-561-74988	Sequence 74988, A
C 553	16	0.5	19	9	US-11-083-784-1503894	Sequence 1503894,	626	16	0.5	201	6	US-10-995-561-76321	Sequence 76321, A
C 554	16	0.5	19	9	US-11-083-784-1503931	Sequence 1503931,	627	16	0.5	201	6	US-10-995-561-76564	Sequence 76564, A
C 555	16	0.5	19	9	US-11-083-784-1527897	Sequence 1527897,	628	16	0.5	201	6	US-10-995-561-77268	Sequence 77268, A
C 556	16	0.5	20	6	US-10-310-914-150695	Sequence 150695, A	629	16	0.5	201	6	US-10-995-561-79646	Sequence 79646, A
C 557	16	0.5	21	6	US-10-750-185-11868	Sequence 11868, A	630	16	0.5	201	6	US-10-995-561-79683	Sequence 79683, A
C 558	16	0.5	21	6	US-10-750-623-11868	Sequence 11868, A	631	16	0.5	201	6	US-10-995-561-79684	Sequence 79684, A
C 559	16	0.5	21	6	US-10-310-914-227799	Sequence 227799,	632	16	0.5	201	6	US-10-995-561-79685	Sequence 79685, A
C 560	16	0.5	21	6	US-10-310-914-455789	Sequence 455789,	633	16	0.5	201	6	US-10-995-561-79686	Sequence 79686, A
C 561	16	0.5	21	6	US-10-310-914-807809	Sequence 807809,	634	16	0.5	201	6	US-10-995-561-79688	Sequence 79688, A
C 562	16	0.5	22	6	US-10-310-914-180185	Sequence 180185,	635	16	0.5	201	6	US-10-995-561-79690	Sequence 79690, A
C 563	16	0.5	22	6	US-10-310-914-108221	Sequence 108221,	636	16	0.5	201	6	US-10-995-561-79706	Sequence 79706, A
C 564	16	0.5	22	6	US-10-310-914-197401	Sequence 197401,	637	16	0.5	201	6	US-10-995-561-81898	Sequence 81898, A
C 565	16	0.5	22	6	US-10-310-914-521990	Sequence 521990,	638	16	0.5	201	7	US-11-124-368A-5162	Sequence 5162, A
C 566	16	0.5	22	6	US-10-310-914-777100	Sequence 777100,	639	16	0.5	201	7	US-11-124-368A-5261	Sequence 5261, A
C 567	16	0.5	22	6	US-10-310-914-1017241	Sequence 1017241,	640	16	0.5	201	7	US-11-124-368A-12561	Sequence 12561, A
C 568	16	0.5	23	6	US-10-310-914-108186	Sequence 108186,	641	16	0.5	201	7	US-11-124-368A-12561	Sequence 12561, A
C 569	16	0.5	23	6	US-10-310-914-108198	Sequence 108198,	642	16	0.5	201	7	US-11-124-368A-15455	Sequence 15455, A
C 570	16	0.5	23	6	US-10-310-914-384576	Sequence 384576,	643	16	0.5	201	7	US-11-124-368A-15455	Sequence 15455, A
C 571	16	0.5	23	6	US-10-310-914-971908	Sequence 971908,	644	16	0.5	201	7	US-11-124-368A-16388	Sequence 16388, A
C 572	16	0.5	24	6	US-10-310-914-149192	Sequence 149192,	645	16	0.5	201	7	US-11-124-368A-16951	Sequence 16951, A
C 573	16	0.5	24	6	US-10-310-914-153952	Sequence 153952,	646	16	0.5	201	7	US-11-124-368A-16951	Sequence 16951, A
C 574	16	0.5	24	6	US-10-310-914-227800	Sequence 227800,	647	16	0.5	201	7	US-11-124-368A-20716	Sequence 20716, A
C 575	16	0.5	24	6	US-10-310-914-353979	Sequence 353979,	648	16	0.5	396	6	US-10-769-744-465	Sequence 465, A
C 576	16	0.5	24	6	US-10-310-914-384676	Sequence 384676,	649	16	0.5	404	7	US-11-000-688-1299	Sequence 1299, A
C 577	16	0.5	25	6	US-10-310-914-971792	Sequence 971792,	650	16	0.5	422	7	US-11-000-688-1371	Sequence 1371, A
C 578	16	0.5	25	6	US-10-310-914-743739	Sequence 743739,	651	16	0.5	493	6	US-10-750-185-1871	Sequence 1871, A
C 579	16	0.5	25	7	US-11-121-849-419242	Sequence 419242,	652	16	0.5	493	6	US-10-750-623-1871	Sequence 1871, A
C 580	16	0.5	25	7	US-11-121-849-593214	Sequence 593214,	653	16	0.5	554	6	US-10-750-623-30481	Sequence 30481, A
C 581	16	0.5	25	7	US-11-121-849-593215	Sequence 593215,	654	16	0.5	554	6	US-10-750-623-30481	Sequence 30481, A
C 582	16	0.5	25	7	US-11-121-849-593216	Sequence 593216,	655	16	0.5	578	7	US-11-000-688-1296	Sequence 1296, A
C 583	16	0.5	25	7	US-11-121-849-606117	Sequence 606117,	656	16	0.5	598	6	US-10-750-185-185	Sequence 185, A
C 584	16	0.5	25	7	US-11-136-527-314800	Sequence 314800,	657	16	0.5	598	6	US-10-750-185-185	Sequence 185, A
C 585	16	0.5	25	7	US-11-136-527-314813	Sequence 314813,	658	16	0.5	598	6	US-10-750-185-185	Sequence 185, A
C 586	16	0.5	25	7	US-11-136-527-350709	Sequence 350709,	659	16	0.5	598	6	US-10-750-623-4113	Sequence 4113, A
C 587	16	0.5	27	6	US-10-310-914-153960	Sequence 153960,	660	16	0.5	598	6	US-10-750-623-19850	Sequence 19850, A
C 588	16	0.5	30	6	US-10-857-780-174	Sequence 174, App	661	16	0.5	598	6	US-10-750-623-19850	Sequence 19850, A
C 589	16	0.5	51	7	US-11-102-743-14	Sequence 14, App1	662	16	0.5	600	6	US-10-750-185-108	Sequence 108, App
C 590	16	0.5	60	6	US-10-310-914-7452	Sequence 7452, App	663	16	0.5	600	6	US-10-750-185-526	Sequence 526, App
C 591	16	0.5	63	6	US-10-310-914A-577	Sequence 577, App	664	16	0.5	600	6	US-10-750-185-2132	Sequence 2132, App
C 592	16	0.5	164	6	US-10-995-561-6005	Sequence 6005, App	665	16	0.5	600	6	US-10-750-623-2224	Sequence 2224, App
C 593	16	0.5	201	6	US-10-995-561-3188	Sequence 3188, App	666	16	0.5	600	6	US-10-750-185-19952	Sequence 19952, App
C 594	16	0.5	201	6	US-10-995-561-5170	Sequence 5170, App	667	16	0.5	600	6	US-10-750-185-20862	Sequence 20862, App
C 595	16	0.5	201	6	US-10-995-561-14580	Sequence 14580, App	668	16	0.5	600	6	US-10-750-623-21279	Sequence 21279, App
C 596	16	0.5	201	6	US-10-995-561-15984	Sequence 15984, App	669	16	0.5	600	6	US-10-750-623-2108	Sequence 2108, App
C 597	16	0.5	201	6	US-10-995-561-16055	Sequence 16055, App	670	16	0.5	600	6	US-10-750-623-2132	Sequence 2132, App
C 598	16	0.5	201	6	US-10-995-561-16305	Sequence 16305, App	671	16	0.5	600	6	US-10-750-623-2132	Sequence 2132, App
C 599	16	0.5	201	6	US-10-995-561-16323	Sequence 16323, App	672	16	0.5	600	6	US-10-750-623-2224	Sequence 2224, App
C 600	16	0.5	201	6	US-10-995-561-16964	Sequence 16964, App	673	16	0.5	600	6	US-10-750-623-19952	Sequence 19952, App
C 601	16	0.5	201	6	US-10-995-561-23382	Sequence 23382, App	674	16	0.5	600	6	US-10-750-623-20862	Sequence 20862, App
C 602	16	0.5	201	6	US-10-995-561-23138	Sequence 23138, App	675	16	0.5	600	6	US-10-750-623-21279	Sequence 21279, App
C 603	16	0.5	201	6	US-10-995-561-26334	Sequence 26334, App	676	16	0.5	600	7	US-11-136-527-6674	Sequence 6674, App
C 604	16	0.5	201	6	US-10-995-561-27814	Sequence 27814, App	677	16	0.5	600	7	US-11-136-527-7766	Sequence 7766, App
C 605	16	0.5	201	6	US-10-995-561-30979	Sequence 30979, App	678	16	0.5	600	7	US-11-128-061-3912	Sequence 3912, App
C 606	16	0.5	201	6	US-10-995-561-30993	Sequence 30993, App	679	16	0.5	636	6	US-10-131-882A-807	Sequence 807, App
C 607	16	0.5	201	6	US-10-995-561-33529	Sequence 33529, App	680	16	0.5	653	6	US-10-750-185-60513	Sequence 60513, App

681	16	0.5	653	6	US-10-750-623-60513	Sequence 60513, A
C 682	-16	0.5	682	6	US-10-750-185-33129	Sequence 33129, A
C 683	-16	0.5	682	6	US-10-750-623-33129	Sequence 33129, A
C 684	-16	0.5	701	6	US-10-750-185-37301	Sequence 37301, A
C 685	-16	0.5	701	6	US-10-750-623-37301	Sequence 37301, A
C 686	-16	0.5	710	6	US-10-750-185-44241	Sequence 44241, A
C 687	-16	0.5	710	6	US-10-750-623-44241	Sequence 44241, A
C 688	-16	0.5	713	6	US-10-750-185-25895	Sequence 25895, A
C 689	-16	0.5	713	6	US-10-750-623-25895	Sequence 25895, A
C 690	-16	0.5	720	6	US-10-750-185-38540	Sequence 38540, A
C 691	-16	0.5	720	6	US-10-750-623-38540	Sequence 38540, A
C 692	-16	0.5	733	6	US-10-750-185-38689	Sequence 38689, A
C 693	-16	0.5	733	6	US-10-750-623-38689	Sequence 38689, A
C 694	-16	0.5	743	6	US-10-750-185-31219	Sequence 31219, A
C 695	-16	0.5	743	6	US-10-750-623-31219	Sequence 31219, A
C 696	-16	0.5	744	6	US-10-512-184-11	Sequence 11, Appl
C 697	-16	0.5	744	6	US-10-454-437-169	Sequence 169, Appl
C 698	-16	0.5	753	6	US-10-750-185-55019	Sequence 55019, A
C 699	-16	0.5	753	6	US-10-750-623-55019	Sequence 55019, A
C 700	-16	0.5	759	6	US-10-750-185-63783	Sequence 63783, A
C 701	-16	0.5	759	6	US-10-750-623-63783	Sequence 63783, A
C 702	-16	0.5	769	6	US-10-750-623-41177	Sequence 41177, A
C 703	-16	0.5	769	6	US-10-750-185-41177	Sequence 41177, A
C 704	-16	0.5	771	6	US-10-467-657-175	Sequence 175, Appl
C 705	-16	0.5	771	6	US-10-467-657-3697	Sequence 3697, Ap
C 706	-16	0.5	772	6	US-10-750-185-26624	Sequence 26624, A
C 707	-16	0.5	772	6	US-10-750-623-26624	Sequence 26624, A
C 708	-16	0.5	783	6	US-10-750-185-27181	Sequence 27181, A
C 709	-16	0.5	783	6	US-10-750-623-27181	Sequence 27181, A
C 710	-16	0.5	789	6	US-10-750-185-29066	Sequence 29066, A
C 711	-16	0.5	789	6	US-10-750-623-29066	Sequence 29066, A
C 712	-16	0.5	795	6	US-10-750-185-59336	Sequence 59336, A
C 713	-16	0.5	795	6	US-10-750-623-59336	Sequence 59336, A
C 714	-16	0.5	795	7	US-11-188-743-14	Sequence 14, Appl
C 715	-16	0.5	806	6	US-10-750-185-25862	Sequence 25862, A
C 716	-16	0.5	806	6	US-10-750-623-25862	Sequence 25862, A
C 717	-16	0.5	812	6	US-10-750-185-38571	Sequence 38571, A
C 718	-16	0.5	812	6	US-10-750-623-38571	Sequence 38571, A
C 719	-16	0.5	821	6	US-10-750-185-52237	Sequence 52237, A
C 720	-16	0.5	821	6	US-10-750-623-52237	Sequence 52237, A
C 721	-16	0.5	832	6	US-10-750-185-37014	Sequence 37014, A
C 722	-16	0.5	832	6	US-10-750-623-37014	Sequence 37014, A
C 723	-16	0.5	860	6	US-10-750-185-45542	Sequence 45542, A
C 724	-16	0.5	860	6	US-10-750-623-45542	Sequence 45542, A
C 725	-16	0.5	867	6	US-10-750-185-28541	Sequence 28541, A
C 726	-16	0.5	867	6	US-10-750-623-28541	Sequence 28541, A
C 727	-16	0.5	884	6	US-10-750-185-43902	Sequence 43902, A
C 728	-16	0.5	884	6	US-10-750-623-43902	Sequence 43902, A
C 729	-16	0.5	897	7	US-11-128-061-270	Sequence 270, Appl
C 730	-16	0.5	913	6	US-10-750-185-62985	Sequence 62985, A
C 731	-16	0.5	913	6	US-10-750-623-62985	Sequence 62985, A
C 732	-16	0.5	938	6	US-10-750-185-58777	Sequence 58777, A
C 733	-16	0.5	938	6	US-10-750-623-58777	Sequence 58777, A
C 734	-16	0.5	939	6	US-10-821-234-271	Sequence 271, Appl
C 735	-16	0.5	939	6	US-10-750-185-33635	Sequence 33635, A
C 736	-16	0.5	939	6	US-10-750-623-33635	Sequence 33635, A
C 737	-16	0.5	958	6	US-10-750-185-57703	Sequence 57703, A
C 738	-16	0.5	958	6	US-10-750-623-57703	Sequence 57703, A
C 739	-16	0.5	958	6	US-10-750-185-31017	Sequence 31017, A
C 740	-16	0.5	960	7	US-10-750-623-31017	Sequence 31017, A
C 741	-16	0.5	960	7	US-11-150-883-20	Sequence 20, Appl
C 742	-16	0.5	961	6	US-10-750-185-38959	Sequence 38959, A
C 743	-16	0.5	961	6	US-10-750-623-38959	Sequence 38959, A
C 744	-16	0.5	968	6	US-10-750-185-32696	Sequence 32696, A
C 745	-16	0.5	968	6	US-10-750-623-32696	Sequence 32696, A
C 746	-16	0.5	977	6	US-10-944-272-80	Sequence 80, Appl
C 747	-16	0.5	982	6	US-10-944-272-81	Sequence 81, Appl
C 748	-16	0.5	991	6	US-10-944-272-82	Sequence 82, Appl
C 749	-16	0.5	996	6	US-10-944-272-83	Sequence 83, Appl
C 750	-16	0.5	996	6	US-10-750-185-48337	Sequence 48337, A
C 751	-16	0.5	996	6	US-10-750-623-48337	Sequence 48337, A
C 752	-16	0.5	1001	6	US-10-750-185-30964	Sequence 30964, A
C 753	-16	0.5	1001	6	US-10-750-623-30964	Sequence 30964, A

754	16	0.5	1026	7	US-11-113-908-93	Sequence 93, Appl
C 755	-16	0.5	1036	6	US-10-750-185-35248	Sequence 35248, A
C 756	-16	0.5	1036	6	US-10-750-623-35248	Sequence 35248, A
C 757	-16	0.5	1048	6	US-10-750-185-30231	Sequence 30231, A
C 758	-16	0.5	1048	6	US-10-750-623-30231	Sequence 30231, A
C 759	-16	0.5	1052	6	US-10-750-185-49803	Sequence 49803, A
C 760	-16	0.5	1052	6	US-10-750-623-49803	Sequence 49803, A
C 761	-16	0.5	1061	6	US-10-750-185-46949	Sequence 46949, A
C 762	-16	0.5	1061	6	US-10-750-623-46949	Sequence 46949, A
C 763	-16	0.5	1085	6	US-10-750-185-30543	Sequence 30543, A
C 764	-16	0.5	1085	6	US-10-750-623-30543	Sequence 30543, A
C 765	-16	0.5	1085	6	US-10-750-185-51776	Sequence 51776, A
C 766	-16	0.5	1085	6	US-10-750-623-51776	Sequence 51776, A
C 767	-16	0.5	1103	7	US-11-136-527-1670	Sequence 1670, Ap
C 768	-16	0.5	1103	6	US-10-750-185-39476	Sequence 39476, A
C 769	-16	0.5	1103	6	US-10-750-623-39476	Sequence 39476, A
C 770	-16	0.5	1115	6	US-10-750-185-34091	Sequence 34091, A
C 771	-16	0.5	1115	6	US-10-750-623-34091	Sequence 34091, A
C 772	-16	0.5	1125	7	US-11-136-527-894	Sequence 894, Appl
C 773	-16	0.5	1132	6	US-10-750-185-27461	Sequence 27461, A
C 774	-16	0.5	1132	6	US-10-750-623-27461	Sequence 27461, A
C 775	-16	0.5	1141	6	US-10-750-185-58935	Sequence 58935, A
C 776	-16	0.5	1141	6	US-10-750-623-58935	Sequence 58935, A
C 777	-16	0.5	1143	6	US-10-525-674-27	Sequence 27, Appl
C 778	-16	0.5	1149	6	US-10-750-185-59099	Sequence 59099, A
C 779	-16	0.5	1151	6	US-10-750-623-45225	Sequence 45225, A
C 780	-16	0.5	1151	6	US-10-750-185-45225	Sequence 45225, A
C 781	-16	0.5	1151	6	US-10-750-623-45225	Sequence 45225, A
C 782	-16	0.5	1155	6	US-10-750-185-35027	Sequence 35027, A
C 783	-16	0.5	1155	6	US-10-750-623-35027	Sequence 35027, A
C 784	-16	0.5	1157	6	US-10-750-185-45746	Sequence 45746, A
C 785	-16	0.5	1157	6	US-10-750-623-45746	Sequence 45746, A
C 786	-16	0.5	1157	6	US-10-750-185-45746	Sequence 45746, A
C 787	-16	0.5	1170	6	US-10-750-623-45375	Sequence 45375, A
C 788	-16	0.5	1170	6	US-10-750-185-45375	Sequence 45375, A
C 789	-16	0.5	1170	6	US-10-750-623-45375	Sequence 45375, A
C 790	-16	0.5	1172	6	US-10-750-185-52801	Sequence 52801, A
C 791	-16	0.5	1172	6	US-10-750-623-52801	Sequence 52801, A
C 792	-16	0.5	1187	6	US-10-750-185-37975	Sequence 37975, A
C 793	-16	0.5	1187	6	US-10-750-623-37975	Sequence 37975, A
C 794	-16	0.5	1199	6	US-10-750-185-51619	Sequence 51619, A
C 795	-16	0.5	1199	6	US-10-750-623-51619	Sequence 51619, A
C 796	-16	0.5	1210	6	US-10-750-185-51932	Sequence 51932, A
C 797	-16	0.5	1210	6	US-10-750-623-51932	Sequence 51932, A
C 798	-16	0.5	1224	6	US-10-750-185-32034	Sequence 32034, A
C 799	-16	0.5	1224	6	US-10-750-623-32034	Sequence 32034, A
C 800	-16	0.5	1225	6	US-10-750-185-60731	Sequence 60731, A
C 801	-16	0.5	1225	6	US-10-750-623-60731	Sequence 60731, A
C 802	-16	0.5	1235	6	US-10-750-185-28369	Sequence 28369, A
C 803	-16	0.5	1235	6	US-10-750-623-28369	Sequence 28369, A
C 804	-16	0.5	1247	6	US-10-118-590-15	Sequence 15, Appl
C 805	-16	0.5	1254	6	US-10-821-234-684	Sequence 684, Appl
C 806	-16	0.5	1263	6	US-10-750-185-33787	Sequence 33787, A
C 807	-16	0.5	1263	6	US-10-750-623-33787	Sequence 33787, A
C 808	-16	0.5	1267	6	US-10-750-185-50045	Sequence 50045, A
C 809	-16	0.5	1267	6	US-10-750-623-50045	Sequence 50045, A
C 810	-16	0.5	1312	6	US-10-750-185-27465	Sequence 27465, A
C 811	-16	0.5	1312	6	US-10-750-623-27465	Sequence 27465, A
C 812	-16	0.5	1334	7	US-11-136-527-3397	Sequence 3397, Ap
C 813	-16	0.5	1334	7	US-10-750-185-57569	Sequence 57569, A
C 814	-16	0.5	1336	6	US-10-750-623-57569	Sequence 57569, A
C 815	-16	0.5	1336	6	US-10-750-185-57274	Sequence 57274, A
C 816	-16	0.5	1342	6	US-10-750-623-57274	Sequence 57274, A
C 817	-16	0.5	1342	6	US-10-750-185-51274	Sequence 51274, A
C 818	-16	0.5	1349	7	US-11-136-527-3183	Sequence 3183, Ap
C 819	-16	0.5	1349	7	US-10-750-185-3183	Sequence 3183, A
C 820	-16	0.5	1361	6	US-10-750-623-35593	Sequence 35593, A
C 821	-16	0.5	1361	6	US-10-750-185-35593	Sequence 35593, A
C 822	-16	0.5	1362	6	US-10-750-623-41591	Sequence 41591, A
C 823	-16	0.5	1362	6	US-10-750-185-41591	Sequence 41591, A
C 824	-16	0.5	1365	7	US-11-037-243-44	Sequence 44, Appl
C 825	-16	0.5	1373	6	US-10-750-185-48083	Sequence 48083, A
C 826	-16	0.5	1373	6	US-10-750-623-48083	Sequence 48083, A

C 827	16	0.5	1373	6	US-10-750-623-48083	Sequence 48083, A	C 900	16	0.5	1693	6	US-10-750-185-39216	Sequence 39216, A
C 828	16	0.5	1376	6	US-10-750-185-55168	Sequence 55168, A	C 901	16	0.5	1693	6	US-10-750-623-30216	Sequence 30216, A
C 829	16	0.5	1376	6	US-10-750-623-55168	Sequence 55168, A	C 902	16	0.5	1707	6	US-10-750-185-60686	Sequence 60686, A
C 830	16	0.5	1380	6	US-10-750-185-35064	Sequence 35064, A	C 903	16	0.5	1707	6	US-10-750-623-60686	Sequence 60686, A
C 831	16	0.5	1380	6	US-10-750-623-35064	Sequence 35064, A	C 904	16	0.5	1716	6	US-10-750-185-26455	Sequence 26455, A
C 832	16	0.5	1397	6	US-10-750-185-37725	Sequence 37725, A	C 905	16	0.5	1716	6	US-10-750-623-26455	Sequence 26455, A
C 833	16	0.5	1397	6	US-10-750-623-37725	Sequence 37725, A	C 906	16	0.5	1718	6	US-10-750-185-33514	Sequence 33514, A
C 834	16	0.5	1400	7	US-11-136-527-7622	Sequence 7622, Ap	C 907	16	0.5	1718	6	US-10-750-623-33514	Sequence 33514, A
C 835	16	0.5	1400	7	US-11-136-527-7954	Sequence 7954, Ap	C 908	16	0.5	1733	6	US-10-750-185-39627	Sequence 39627, A
C 836	16	0.5	1400	7	US-11-136-527-7959	Sequence 7959, Ap	C 909	16	0.5	1733	6	US-10-750-623-39627	Sequence 39627, A
C 837	16	0.5	1400	7	US-11-136-527-8084	Sequence 8084, Ap	C 910	16	0.5	1734	6	US-10-750-185-35310	Sequence 35310, A
C 838	16	0.5	1400	7	US-11-136-527-8091	Sequence 8091, Ap	C 911	16	0.5	1734	6	US-10-750-623-35310	Sequence 35310, A
C 839	16	0.5	1404	6	US-10-750-185-41344	Sequence 41344, A	C 912	16	0.5	1741	6	US-10-750-185-39483	Sequence 39483, A
C 840	16	0.5	1404	6	US-10-750-623-41344	Sequence 41344, A	C 913	16	0.5	1741	6	US-10-750-623-39483	Sequence 39483, A
C 841	16	0.5	1406	6	US-10-750-185-38066	Sequence 38066, A	C 914	16	0.5	1745	6	US-10-750-185-50271	Sequence 50271, A
C 842	16	0.5	1406	6	US-10-750-623-38066	Sequence 38066, A	C 915	16	0.5	1745	6	US-10-750-623-50271	Sequence 50271, A
C 843	16	0.5	1411	6	US-10-750-185-59086	Sequence 59086, A	C 916	16	0.5	1755	6	US-10-750-185-60604	Sequence 60604, A
C 844	16	0.5	1411	6	US-10-750-623-59086	Sequence 59086, A	C 917	16	0.5	1755	6	US-10-750-623-60604	Sequence 60604, A
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C 847	16	0.5	1420	6	US-10-750-185-58111	Sequence 58111, A	C 920	16	0.5	1766	6	US-10-750-185-55411	Sequence 55411, A
C 848	16	0.5	1420	6	US-10-750-623-58111	Sequence 58111, A	C 921	16	0.5	1766	6	US-10-750-623-55411	Sequence 55411, A
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C 850	16	0.5	1437	6	US-10-750-623-43877	Sequence 43877, A	C 923	16	0.5	1775	6	US-10-750-623-48024	Sequence 48024, A
C 851	16	0.5	1437	6	US-10-798-579A-3	Sequence 3, Appl1	C 924	16	0.5	1777	6	US-10-750-185-64049	Sequence 64049, A
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C 853	16	0.5	1466	6	US-10-750-185-37048	Sequence 37048, A	C 926	16	0.5	1784	6	US-10-750-185-34508	Sequence 34508, A
C 854	16	0.5	1466	6	US-10-750-623-37048	Sequence 37048, A	C 927	16	0.5	1784	6	US-10-750-623-34508	Sequence 34508, A
C 855	16	0.5	1473	6	US-10-750-185-45340	Sequence 45340, A	C 928	16	0.5	1785	7	US-11-188-743-13	Sequence 13, Appl1
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C 858	16	0.5	1477	6	US-10-750-623-28868	Sequence 28868, A	C 931	16	0.5	1822	6	US-10-750-185-44372	Sequence 44372, A
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C 863	16	0.5	1494	6	US-10-750-185-38691	Sequence 38691, A	C 936	16	0.5	1840	6	US-10-750-623-64083	Sequence 64083, A
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C 865	16	0.5	1500	7	US-11-087-100-7	Sequence 7, Appl1	C 938	16	0.5	1848	6	US-10-512-184-25	Sequence 25, Appl1
C 866	16	0.5	1500	7	US-11-087-084-7	Sequence 7, Appl1	C 939	16	0.5	1857	6	US-10-750-185-47431	Sequence 47431, A
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C 868	16	0.5	1504	6	US-10-750-185-44259	Sequence 44259, A	C 941	16	0.5	1859	6	US-10-750-185-34982	Sequence 34982, A
C 869	16	0.5	1504	6	US-10-750-623-44259	Sequence 44259, A	C 942	16	0.5	1859	6	US-10-750-623-34982	Sequence 34982, A
C 870	16	0.5	1505	6	US-10-750-185-64442	Sequence 64442, A	C 943	16	0.5	1859	6	US-10-750-185-61933	Sequence 61933, A
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C 873	16	0.5	1526	6	US-10-750-623-24606	Sequence 24606, A	C 946	16	0.5	1865	6	US-10-750-185-52204	Sequence 52204, A
C 874	16	0.5	1536	6	US-10-750-185-60649	Sequence 60649, A	C 947	16	0.5	1885	6	US-10-750-623-51776	Sequence 51776, A
C 875	16	0.5	1536	6	US-10-750-623-60649	Sequence 60649, A	C 948	16	0.5	1885	6	US-10-750-623-51776	Sequence 51776, A
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C 877	16	0.5	1565	6	US-10-750-623-44536	Sequence 44536, A	C 950	16	0.5	1887	6	US-10-750-623-31786	Sequence 31786, A
C 878	16	0.5	1571	6	US-10-750-185-59692	Sequence 59692, A	C 951	16	0.5	1896	6	US-10-750-185-29524	Sequence 29524, A
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C 880	16	0.5	1581	6	US-10-750-185-40863	Sequence 40863, A	C 953	16	0.5	1903	6	US-10-750-185-37484	Sequence 37484, A
C 881	16	0.5	1581	6	US-10-750-623-51037	Sequence 51037, A	C 954	16	0.5	1903	6	US-10-750-623-37484	Sequence 37484, A
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C 893	16	0.5	1654	7	US-11-122-144-3	Sequence 3, Appl1	C 966	16	0.5	1990	6	US-10-750-185-64598	Sequence 64598, A
C 894	16	0.5	1670	6	US-10-750-185-57206	Sequence 57206, A	C 967	16	0.5	1990	6	US-10-750-623-64598	Sequence 64598, A
C 895	16	0.5	1670	6	US-10-750-623-57206	Sequence 57206, A	C 968	16	0.5	2000	7	US-11-194-246-380	Sequence 380, App
C 896	16	0.5	1682	6	US-10-750-185-39703	Sequence 39703, A	C 969	16	0.5	2002	6	US-10-750-185-52154	Sequence 52154, A
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C 975      16      0.5      2030      6      US-10-750-623-35998      Sequence 35998, A
C 976      16      0.5      2038      6      US-10-750-185-40987      Sequence 40987, A
C 977      16      0.5      2038      6      US-10-750-623-40987      Sequence 40987, A
C 978      16      0.5      2045      6      US-10-750-185-47809      Sequence 47809, A
C 979      16      0.5      2045      6      US-10-750-623-47809      Sequence 47809, A
C 980      16      0.5      2057      6      US-10-118-590-27      Sequence 27, Appl
C 981      16      0.5      2085      6      US-10-750-185-53162      Sequence 53162, A
C 982      16      0.5      2085      6      US-10-750-623-53162      Sequence 53162, A
C 983      16      0.5      2100      6      US-10-750-185-54849      Sequence 54849, A
C 984      16      0.5      2100      6      US-10-750-623-54849      Sequence 54849, A
C 985      16      0.5      2126      7      US-11-136-527-3324      Sequence 3324, Ap
C 986      16      0.5      2139      6      US-10-453-372-47      Sequence 47, Appl
C 987      16      0.5      2145      6      US-10-750-185-30137      Sequence 30137, A
C 988      16      0.5      2161      6      US-10-750-623-30137      Sequence 30137, A
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C 990      16      0.5      2170      6      US-10-750-623-37376      Sequence 37376, A
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C 992      16      0.5      2179      6      US-10-750-623-53966      Sequence 53966, A
C 993      16      0.5      2179      6      US-10-750-185-46423      Sequence 46423, A
C 994      16      0.5      2184      6      US-10-750-623-46423      Sequence 46423, A
C 995      16      0.5      2184      6      US-10-467-657-1441      Sequence 1441, Ap
C 996      16      0.5      2194      6      US-10-775-185-245      Sequence 245, App
C 997      16      0.5      2196      6      US-10-750-623-30957      Sequence 30957, A
C 998      16      0.5      2196      6      US-10-750-623-30957      Sequence 30957, A
C 999      16      0.5      2209      6      US-10-750-185-62656      Sequence 62656, A
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## ALIGNMENTS

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RESULT 1
US-10-750-185-30474
/ Sequence 30474, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30474
/ LENGTH: 1219
/ TYPE: DNA
/ ORGANISM: Bovine 19866880607526
US-10-750-185-30474

Query Match      1.0%; Score 34; DB 6; Length 1219;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      516      TCTGCCAGACGAGACCTTCTGCTTTTGACAT 549
DB      1161      TCTGCCAGACGAGACCTTCTGCTTTTGACAT 1194
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RESULT 2
US-10-750-623-30474
/ Sequence 30474, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
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/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30474
/ LENGTH: 1219
/ TYPE: DNA
/ ORGANISM: Bovine 19866880607526
US-10-750-623-30474

Query Match      1.0%; Score 34; DB 6; Length 1219;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1161      TCTGCCAGACGAGACCTTCTGCTTTTGACAT 1194
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RESULT 3
US-10-310-914A-213685/C
/ Sequence 213685, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Kyuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087,0200,CEUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 213685
/ LENGTH: 25
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-213685
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Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      25      AAATCTACTTTCTTCTTACTACTACA 1
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RESULT 4
US-11-121-849-177180
/ Sequence 177180, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded 8
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177180

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3009 GCAGGAGATGCAGTCTCTTAA 3033
DB 1 GCAGGAGATGCAGTCTCTTAA 25

RESULT 5
US-11-121-849-177181
; Sequence 177181, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177181

Query Match
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3019 GCAGGTCTCTTAAAGCATGATG 3043
DB 1 GCAGGTCTCTTAAAGCATGATG 25

RESULT 6
US-11-121-849-177182
; Sequence 177182, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177182

Query Match
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3071 TGTATATGCTCCACACTACGCT 3095
DB 1 TGTATATGCTCCACACTACGCT 3095
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DB 1 TGTATATGCTCCACACTACGCT 25

RESULT 7
US-11-121-849-177183
; Sequence 177183, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177183
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177183

Query Match
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TGCTCCACACTACGCTGTGATAACA 25

RESULT 8
US-11-121-849-177184
; Sequence 177184, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177184

Query Match
Best Local Similarity 100.0%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GATAACACAAACCTCAGATTACG 25

RESULT 9
US-11-121-849-177185
; Sequence 177185, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
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; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177185

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3109 CTCAGTATTCACTATTATAGGCAC 3133
DB      1 CTCAGTATTCACTATTATAGGCAC 25
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RESULT 10
US-11-121-849-177186
; Sequence 177186, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177186
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177186

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3124 TTAGGCACACTAGTTTATACGCA 3148
DB      1 TTAGGCACACTAGTTTATACGCA 25
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RESULT 11
US-11-121-849-177187
; Sequence 177187, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177187
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177187

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3140 TATACGCACTACTGCTTACTACT 3164
DB      1 TATACGCACTACTGCTTACTACT 25
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RESULT 12
US-11-121-849-177188
; Sequence 177188, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177188
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177188

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3166 GACTGTTTGTGGCAATATCTTT 3190
DB      1 GACTGTTTGTGGCAATATCTTT 25
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RESULT 13
US-11-121-849-177189
; Sequence 177189, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177189
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177189

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3213 GAGGTTCAATACATACATCGA 3237
DB      1 GAGGTTCAATACATACATCGA 25
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RESULT 14
US-11-121-849-177190
; Sequence 177190, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
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; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177190
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177190

Query Match          0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3245 TACTTTCTGTTACTACACAAAGC 3269
DB      1 TACTTTCTGTTACTACACAAAGC 25

RESULT 15
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; Sequence 213670, Application US/10310914A
; Publication No.: US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213670
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-213670

Query Match          0.7%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2907 TTGCAACAAGCATAGCTTACTTA 2930
DB      24 TTGCAACAAGCATAGCTTACTTA 1
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Search completed: January 14, 2006, 05:40:21  
Job time : 546 secs

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C 126	19	0.6	516	5	US-10-027-632-43105	Sequence 43105, A	199	19	0.6	738	5	US-10-027-632-143305	Sequence 143305, A
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158	19	0.6	593	4	US-09-925-065A-452970	Sequence 452970, A	231	19	0.6	2403	6	US-10-369-493-42725	Sequence 42725, A
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162	19	0.6	597	4	US-09-925-065A-425667	Sequence 425667, A	C 235	19	0.6	3077	8	US-10-473-136-209	Sequence 136-209
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243	19	0.6	5645	10	US-11-097-143-2356	Sequence 2356, Ap	18	0.5	201	8	US-10-741-600-56428	Sequence 56428, A
244	19	0.6	5981	6	US-10-311-455-1736	Sequence 1736, Ap	18	0.5	201	8	US-10-741-600-56434	Sequence 56434, A
245	19	0.6	5997	7	US-10-221-613-1170	Sequence 1170, App	18	0.5	201	8	US-10-741-600-56550	Sequence 56550, A
246	19	0.6	6077	6	US-10-311-455-11219	Sequence 1219, Ap	18	0.5	238	8	US-10-425-115-13017	Sequence 13017, A
247	19	0.6	6077	6	US-10-311-455-1827	Sequence 1827, Ap	18	0.5	250	3	US-09-960-359-4707	Sequence 4707, Ap
248	19	0.6	6123	6	US-10-311-455-1009	Sequence 1009, Ap	18	0.5	256	7	US-10-424-559-119230	Sequence 119230, Ap
249	19	0.6	6381	6	US-10-311-455-940	Sequence 940, App	18	0.5	267	8	US-10-425-115-68194	Sequence 68194, A
250	19	0.6	6381	6	US-10-240-485-72	Sequence 72, App	18	0.5	284	8	US-10-425-115-160881	Sequence 160881, A
251	19	0.6	6923	7	US-10-221-613-158	Sequence 158, App	18	0.5	320	8	US-10-425-115-18484	Sequence 138484, A
252	19	0.6	7089	5	US-10-339-676-67	Sequence 67, App	18	0.5	350	7	US-10-242-535A-19264	Sequence 19264, A
253	19	0.6	7089	5	US-10-240-453-71	Sequence 71, App	18	0.5	354	7	US-10-085-782A-19264	Sequence 19264, A
254	19	0.6	7659	6	US-10-311-455-162	Sequence 162, App	18	0.5	354	7	US-10-424-559-43873	Sequence 43873, A
255	19	0.6	7969	7	US-10-221-714A-401	Sequence 401, App	18	0.5	360	7	US-10-424-559-117094	Sequence 117094, A
256	19	0.6	7969	7	US-10-433-793-67	Sequence 67, App	18	0.5	366	7	US-10-437-963-71111	Sequence 71111, A
257	19	0.6	8049	6	US-10-311-455-2010	Sequence 2010, Ap	18	0.5	366	3	US-09-732-627A-1075	Sequence 1075, Ap
258	19	0.6	8143	6	US-10-311-455-1869	Sequence 1869, Ap	18	0.5	368	3	US-09-764-869-318	Sequence 318, App
259	19	0.6	8693	5	US-10-172-086-38	Sequence 38, App	18	0.5	368	5	US-10-091-504-318	Sequence 318, App
260	19	0.6	8693	6	US-10-311-455-1484	Sequence 1484, Ap	18	0.5	368	6	US-10-227-557-318	Sequence 318, App
261	19	0.6	8693	7	US-10-311-507-70	Sequence 70, App	18	0.5	386	4	US-09-925-065A-808301	Sequence 808301, A
262	19	0.6	8693	8	US-10-480-846-38	Sequence 38, App	18	0.5	386	4	US-09-925-065A-808302	Sequence 808302, A
263	19	0.6	8998	6	US-10-311-455-1679	Sequence 1679, Ap	18	0.5	387	8	US-10-425-115-46338	Sequence 46338, A
264	19	0.6	11029	7	US-10-221-714A-135	Sequence 135, App	18	0.5	391	9	US-10-972-079-71317	Sequence 71317, A
265	19	0.6	11187	7	US-10-240-453-325	Sequence 325, App	18	0.5	396	4	US-09-925-065A-386158	Sequence 386158, A
266	19	0.6	11327	7	US-10-221-714A-154	Sequence 154, App	18	0.5	426	7	US-10-424-559-39214	Sequence 39214, A
267	19	0.6	11327	7	US-10-311-455-867	Sequence 867, App	18	0.5	429	5	US-10-027-632-182962	Sequence 182962, A
268	19	0.6	12017	3	US-09-735-927-3	Sequence 3, App	18	0.5	435	8	US-10-425-115-97008	Sequence 97008, A
269	19	0.6	13712	6	US-10-311-455-1504	Sequence 3, App	18	0.5	437	9	US-10-357-930-9579	Sequence 9579, Ap
270	19	0.6	13712	6	US-10-257-166-34	Sequence 1504, Ap	18	0.5	437	9	US-10-972-079-71316	Sequence 71316, A
271	19	0.6	17893	6	US-10-311-455-1337	Sequence 1337, Ap	18	0.5	437	9	US-09-925-065A-188733	Sequence 188733, A
272	19	0.6	18133	6	US-10-311-455-913	Sequence 913, App	18	0.5	437	9	US-10-972-079-71316	Sequence 71316, A
273	19	0.6	18133	7	US-10-257-166-99	Sequence 99, App	18	0.5	439	3	US-09-864-701-10523	Sequence 10523, A
274	19	0.6	18218	6	US-10-311-455-1921	Sequence 1921, Ap	18	0.5	453	3	US-09-864-701-10523	Sequence 10523, A
275	19	0.6	21354	7	US-10-221-714A-512	Sequence 512, App	18	0.5	458	8	US-10-424-559-64012	Sequence 64012, A
276	19	0.6	23576	5	US-10-087-192-313	Sequence 313, App	18	0.5	458	8	US-10-425-115-124660	Sequence 124660, A
277	19	0.6	23899	10	US-11-097-143-12784	Sequence 12784, A	18	0.5	464	3	US-09-764-887-1122	Sequence 1122, App
278	19	0.6	34769	7	US-10-221-714A-474	Sequence 474, App	18	0.5	464	4	US-10-073-961-122	Sequence 122, App
279	19	0.6	34769	7	US-10-221-714A-501	Sequence 501, App	18	0.5	465	4	US-09-925-065A-355543	Sequence 355543, A
280	19	0.6	38045	9	US-10-493-759-6	Sequence 6, App	18	0.5	465	4	US-09-925-065A-355544	Sequence 355544, A
281	19	0.6	50002	5	US-10-087-192-994	Sequence 994, App	18	0.5	465	4	US-10-424-535A-265630	Sequence 265630, A
282	19	0.6	50002	7	US-10-322-281-601	Sequence 601, App	18	0.5	465	7	US-10-085-782A-266610	Sequence 266610, A
283	19	0.6	52001	7	US-10-317-273-11	Sequence 11, App	18	0.5	465	7	US-10-357-930-30782	Sequence 30782, A
284	19	0.6	56840	7	US-10-322-281-85	Sequence 85, App	18	0.5	465	8	US-10-357-930-30782	Sequence 30782, A
285	19	0.6	70000	7	US-10-210-723-13	Sequence 13, App	18	0.5	465	8	US-10-357-930-30782	Sequence 30782, A
286	19	0.6	107613	7	US-10-333-069-1	Sequence 1, App	18	0.5	466	7	US-10-424-559-72082	Sequence 72082, A
287	19	0.6	114693	8	US-10-473-392-3	Sequence 3, App	18	0.5	471	4	US-09-925-065A-257642	Sequence 257642, A
288	19	0.6	186854	4	US-10-872-156-34	Sequence 34, App	18	0.5	474	4	US-09-925-065A-796671	Sequence 796671, A
289	19	0.6	203654	3	US-09-820-905-3	Sequence 3, App	18	0.5	476	4	US-10-425-115-17357	Sequence 17357, A
290	19	0.6	203654	9	US-10-473-338A-3	Sequence 3, App	18	0.5	480	4	US-09-925-065A-662519	Sequence 662519, A
291	19	0.6	244196	8	US-10-741-600-17745	Sequence 1, App	18	0.5	485	4	US-09-925-065A-98448	Sequence 98448, A
292	19	0.6	304905	7	US-10-271-416-1	Sequence 1, App	18	0.5	485	4	US-09-925-065A-98448	Sequence 98448, A
293	19	0.6	366710	8	US-10-719-993-6792	Sequence 6792, Ap	18	0.5	486	3	US-09-764-887-586	Sequence 586, App
294	19	0.6	385320	8	US-10-741-600-17796	Sequence 17796, A	18	0.5	486	3	US-09-764-887-587	Sequence 587, App
295	19	0.6	447894	9	US-10-723-670-1	Sequence 1, App	18	0.5	486	5	US-10-073-961-586	Sequence 586, App
296	19	0.6	3673778	6	US-10-312-841-2	Sequence 2, App	18	0.5	486	5	US-09-925-065A-779212	Sequence 779212, A
297	18	0.5	21	6	US-10-032-585-518	Sequence 518, Ap	18	0.5	488	4	US-09-925-065A-779213	Sequence 779213, A
298	18	0.5	25	10	US-11-036-317-650286	Sequence 650286, A	18	0.5	488	4	US-09-925-065A-779213	Sequence 779213, A
299	18	0.5	25	10	US-11-036-317-815617	Sequence 815617, A	18	0.5	488	4	US-09-925-065A-779213	Sequence 779213, A
300	18	0.5	25	10	US-11-036-317-844982	Sequence 844982, A	18	0.5	492	4	US-09-925-065A-990640	Sequence 990640, A
301	18	0.5	147	3	US-10-674-124A-3444	Sequence 3444, Ap	18	0.5	497	4	US-09-925-065A-759582	Sequence 759582, A
302	18	0.5	181	3	US-09-983-965-2498	Sequence 2499, Ap	18	0.5	497	4	US-09-925-065A-759583	Sequence 759583, A
303	18	0.5	201	8	US-10-719-993-9141	Sequence 9141, Ap	18	0.5	497	4	US-09-925-065A-759584	Sequence 759584, A
304	18	0.5	201	8	US-10-719-993-9293	Sequence 9293, Ap	18	0.5	513	7	US-10-424-559-53560	Sequence 53560, A
305	18	0.5	201	8	US-10-719-993-13062	Sequence 13062, A	18	0.5	514	4	US-09-925-065A-501299	Sequence 501299, A
306	18	0.5	201	8	US-10-719-993-18070	Sequence 18070, A	18	0.5	514	4	US-09-925-065A-501300	Sequence 501300, A
307	18	0.5	201	8	US-10-719-993-20779	Sequence 20779, A	18	0.5	514	4	US-09-925-065A-501301	Sequence 501301, A
308	18	0.5	201	8	US-10-741-600-16350	Sequence 16350, A	18	0.5	516	9	US-10-501-282-4519	Sequence 4519, Ap
309	18	0.5	201	8	US-10-741-600-16354	Sequence 16354, A	18	0.5	519	9	US-10-972-079-71315	Sequence 71315, A
310	18	0.5	201	8	US-10-741-600-16360	Sequence 16360, A	18	0.5	523	4	US-09-925-065A-520669	Sequence 520669, A
311	18	0.5	201	8	US-10-741-600-16367	Sequence 16367, A	18	0.5	524	4	US-09-925-065A-505383	Sequence 505383, A
312	18	0.5	201	8	US-10-741-600-16371	Sequence 16371, A	18	0.5	525	4	US-09-925-065A-277986	Sequence 277986, A
313	18	0.5	201	8	US-10-741-600-16377	Sequence 16377, A	18	0.5				
314	18	0.5	201	8	US-10-741-600-40612	Sequence 40612, A	18	0.5				
315	18	0.5	201	8	US-10-741-600-56400	Sequence 56400, A	18	0.5				

389	18	0.5	526	4	US-09-925-065A-431365	Sequence 431365,	462	18	0.5	577	4	US-09-925-065A-531646	Sequence 531646,
390	18	0.5	526	4	US-09-925-065A-431366	Sequence 431366,	463	18	0.5	578	4	US-09-925-065A-437884	Sequence 437884, A
391	18	0.5	529	4	US-09-925-065A-163141	Sequence 163141,	464	18	0.5	579	4	US-09-925-065A-368035	Sequence 368035
392	18	0.5	529	4	US-09-925-065A-387151	Sequence 387151,	465	18	0.5	579	4	US-09-925-065A-368037	Sequence 368037,
393	18	0.5	531	4	US-09-925-065A-747254	Sequence 747254,	466	18	0.5	579	6	US-10-027-632-770338	Sequence 770338
394	18	0.5	532	4	US-09-925-065A-750083	Sequence 750083,	467	18	0.5	579	6	US-10-027-632-770338	Sequence 770338
395	18	0.5	534	6	US-10-156-761-6745	Sequence 6745, Ap	468	18	0.5	580	4	US-09-925-065A-651243	Sequence 651243,
396	18	0.5	537	8	US-10-425-115-154372	Sequence 154372,	469	18	0.5	581	4	US-09-925-065A-125212	Sequence 125212,
397	18	0.5	540	4	US-09-925-065A-578152	Sequence 578152,	470	18	0.5	582	4	US-09-925-065A-311094	Sequence 311094,
398	18	0.5	541	4	US-09-925-065A-278368	Sequence 278368,	471	18	0.5	582	4	US-09-925-065A-680051	Sequence 680051,
399	18	0.5	542	9	US-10-972-079-69712	Sequence 69712, A	472	18	0.5	582	4	US-09-925-065A-793814	Sequence 793814,
400	18	0.5	543	4	US-09-925-065A-163561	Sequence 163561,	473	18	0.5	582	7	US-10-282-122A-310339	Sequence 310339, A
401	18	0.5	543	4	US-09-925-065A-163562	Sequence 163562,	474	18	0.5	585	4	US-09-925-065A-166114	Sequence 166114,
402	18	0.5	544	4	US-09-925-065A-510840	Sequence 510840,	475	18	0.5	585	4	US-09-925-065A-560038	Sequence 560038,
403	18	0.5	544	4	US-09-925-065A-510841	Sequence 510841,	476	18	0.5	586	4	US-09-925-065A-560035	Sequence 460035,
404	18	0.5	544	4	US-09-925-065A-831478	Sequence 831478,	477	18	0.5	586	4	US-09-925-065A-460037	Sequence 460037,
405	18	0.5	545	4	US-09-925-065A-531644	Sequence 531644,	478	18	0.5	586	4	US-09-925-065A-460038	Sequence 460038,
406	18	0.5	546	4	US-09-925-065A-759761	Sequence 759761,	479	18	0.5	586	4	US-09-925-065A-828852	Sequence 828852,
407	18	0.5	546	4	US-09-925-065A-759762	Sequence 759762,	480	18	0.5	586	4	US-09-925-065A-954731	Sequence 954731,
408	18	0.5	546	5	US-10-027-632-191445	Sequence 191445,	481	18	0.5	586	5	US-10-027-632-258363	Sequence 258363,
409	18	0.5	546	5	US-10-027-632-191446	Sequence 191446,	482	18	0.5	586	6	US-10-027-632-548363	Sequence 548363,
410	18	0.5	546	5	US-10-027-632-191447	Sequence 191447,	483	18	0.5	587	4	US-09-925-065A-543308	Sequence 543308,
411	18	0.5	546	6	US-10-027-632-191445	Sequence 191445,	484	18	0.5	587	4	US-09-925-065A-766334	Sequence 766334,
412	18	0.5	546	6	US-10-027-632-191446	Sequence 191446,	485	18	0.5	588	5	US-10-027-632-16758	Sequence 16758, A
413	18	0.5	546	6	US-10-027-632-191447	Sequence 191447,	486	18	0.5	588	6	US-10-027-632-16758	Sequence 16758, A
414	18	0.5	547	4	US-09-925-065A-26823	Sequence 26823, A	487	18	0.5	589	5	US-09-925-065A-635723	Sequence 635723,
415	18	0.5	547	4	US-09-925-065A-653247	Sequence 653247,	488	18	0.5	589	5	US-10-027-632-252439	Sequence 252439,
416	18	0.5	548	4	US-09-925-065A-771081	Sequence 771081,	489	18	0.5	589	6	US-10-027-632-252439	Sequence 252439,
417	18	0.5	548	4	US-09-925-065A-835486	Sequence 835486,	490	18	0.5	590	4	US-09-925-065A-244641	Sequence 244641,
418	18	0.5	550	3	US-09-825-476-59	Sequence 59, App1	491	18	0.5	592	4	US-09-925-065A-265164	Sequence 265164,
419	18	0.5	550	4	US-09-925-065A-297403	Sequence 297403,	492	18	0.5	592	5	US-10-027-632-83215	Sequence 83215, A
420	18	0.5	550	4	US-09-925-065A-505832	Sequence 505832,	493	18	0.5	592	5	US-10-027-632-83215	Sequence 83215, A
421	18	0.5	550	4	US-09-925-065A-505832	Sequence 505832,	494	18	0.5	592	6	US-10-027-632-83215	Sequence 83215, A
422	18	0.5	550	4	US-09-925-065A-515913	Sequence 515913,	495	18	0.5	592	6	US-10-027-632-116052	Sequence 116052,
423	18	0.5	550	4	US-09-925-065A-515914	Sequence 615913,	496	18	0.5	593	4	US-09-925-065A-491113	Sequence 491113,
424	18	0.5	553	4	US-09-925-065A-335047	Sequence 335047,	497	18	0.5	593	4	US-09-925-065A-837928	Sequence 837928,
425	18	0.5	553	4	US-09-925-065A-335048	Sequence 335048,	498	18	0.5	594	4	US-09-925-065A-228254	Sequence 228254,
426	18	0.5	556	4	US-09-925-065A-333584	Sequence 333584,	499	18	0.5	594	4	US-09-925-065A-740965	Sequence 740965,
427	18	0.5	557	3	US-09-864-761-12304	Sequence 12304, A	500	18	0.5	594	4	US-09-925-065A-911390	Sequence 911390,
428	18	0.5	557	5	US-10-027-632-85793	Sequence 85793, A	501	18	0.5	595	4	US-09-925-065A-462082	Sequence 462082,
429	18	0.5	557	5	US-10-027-632-85794	Sequence 85794, A	502	18	0.5	595	4	US-09-925-065A-850334	Sequence 850334,
430	18	0.5	557	5	US-10-027-632-85795	Sequence 85795, A	503	18	0.5	596	4	US-09-925-065A-832537	Sequence 832537,
431	18	0.5	557	5	US-10-027-632-85796	Sequence 85796, A	504	18	0.5	596	5	US-10-027-632-210197	Sequence 210197,
432	18	0.5	557	5	US-10-027-632-320345	Sequence 320345,	505	18	0.5	596	6	US-10-027-632-210197	Sequence 210197,
433	18	0.5	557	5	US-10-027-632-320346	Sequence 320346,	506	18	0.5	596	8	US-10-425-115-26946	Sequence 26946, A
434	18	0.5	557	5	US-10-027-632-320347	Sequence 320347,	507	18	0.5	597	4	US-09-925-065A-663245	Sequence 663245,
435	18	0.5	557	5	US-10-027-632-320348	Sequence 320348,	508	18	0.5	597	4	US-09-925-065A-663246	Sequence 663246,
436	18	0.5	557	6	US-10-027-632-85793	Sequence 85793, A	509	18	0.5	598	4	US-09-925-065A-258517	Sequence 258517,
437	18	0.5	557	6	US-10-027-632-85794	Sequence 85794, A	510	18	0.5	598	4	US-09-925-065A-312902	Sequence 312902,
438	18	0.5	557	6	US-10-027-632-85795	Sequence 85795, A	511	18	0.5	598	4	US-09-925-065A-886407	Sequence 886407,
439	18	0.5	557	6	US-10-027-632-85796	Sequence 85796, A	512	18	0.5	598	4	US-09-925-065A-911390	Sequence 911390,
440	18	0.5	557	6	US-10-027-632-320345	Sequence 320345,	513	18	0.5	599	9	US-10-972-079-11314	Sequence 71314, A
441	18	0.5	557	6	US-10-027-632-320346	Sequence 320346,	514	18	0.5	599	9	US-10-972-079-77431	Sequence 77431, A
442	18	0.5	557	6	US-10-027-632-320347	Sequence 320347,	515	18	0.5	599	9	US-10-972-079-77431	Sequence 77431, A
443	18	0.5	557	6	US-10-027-632-320348	Sequence 320348,	516	18	0.5	600	4	US-09-925-065A-31068	Sequence 31068, A
444	18	0.5	559	6	US-10-027-632-231092	Sequence 231092,	517	18	0.5	600	9	US-10-972-079-4468	Sequence 6468, Ap
445	18	0.5	559	6	US-10-027-632-231092	Sequence 231092,	518	18	0.5	600	9	US-10-972-079-4469	Sequence 4469, Ap
446	18	0.5	562	4	US-09-925-065A-419799	Sequence 419799,	519	18	0.5	600	9	US-10-972-079-6470	Sequence 6470, Ap
447	18	0.5	563	4	US-09-925-065A-402538	Sequence 402538,	520	18	0.5	600	9	US-10-972-079-15654	Sequence 15654, Ap
448	18	0.5	563	7	US-10-425-114-15172	Sequence 15172, A	521	18	0.5	600	9	US-10-972-079-15655	Sequence 15655, A
449	18	0.5	567	4	US-09-925-065A-628991	Sequence 628991,	522	18	0.5	600	9	US-10-972-079-15656	Sequence 15656, A
450	18	0.5	567	4	US-09-925-065A-659861	Sequence 659861,	523	18	0.5	600	9	US-10-972-079-15657	Sequence 15657, A
451	18	0.5	567	4	US-09-925-065A-396342	Sequence 396342,	524	18	0.5	600	9	US-10-972-079-15658	Sequence 15658, A
452	18	0.5	568	4	US-09-925-065A-626467	Sequence 626467,	525	18	0.5	600	9	US-10-972-079-15659	Sequence 15659, A
453	18	0.5	568	4	US-09-925-065A-626468	Sequence 626468,	526	18	0.5	600	9	US-10-972-079-15660	Sequence 15660, A
454	18	0.5	568	4	US-09-925-065A-626468	Sequence 626468,	527	18	0.5	600	9	US-10-972-079-22352	Sequence 22352, A
455	18	0.5	571	5	US-10-027-632-74614	Sequence 74614, A	528	18	0.5	600	9	US-10-972-079-46982	Sequence 46982, A
456	18	0.5	571	5	US-10-027-632-74615	Sequence 74615, A	529	18	0.5	600	9	US-10-972-079-77435	Sequence 77435, A
457	18	0.5	571	6	US-10-027-632-74616	Sequence 74616, A	530	18	0.5	600	9	US-10-972-079-77437	Sequence 77437, A
458	18	0.5	571	6	US-10-027-632-74615	Sequence 74615, A	531	18	0.5	600	10	US-11-060-756-3614	Sequence 3614, Ap
459	18	0.5	573	8	US-10-425-115-97811	Sequence 97811, A	532	18	0.5	600	10	US-11-060-756-7886	Sequence 7886, Ap
460	18	0.5	575	4	US-09-925-065A-448940	Sequence 448940,	533	18	0.5	601	9	US-10-893-315-791	Sequence 791, App
461	18	0.5	577	4	US-09-925-065A-531645	Sequence 531645,	534	18	0.5	601	9	US-10-893-315-792	Sequence 792, App

C 535	18	0.5	602	4	US-09-925-065A-761350	Sequence 761350,
C 536	18	0.5	603	3	US-09-867-701-10566	Sequence 10566, A
C 537	18	0.5	603	4	US-09-925-065A-70200	Sequence 750200, A
C 538	18	0.5	604	5	US-10-027-632-98442	Sequence 98442, A
C 539	18	0.5	604	6	US-10-027-632-98442	Sequence 98442, A
C 540	18	0.5	605	4	US-09-925-065A-145695	Sequence 145695, A
C 541	18	0.5	606	4	US-09-925-065A-136343	Sequence 136343, A
C 542	18	0.5	606	4	US-09-925-065A-132660	Sequence 132660, A
C 543	18	0.5	608	4	US-09-925-065A-249192	Sequence 249192, A
C 544	18	0.5	608	4	US-09-925-065A-249193	Sequence 249193, A
C 545	18	0.5	608	4	US-09-925-065A-249194	Sequence 249194, A
C 546	18	0.5	609	4	US-09-925-065A-383337	Sequence 383337, A
C 547	18	0.5	609	4	US-09-925-065A-383338	Sequence 383338, A
C 548	18	0.5	609	4	US-09-925-065A-802829	Sequence 802829, A
C 549	18	0.5	614	4	US-09-925-065A-84805	Sequence 84805, A
C 550	18	0.5	616	4	US-09-925-065A-518162	Sequence 518162, A
C 551	18	0.5	619	4	US-09-925-065A-886041	Sequence 886041, A
C 552	18	0.5	620	4	US-09-925-065A-289603	Sequence 289603, A
C 553	18	0.5	621	4	US-09-925-065A-49487	Sequence 49487, A
C 554	18	0.5	622	4	US-09-925-065A-224170	Sequence 224170, A
C 555	18	0.5	622	4	US-09-925-065A-503250	Sequence 503250, A
C 556	18	0.5	624	4	US-09-925-065A-493027	Sequence 493027, A
C 557	18	0.5	624	4	US-09-925-065A-493028	Sequence 493028, A
C 558	18	0.5	624	4	US-09-925-065A-493029	Sequence 493029, A
C 559	18	0.5	624	6	US-10-027-632-199955	Sequence 199955, A
C 560	18	0.5	624	6	US-10-027-632-199955	Sequence 199955, A
C 561	18	0.5	626	4	US-09-925-065A-448976	Sequence 448976, A
C 562	18	0.5	626	4	US-09-925-065A-448977	Sequence 448977, A
C 563	18	0.5	627	4	US-09-925-065A-822960	Sequence 822960, A
C 564	18	0.5	629	6	US-10-369-493-30352	Sequence 30352, A
C 565	18	0.5	635	8	US-10-425-115-166201	Sequence 166201, A
C 566	18	0.5	637	4	US-09-925-065A-531366	Sequence 531366, A
C 567	18	0.5	637	4	US-09-925-065A-531367	Sequence 531367, A
C 568	18	0.5	639	4	US-09-925-065A-656975	Sequence 656975, A
C 569	18	0.5	641	5	US-10-027-632-127010	Sequence 127010, A
C 570	18	0.5	641	5	US-10-027-632-127011	Sequence 127011, A
C 571	18	0.5	641	5	US-10-027-632-127011	Sequence 127011, A
C 572	18	0.5	641	5	US-10-027-632-127012	Sequence 127012, A
C 573	18	0.5	641	6	US-10-027-632-127011	Sequence 127011, A
C 574	18	0.5	641	6	US-10-027-632-127011	Sequence 127011, A
C 575	18	0.5	641	6	US-10-027-632-127012	Sequence 127012, A
C 576	18	0.5	642	6	US-10-311-455-2351	Sequence 2351, Ap
C 577	18	0.5	643	4	US-09-925-065A-777841	Sequence 777841, A
C 578	18	0.5	647	4	US-09-925-065A-880138	Sequence 880138, A
C 579	18	0.5	647	4	US-09-925-065A-880139	Sequence 880139, A
C 580	18	0.5	647	4	US-09-925-065A-880140	Sequence 880140, A
C 581	18	0.5	647	4	US-09-925-065A-908047	Sequence 908047, A
C 582	18	0.5	650	5	US-10-027-632-205556	Sequence 205556, A
C 583	18	0.5	650	5	US-10-027-632-205557	Sequence 205557, A
C 584	18	0.5	650	6	US-10-027-632-205556	Sequence 205556, A
C 585	18	0.5	651	7	US-10-027-632-205557	Sequence 205557, A
C 586	18	0.5	651	7	US-10-027-632-205557	Sequence 205557, A
C 587	18	0.5	653	4	US-09-925-065A-710566	Sequence 710566, A
C 588	18	0.5	654	4	US-09-925-065A-674464	Sequence 674464, A
C 589	18	0.5	656	4	US-09-925-065A-547521	Sequence 547521, A
C 590	18	0.5	656	4	US-09-925-065A-547522	Sequence 547522, A
C 591	18	0.5	659	4	US-09-925-065A-546173	Sequence 546173, A
C 592	18	0.5	659	4	US-09-925-065A-546174	Sequence 546174, A
C 593	18	0.5	663	5	US-10-027-632-114958	Sequence 114958, A
C 594	18	0.5	663	5	US-10-027-632-114959	Sequence 114959, A
C 595	18	0.5	663	5	US-10-027-632-114960	Sequence 114960, A
C 596	18	0.5	663	6	US-10-027-632-114958	Sequence 114958, A
C 597	18	0.5	663	6	US-10-027-632-114959	Sequence 114959, A
C 598	18	0.5	663	6	US-10-027-632-114960	Sequence 114960, A
C 599	18	0.5	663	8	US-10-767-795-1079	Sequence 1079, Ap
C 600	18	0.5	668	4	US-09-925-065A-503249	Sequence 503249, A
C 601	18	0.5	670	5	US-10-027-632-38347	Sequence 38347, A
C 602	18	0.5	670	5	US-10-027-632-38348	Sequence 38348, A
C 603	18	0.5	670	5	US-10-027-632-38349	Sequence 38349, A
C 604	18	0.5	670	5	US-10-027-632-38350	Sequence 38350, A
C 605	18	0.5	670	6	US-10-027-632-38347	Sequence 38347, A
C 606	18	0.5	670	6	US-10-027-632-38348	Sequence 38348, A
C 607	18	0.5	670	6	US-10-027-632-38349	Sequence 38349, A

C 681	18	0.5	1064	6	US-10-027-632-249870	Sequence 249870,	C 754	18	0.5	2341	3	US-09-881-752A-147	Sequence 147, App
C 682	18	0.5	1067	7	US-10-424-599-141079	Sequence 141079,	C 755	18	0.5	2342	9	US-10-479-081-109	Sequence 109, App
C 683	18	0.5	1080	5	US-10-027-632-250694	Sequence 250694,	C 756	18	0.5	2469	10	US-11-037-143-33346	Sequence 33346, A
C 684	18	0.5	1080	5	US-10-027-632-250695	Sequence 250695,	C 757	18	0.5	2471	4	US-09-925-065A-718681	Sequence 718681,
C 685	18	0.5	1080	5	US-10-027-632-250696	Sequence 250696,	C 758	18	0.5	2503	6	US-10-131-827-8881	Sequence 8881, App
C 686	18	0.5	1080	5	US-10-027-632-250697	Sequence 250697,	C 759	18	0.5	2610	7	US-10-425-114-44603	Sequence 34603, A
C 687	18	0.5	1080	6	US-10-027-632-250694	Sequence 250694,	C 760	18	0.5	2625	8	US-10-425-114-4603	Sequence 58916, A
C 688	18	0.5	1080	6	US-10-027-632-250695	Sequence 250695,	C 761	18	0.5	2651	3	US-09-953-118-18916	Sequence 15916, App
C 689	18	0.5	1080	6	US-10-027-632-250696	Sequence 250696,	C 762	18	0.5	2651	6	US-10-101-018-5	Sequence 19, App
C 690	18	0.5	1080	6	US-10-027-632-250697	Sequence 250697,	C 763	18	0.5	2651	6	US-10-446-373-19	Sequence 19, App
C 691	18	0.5	1089	4	US-09-925-065A-679937	Sequence 679937,	C 764	18	0.5	2718	10	US-11-037-143-31640	Sequence 31640, A
C 692	18	0.5	1093	4	US-09-925-065A-57904	Sequence 57904, A	C 765	18	0.5	2742	4	US-09-925-065A-707746	Sequence 707746,
C 693	18	0.5	1119	7	US-10-398-221-1766	Sequence 1766, App	C 766	18	0.5	2764	2	US-08-961-527-240	Sequence 240, App
C 694	18	0.5	1120	7	US-10-437-963-58830	Sequence 58830, A	C 767	18	0.5	2764	7	US-10-158-844-240	Sequence 240, App
C 695	18	0.5	1122	7	US-10-425-114-34842	Sequence 34842, A	C 768	18	0.5	2784	5	US-10-027-632-112170	Sequence 112170,
C 696	18	0.5	1126	4	US-09-925-065A-64472	Sequence 64472, A	C 769	18	0.5	2784	6	US-10-027-632-112170	Sequence 112170,
C 697	18	0.5	1133	4	US-10-425-114-9028	Sequence 9028, App	C 770	18	0.5	2784	6	US-10-027-632-112170	Sequence 112170,
C 698	18	0.5	1135	4	US-09-925-065A-547744	Sequence 547744,	C 771	18	0.5	2893	4	US-09-925-065A-713677	Sequence 713677,
C 699	18	0.5	1140	6	US-10-424-599-129489	Sequence 129489, A	C 772	18	0.5	3090	7	US-10-424-599-35642	Sequence 35642, A
C 700	18	0.5	1163	7	US-10-424-599-119411	Sequence 119411,	C 773	18	0.5	3102	10	US-11-037-143-20278	Sequence 20278, A
C 701	18	0.5	1163	7	US-10-425-115-10913	Sequence 10913,	C 774	18	0.5	3152	10	US-11-037-143-40583	Sequence 40583, A
C 702	18	0.5	1199	8	US-10-425-115-10913	Sequence 10913,	C 775	18	0.5	3191	7	US-10-424-599-35990	Sequence 35990, A
C 703	18	0.5	1203	8	US-10-425-115-142063	Sequence 142063,	C 776	18	0.5	3261	8	US-10-357-930-21399	Sequence 21399, A
C 704	18	0.5	1205	7	US-10-425-114-1115	Sequence 1115, App	C 777	18	0.5	3261	8	US-10-357-930-22596	Sequence 22596, A
C 705	18	0.5	1207	5	US-10-027-632-266168	Sequence 266168,	C 778	18	0.5	3261	8	US-10-357-930-27240	Sequence 27240, A
C 706	18	0.5	1207	6	US-10-027-632-266168	Sequence 266168,	C 779	18	0.5	3261	8	US-10-357-930-18438	Sequence 18438, A
C 707	18	0.5	1216	4	US-09-925-065A-91026	Sequence 91026, A	C 780	18	0.5	3262	5	US-10-198-846-12565	Sequence 12565, A
C 708	18	0.5	1216	4	US-09-925-065A-91027	Sequence 91027, A	C 781	18	0.5	3346	4	US-09-925-065A-70539	Sequence 70539,
C 709	18	0.5	1238	4	US-09-925-065A-289664	Sequence 289664,	C 782	18	0.5	3346	4	US-09-925-065A-705840	Sequence 705840,
C 710	18	0.5	1267	8	US-10-723-860-7219	Sequence 7219, App	C 783	18	0.5	3363	9	US-10-994-726-12	Sequence 12, App
C 711	18	0.5	1277	5	US-10-027-632-124926	Sequence 124926,	C 784	18	0.5	3441	7	US-10-994-726-11	Sequence 11, App
C 712	18	0.5	1277	6	US-10-027-632-124926	Sequence 124926,	C 785	18	0.5	3445	9	US-10-425-114-9898	Sequence 9898, App
C 713	18	0.5	1290	8	US-10-425-114-12690	Sequence 12690, A	C 786	18	0.5	3463	3	US-09-863-040-3	Sequence 3, App
C 714	18	0.5	1308	8	US-10-425-115-65896	Sequence 65896, A	C 787	18	0.5	3463	6	US-10-454-210-3	Sequence 3, App
C 715	18	0.5	1312	4	US-09-925-065A-77470	Sequence 77470, A	C 788	18	0.5	3463	7	US-10-424-599-35646	Sequence 35646, A
C 716	18	0.5	1467	3	US-09-974-879-40	Sequence 879, App	C 789	18	0.5	3524	7	US-10-424-599-944249	Sequence 944249
C 717	18	0.5	1467	3	US-09-305-736-40	Sequence 40, App	C 790	18	0.5	3626	3	US-09-900-237-29	Sequence 29, App
C 718	18	0.5	1467	3	US-09-818-683-40	Sequence 40, App	C 791	18	0.5	3985	8	US-10-723-860-3313	Sequence 2313, App
C 719	18	0.5	1467	3	US-09-818-683-40	Sequence 40, App	C 792	18	0.5	3986	3	US-10-741-600-742	Sequence 742, App
C 720	18	0.5	1467	7	US-10-621-401-40	Sequence 40, App	C 793	18	0.5	3992	8	US-09-944-807-9	Sequence 9, App
C 721	18	0.5	1506	4	US-09-925-065A-73167	Sequence 73167, A	C 794	18	0.5	3992	6	US-10-007-926A-292	Sequence 292, App
C 722	18	0.5	1506	4	US-09-925-065A-73168	Sequence 73168, A	C 795	18	0.5	3992	8	US-10-874-015-9	Sequence 9, App
C 723	18	0.5	1506	4	US-09-925-065A-73169	Sequence 73169, A	C 796	18	0.5	3992	8	US-10-450-763-15470	Sequence 15470, A
C 724	18	0.5	1506	4	US-09-925-065A-73170	Sequence 73170, A	C 797	18	0.5	3992	8	US-10-741-600-743	Sequence 743, App
C 725	18	0.5	1506	4	US-09-925-065A-73171	Sequence 73171, A	C 798	18	0.5	4008	6	US-10-101-510-544	Sequence 544, App
C 726	18	0.5	1506	4	US-09-925-065A-73172	Sequence 73172, A	C 799	18	0.5	4240	8	US-10-723-860-6517	Sequence 6517, App
C 727	18	0.5	1560	3	US-09-900-237-27	Sequence 27, App	C 800	18	0.5	4298	3	US-09-823-245A-622	Sequence 622, App
C 728	18	0.5	1616	7	US-10-437-963-71962	Sequence 71962, A	C 801	18	0.5	4614	6	US-10-369-493-25085	Sequence 25085, A
C 729	18	0.5	1619	6	US-10-437-963-25784	Sequence 25784, A	C 802	18	0.5	4614	6	US-10-369-493-25085	Sequence 25085, A
C 730	18	0.5	1624	7	US-10-424-599-62203	Sequence 62203, A	C 803	18	0.5	5118	10	US-11-037-143-23120	Sequence 23120, A
C 731	18	0.5	1682	7	US-10-425-114-31727	Sequence 31727, App	C 804	18	0.5	5218	6	US-10-311-455-1240	Sequence 1240, App
C 732	18	0.5	1795	8	US-10-425-115-91943	Sequence 91943, A	C 805	18	0.5	5274	10	US-11-037-143-40582	Sequence 40582, A
C 733	18	0.5	1797	8	US-10-425-115-65718	Sequence 65718, A	C 806	18	0.5	5327	7	US-10-437-963-18854	Sequence 18854, A
C 734	18	0.5	1866	4	US-09-925-065A-677936	Sequence 677936,	C 807	18	0.5	5336	6	US-10-311-455-4071	Sequence 4071, App
C 735	18	0.5	1866	4	US-09-925-065A-677937	Sequence 677937,	C 808	18	0.5	5394	7	US-10-398-221-8837	Sequence 8837, App
C 736	18	0.5	1893	4	US-09-925-065A-82882	Sequence 82882, A	C 809	18	0.5	5497	10	US-11-037-143-4135	Sequence 4135, App
C 737	18	0.5	1909	7	US-10-424-599-118404	Sequence 118404, A	C 810	18	0.5	5864	9	US-10-324-035-16	Sequence 16, App
C 738	18	0.5	1934	7	US-10-424-599-61023	Sequence 61023, A	C 811	18	0.5	5969	5	US-10-172-086-46	Sequence 46, App
C 739	18	0.5	1936	10	US-11-011-522-5	Sequence 5, App	C 812	18	0.5	5969	7	US-10-240-5899A-136	Sequence 136, App
C 740	18	0.5	1957	7	US-10-424-599-76825	Sequence 76825, A	C 813	18	0.5	5969	7	US-10-311-507-84	Sequence 84, App
C 741	18	0.5	2000	3	US-09-938-842A-2953	Sequence 2953, App	C 814	18	0.5	5969	8	US-10-480-846-46	Sequence 46, App
C 742	18	0.5	2000	3	US-09-938-842A-2953	Sequence 2953, App	C 815	18	0.5	6078	8	US-10-425-115-91405	Sequence 91405, A
C 743	18	0.5	2033	4	US-09-925-065A-78860	Sequence 78860, A	C 816	18	0.5	6112	6	US-10-311-455-445	Sequence 445, App
C 744	18	0.5	2033	4	US-10-425-114-31617	Sequence 31617, A	C 817	18	0.5	6290	6	US-10-311-455-1020	Sequence 1020, App
C 745	18	0.5	2106	7	US-10-282-122A-20788	Sequence 20788, A	C 818	18	0.5	6390	9	US-10-450-763-15469	Sequence 15469, A
C 746	18	0.5	2106	7	US-10-282-122A-20788	Sequence 20788, A	C 819	18	0.5	6390	9	US-10-450-763-15469	Sequence 15469, A
C 747	18	0.5	2186	7	US-10-437-963-33978	Sequence 33978, A	C 820	18	0.5	6409	7	US-10-221-714A-217	Sequence 217, App
C 748	18	0.5	2186	7	US-09-925-065A-55975	Sequence 55975, A	C 821	18	0.5	6568	3	US-09-880-107-1535	Sequence 1535, App
C 749	18	0.5	2269	8	US-10-425-115-1903	Sequence 1903, App	C 822	18	0.5	6568	3	US-09-911-826A-1	Sequence 1, App
C 750	18	0.5	2280	7	US-10-335-977-3392	Sequence 3393, App	C 823	18	0.5	6668	5	US-10-956-157-1884	Sequence 1884, App
C 751	18	0.5	2286	7	US-10-335-977-3393	Sequence 3393, App	C 824	18	0.5	6668	5	US-10-198-846-11542	Sequence 11542, A
C 752	18	0.5	2336	4	US-09-925-065A-724029	Sequence 724029,	C 825	18	0.5	6693	9	US-10-887-553A-670	Sequence 670, App
C 753	18	0.5	2336	4	US-09-925-065A-724030	Sequence 724030,	C 826	18	0.5	6758	8	US-10-778-804-7	Sequence 7, App



827	18	0.5	7000	6	US-10-101-510-340	Sequence 340, App	C 900	18	0.5	149000	8	US-10-741-600-17780	Sequence 17780, A
828	18	0.5	7016	5	US-10-205-823-364	Sequence 364, App	C 901	18	0.5	150298	9	US-10-981-277-52	Sequence 52, Appl
829	18	0.5	7016	10	US-11-051-454-364	Sequence 364, App	C 902	18	0.5	150351	9	US-10-322-281-453	Sequence 453, App
830	18	0.5	7096	5	US-10-090-983-3	Sequence 3, Appl	C 903	18	0.5	155074	5	US-10-026-188-6	Sequence 6, Appl
831	18	0.5	7134	6	US-10-311-455-455	Sequence 455, App	C 904	18	0.5	158091	8	US-10-235-192A-38	Sequence 38, Appl
832	18	0.5	7781	6	US-10-311-455-141	Sequence 1141, Ap	C 905	18	0.5	175737	8	US-10-723-860-1753	Sequence 1753, Ap
833	18	0.5	7812	3	US-09-070-927A-25	Sequence 25, Appl	C 906	18	0.5	175737	9	US-10-783-271-34	Sequence 34, Appl
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835	18	0.5	8130	10	US-11-097-143-31639	Sequence 31639, A	C 908	18	0.5	185035	9	US-10-756-149-2896	Sequence 2896, Ap
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839	18	0.5	9524	7	US-10-257-166-75	Sequence 75, Appl	C 912	18	0.5	207557	9	US-10-893-315-148	Sequence 148, App
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844	18	0.5	15400	6	US-10-090-002-3	Sequence 3, Appl	C 917	18	0.5	230093	8	US-10-719-993-6661	Sequence 6661, Ap
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847	18	0.5	15941	6	US-10-380-935-35	Sequence 35, Appl	C 920	18	0.5	245531	7	US-10-737-318-16	Sequence 16, Appl
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866	18	0.5	41922	6	US-10-024-396-13	Sequence 13, Appl	C 939	18	0.5	3673778	6	US-10-312-841-2	Sequence 2, Appl
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## ALIGNMENTS

RESULT 1  
US-10-007-270-1  
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GENERAL INFORMATION:  
APPLICANT: Hageman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
APPLICANT: University of Iowa Research Foundation  
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NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 3330  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA, isoform A  
US-10-007-270-1

Query Match 100.0%; Score 3330; DB 5; Length 3330;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3241 ATCTTACTTTCTTGTACTATACAAAGCTATTTTAAAGAAATGATGATGATGAG 3300  
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Db 3241 ATCTTACTTTCTTGTACTATACAAAGCTATTTTAAAGAAATGATGATGATGAG 3300  
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Db 3301 GGGGAAGTTGTACTATGACATTAATCAAT 3330

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/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ APPLICANT: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-00012005
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ PRIOR FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 2887
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform B
US-10-007-270-3
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Query Match      74.4%; Score 2476; DB 5; Length 2887;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 310 AGATGTTGCCAAGTCTCACTTGGGCTTTCCTCTCACTCGTGAATGACACCTCTCTCA 369
QY 813 TGAATTTCTGATATATACCTCAACGACACCAAGATCCTTACACAGAAAGAAACAGA 872
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QY 873 ATTGCTGTGTGGAGAGACAGAGGCTGAGCTCAGCGTCTCTGTGTAAACCAAGATT 932
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QY 933 CAAGGACAGCTGCTGACCTCCAGTCCCATTTATTCAGAGGCTTACAGGAAAGTCCCA 992
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DB 550 ACTTCAGATGCAAAAGATATTTAAGAACTTCAGAGATTCAAAAAATCATGTGTAGG 609
QY 1053 ATTAGACCAAAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCACTTACGGCCAT 1112
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QY 1173 CAACAAATTTGAAGTGAAGAACTTATCATGAAACCATGAGAGAGACAAACACAGA 1232
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DB 790 AATCTATCTCAACGCTACAGACTCTCAAAAGGCTGATCAGAAAGCATGAGAAAGACA 849
QY 1293 ATCTTGAATGTGGGGACAAATTCAGTTCACTGATGAATTGCTGATGCTCCAGCCCT 1352
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DB 970 TTTGAGTCCAGAACTTCTCTCTGTGTAACCCCAAGCTTGAACAAGTGAACGAGACAGA 1029
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QY 1593 AATGGCACTGACCAACAAAGCTATGATCAAGGCTCAACATCCCAACCAAGATTTATTC 1652
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QY 1833 GGAGGATACCACTCCCTGTCTAGCTTACAGATATATACCACTAGTTCTATGACCATTCG 1892
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DB 1450 CCCCAAGGGCCGAGAGCTGTATGATGTTCTTCAAGTCTGCGTGTGTGTAACATGGCTTCTC 1509
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DB 1510 CAAGCACTGTGTAACAAAGAGCTCTGTGAGTACCGAGCTCTGAGGCAAAATTCACACA 1569
QY 2013 GCTGCTGTGTCATATCTACGATTCACATCTTAACAGATTTTAAGCAACTTGAATTACTTAA 2072
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Db 2170 AGGCTATCTCAAGAGATGATTTGCTTCTCAAGAGAAATGAGACAGGCTATTTCA 2229
QY 2673 GGTTCATCAAAATTCACACATACAGTCAACCTGAGATGACGACACACATATTTCA 2732
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Db 2410 TGATCATAGCCAGGTTTGTCTTCCACTTCCGTAAGAAATTTTACTCAAGATATTGCA 2469
QY 2913 ACAAGCATAGCTTACTTATTTGTTAGGAGCTGAACAATTTTATTTGGAGCAAACTTTA 2972
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Db 2710 TCTGATTAACACAAACCTGAGTATGATGATGATGATGATGATGATGATGATGATGAT 2769
QY 3213 GAGGTTCAAGATACATACATGAGAAATCTTACTTTCTTGTATCTACACAAAGCTAT 3272
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IPM 150 isoform A variant cDNA sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2440)
US-10-007-270-27
Query Match 62.9%; Score 2094; DB 5; Length 3261;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2574; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

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Db 3204 TTTAAAGAGATGCTATGTTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3261

RESULT 4  
US-10-007-270-5  
Sequence 5, Application US/10007270  
Publication No. US20020160954A1  
GENERAL INFORMATION:  
APPLICANT: Hageman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
TITLE OF INVENTION: University of Iowa Research Foundation  
FILE REFERENCE: 020618-000120US  
CURRENT APPLICATION NUMBER: US/10/007,270  
CURRENT FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US 09/430,195  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 09/183,972  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 2244  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
NAME/KEY: misc\_feature  
LOCATION: (1)-(2244)  
OTHER INFORMATION: n is a, c, g, or t.  
US-10-007-270-5

Query Match 45.1%; Score 1503; DB 5; Length 2244;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2123; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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QY 150 GAGCTAATTTTGTGTTTGGATTTTCTCCAGATTTCAGAAACCAAGAATATCTCATTA 209  
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QY 450 GGGAAAGCATATGCGATCTTTCTGATTCGATTCCTTCGACACAGGGGATATCAGACTGGG 509  
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| | | | |  
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QY 1650 TTCTGCAATCAGCAACTGAGCTGTGGAAATTTCAATCCTCAGCTGATCTTCAGATGACAG 1709  
| | | | |  
Db 1669 TTCTGCAATCAGCAACTGAGCTGTGGAAATTTCAATCCTCAGCTGATCTTCAGATGACAG 1728  
| | | | |  
QY 1710 CCGATCAAGTGCAGGTGCGGAATATGTGTACACCTTAATGAAATGATCTGTCTGA 1769  
| | | | |  
Db 1729 CCGATCAAGTGCAGGTGCGGAATATGTGTACACCTTAATGAAATGATCTGTCTGA 1788  
| | | | |  
QY 1770 CACTCTGCCCCCATCTGAGTACAGAGCTCAGAGAAATATGTTCTGCCCCAGATCATTT 1829  
| | | | |  
Db 1789 CACTCTGCCCCCATCTGAGTACAGAGCTCAGAGAAATATGTTCTGCCCCAGATCATTT 1848  
| | | | |  
QY 1830 CTTGAGAGATACCACTCTGTCTCAGCTTTACAGTATATACCACTAATTTATGACCAT 1889  
| | | | |  
Db 1849 CTTGAGAGATACCACTCTGTCTCAGCTTTACAGTATATACCACTAATTTATGACCAT 1908  
| | | | |  
QY 1890 TGCCCCCAAGGGCCGAGAGCTGTGATGTCTTCAAGTCTGCTGTCTAACATGGCCTT 1949  
| | | | |  
Db 1909 TGCCCCCAAGGGCCGAGAGCTGTGATGTCTTCAAGTCTGCTGTCTAACATGGCCTT 1968  
| | | | |  
QY 1950 CTCCAGAGACCTGTTCACAAAGAGCTCTGAGATTCAGAGCTCTGAGCAACAAATTAC 2009  
| | | | |  
Db 1969 CTCCAGAGACCTGTTCACAAAGAGCTCTGAGATTCAGAGCTCTGAGCAACAAATTAC 2028  
| | | | |  
QY 2010 ACAGCTGCTGTTCATATCTACAGATCAATCTTAACAGATTTAAGCACTTGAATATCT 2069  
| | | | |  
Db 2029 ACAGCTGCTGTTCATATCTACAGATCAATCTTAACAGATTTAAGCACTTGAATATCT 2088  
| | | | |  
QY 2070 TAACTTCAGAAAGGAGTGTGATTTGAAATGAGAAATGAAATTTGTAAGTCTGTGCC 2129  
| | | | |  
Db 2089 TAACTTCAGAAAGGAGTGTGATTTGAAATGAGAAATGAAATTTGTAAGTCTGTGCC 2148  
| | | | |  
QY 2130 GTATTAACCTGACCAAGGCTGTGACAGGGGCTTTGAGAGATTTTGTCTGTGACGCCA 2189  
| | | | |  
Db 2149 GTATTAACCTGACCAAGGCTGTGACAGGGGCTTTGAGAGATTTTGTCTGTGACGCCA 2208  
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QY 2190 ACAACTCATCTGAAAAATGACAGCTACTCTCTC 2223  
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Db 2209 ACAACTCATCTGAAAAATGACAGCTACTCTCTC 2242  
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Query Match 5.9%; Score 197; DB 5; Length 596;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matched 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TAAACCAAGAGGTATCCTCAATCATCTGGATCAATATATATATATTTTTCACATTTC 60
Db 525 TAAACCAAGAGGTATCTCTCATCATCTGGATCAATATATATATATATTTTTCACATTTC 466

Cy 61 TGTTACTTTTAAATAGATTGGAGTTGTTCTGTATTTGTTATCAGAAATTAACCAATGCAC 120
Db 465 TGTTACTTTTAAATAGATTGGAGTTGTTCTGTATTTGTTATCAGAAATTAACCAATGCAC 406

Cy 121 AAAAGCCAGATGATATTGGAAACTAGAAAGACTATATTTTGTTTTGGATTTTCTCCA 180
Db 405 AAAAGCCAGAAATGATATTGGAAACTAGAAAGACTATATTTTGTTTTGGATTTTCTCCA 346

Cy 181 AGTTCAGGAACCAAG 197
Db 345 AGTTCAGGAACCAAG 329

RESULT 6
US-10-027-632-286848/C
; Sequence 286848, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24

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	Query Match	5.9%; Score 197; DB 6; Length 596;
	Best Local Similarity	100.0%; Pred. No. 3.2e-92;
	Matches 197; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 TAAACAGAAAGTTATCTCATCATCATCTGGTATCAATATATTAATATTTTTCACATTTC	60
Db	525 TAAACAGAAAGTTATCTCTCATCATCATCTGGTATCAATATATTAATATTTTTCACATTTC	466
Qy	61 TGTACTTTTTTAANGAATTTGAGGTGTTCTGTGATTTGTTATTCAGAAATTACCAATGCAC	120
Db	465 TGTACTTTTTTAANGAATTTGAGGTGTTCTGTGATTTGTTATTCAGAAATTACCAATGCAC	406
Qy	121 AAAAGCAGATGATTTTGGAAACTAGAAAGCATTTTGTGTTTGGATTTTCTCCA	180
Db	405 AAAAGCAGATGATTTTGGAAACTAGAAAGCATTTTGTGTTTGGATTTTCTCCA	346
Qy	181 AGTTCAAGAACCAACAAAG	197
Db	345 AGTTCAAGAACCAACAAAG	329

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RESULT 7
US-10-007-270-7
; Sequence 7, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US//10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: Human IMPG1 gene, regulatory region
; NAME/KEY: misc.feature
; LOCATION: (1)..(1858)
; OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-7

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Query Match          5.9%; Score 197; DB 5; Length 1858;
Best Local Similarity 100.0%; Pred. No. 3.5e-92;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TAAACAGAAAGGTTATCTTCATCATCTGGTATCAATATATATATTTTTCACATTC 60
          TAAACAGAAAGGTTATCTTCATCATCTGGTATCAATATATATATTTTTCACATTC 1129
qb      1070 TAAACAGAAAGGTTATCTTCATCATCTGGTATCAATATATATATTTTTCACATTC 1129

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; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223807
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-223807

Query Match      2.4%; Score 79; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 5.4e-30; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0;

QY      1327 GAATTCGTGATCACTGCCAGCCTTTGTCCTGACACCCAAATCAGAGCTGCCACATCT 1386
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DB      308 GAATTCGTGGATCAGCGCCAGCCTTTGGTCTCTGACACCCAAATCAGAGCTGCCACATCT 367

QY      1387 TTTCCTGTTATACAGAG 1405
      |||||
DB      368 TTTCCTGTTATACAGAG 386

RESULT 10
US-09-925-065A-462444
; Sequence 462444, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462444
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-462444

Query Match      2.0%; Score 67; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      626 AGAAATATGAATATCTGACAGAGACACTTGGAGAGCCCTGTAATACCATTCATTCATT 685
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DB      215 AGAAATATGAATATCTGACAGAGACACTTGGAGAGCCCTGTAATACCATTCATTCATT 274

QY      686 TCAACAG 692
      |||||
DB      275 TCAACAG 281

RESULT 11
US-09-908-975-16399
; Sequence 16399, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli

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/ APPLICANT: MINTZ, Liat
/ APPLICANT: FAIGER, Simchon
/ TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
/ TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
/ FILE REFERENCE: 36688-0005
/ CURRENT APPLICATION NUMBER: US 09/908,975
/ PRIOR FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 16399
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-908-975-16399

Query Match      1.8%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4,9e-20;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3009 GCAGGAGATGCGAGGTCTCTCTTAACGATGATGTAGTGTAGGCACTGTAGTG 3068
Db      1 GCAGGAGATGCGAGGTCTCTCTTAACGATGATGTAGTGTAGGCACTGTAGTG 60

RESULT 12
US-09-925-065A-127697
/ Sequence 127697, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCES: 108827.135
/ CURRENT APPLICATION NUMBER: US 09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 127697
/ LENGTH: 586
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-127697

Query Match      1.0%; Score 33; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US 09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 127698
/ LENGTH: 586
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-127698

Query Match      1.0%; Score 33; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      595 GCAGGATTAACGAGAGTTCCCTGACG 627
Db      221 GCAGGATTAACGAGAGTTCCCTGACG 253

RESULT 14
US-10-007-270-10
/ Sequence 10, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ TITLE OF INVENTION: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-000120US
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ CURRENT FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ PRIOR FILING DATE: 1998-10-29
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10
/ LENGTH: 1726
/ TYPE: DNA
/ ORGANISM: Mus sp.
/ FEATURE:
/ OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D
US-10-007-270-10

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Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1001 TGCAAAAGATATTTAAGAACTTCAGGATTC 1032
Db      726 TGCAAAAGATATTTAAGAACTTCAGGATTC 757

RESULT 15
US-10-007-270-8
/ Sequence 8, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
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; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3668
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3668)
; OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-8

Query Match      1.0%; Score 32; DB 5; Length 3668;
Best Local Similarity 100.0%; Pred.No.3.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1001 TGCATAAGATATTAGAAACTTCAGATTTC 1032
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Db      1013 TGCATAAGATATTAGAAACTTCAGATTTC 1044
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Title: US-10-007-270-1

Perfect score: 3330

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Minimum DB seq length: 0

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	20	0.6	601	3 US-09-949-016-35114	Sequence 35114, A
4	20	0.6	601	3 US-09-949-016-35115	Sequence 35115, A
5	20	0.6	601	3 US-09-949-016-142318	Sequence 142318, A
6	20	0.6	601	3 US-09-949-016-142319	Sequence 142319, A
7	20	0.6	601	3 US-09-949-016-142320	Sequence 142320, A
8	20	0.6	601	3 US-09-949-016-161496	Sequence 161496, A
9	20	0.6	1399	3 US-08-617-785-5	Sequence 5, Appl1
10	20	0.6	1399	3 US-09-817-464-5	Sequence 5, Appl1
11	20	0.6	2679	2 US-07-977-434-11	Sequence 11, Appl1
12	20	0.6	2679	2 US-08-458-819-11	Sequence 11, Appl1
13	20	0.6	2679	6 PCT-US91-07035-11	Sequence 11, Appl1
14	20	0.6	3021	3 US-09-016-434-1118	Sequence 11, Appl1
15	20	0.6	3804	3 US-08-617-785-3	Sequence 11, Appl1
16	20	0.6	3804	3 US-09-817-464-3	Sequence 11, Appl1
17	20	0.6	31229	3 US-09-949-016-12619	Sequence 12619, A
18	20	0.6	31231	3 US-09-949-016-15766	Sequence 15766, A
19	20	0.6	79595	3 US-09-949-016-15318	Sequence 15318, A
20	20	0.6	84495	3 US-09-797-906-3	Sequence 3, Appl1
21	20	0.6	148794	3 US-09-949-016-12751	Sequence 12751, A
22	20	0.6	240157	3 US-09-949-016-16264	Sequence 16264, A
23	19	0.6	233	3 US-09-513-999C-2939	Sequence 2939, Ap
24	19	0.6	466	3 US-09-513-999C-12117	Sequence 12117, A

25	19	0.6	601	3 US-09-949-016-25052	Sequence 25052, A
26	19	0.6	601	3 US-09-949-016-60789	Sequence 60789, A
27	19	0.6	601	3 US-09-949-016-144765	Sequence 144765, A
28	19	0.6	700	3 US-09-735-271-1232	Sequence 1232, Ap
29	19	0.6	837	3 US-09-252-991A-15872	Sequence 15872, A
30	19	0.6	1029	3 US-09-248-796A-5023	Sequence 5023, Ap
31	19	0.6	1158	3 US-09-252-991A-15820	Sequence 15820, A
32	19	0.6	1281	3 US-09-711-164-209	Sequence 209, Ap
33	19	0.6	1201	3 US-09-424-978B-10	Sequence 10, Appl
34	19	0.6	2570	3 US-09-252-991A-15898	Sequence 15898, A
35	19	0.6	7987	3 US-09-949-016-15299	Sequence 15299, A
36	19	0.6	9615	3 US-09-949-016-17282	Sequence 17282, A
37	19	0.6	36148	3 US-09-949-016-13969	Sequence 12969, A
38	19	0.6	43993	3 US-09-949-016-13172	Sequence 12172, A
39	19	0.6	43983	3 US-09-949-016-13106	Sequence 13406, A
40	19	0.6	49389	3 US-09-949-016-12547	Sequence 12547, A
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42	19	0.6	49389	3 US-09-949-016-13445	Sequence 13445, A
43	19	0.6	58879	3 US-09-949-016-16052	Sequence 16052, A
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47	19	0.6	101015	3 US-09-949-016-16981	Sequence 16981, A
48	19	0.6	147840	3 US-09-949-016-15236	Sequence 15236, A
49	19	0.6	171700	3 US-09-949-016-12276	Sequence 12276, A
50	19	0.6	171701	3 US-09-949-016-15835	Sequence 15835, A
51	19	0.6	188636	3 US-09-949-002-661	Sequence 661, App
52	19	0.6	283538	3 US-09-949-016-13506	Sequence 13506, A
53	19	0.6	312470	3 US-09-949-016-14043	Sequence 14043, A
54	19	0.6	336024	3 US-09-949-016-12373	Sequence 12373, A
55	19	0.6	451924	3 US-09-949-016-12896	Sequence 12896, A
56	19	0.6	451925	3 US-09-949-016-17305	Sequence 17305, A
57	19	0.6	526	3 US-09-513-999C-9118	Sequence 9118, Ap
58	18	0.5	550	3 US-08-642-274D-59	Sequence 59, Appl
59	18	0.5	550	3 US-08-952-014C-59	Sequence 59, Appl
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61	18	0.5	601	3 US-09-949-016-22752	Sequence 22752, A
62	18	0.5	601	3 US-09-949-016-37235	Sequence 37235, A
63	18	0.5	601	3 US-09-949-016-78490	Sequence 78490, A
64	18	0.5	601	3 US-09-949-016-86336	Sequence 86336, A
65	18	0.5	601	3 US-09-949-016-91903	Sequence 91903, A
66	18	0.5	601	3 US-09-949-016-91904	Sequence 91904, A
67	18	0.5	601	3 US-09-949-016-91905	Sequence 91905, A
68	18	0.5	601	3 US-09-949-016-131939	Sequence 131939, A
69	18	0.5	601	3 US-09-949-016-131956	Sequence 131956, A
70	18	0.5	601	3 US-09-949-016-131973	Sequence 131973, A
71	18	0.5	601	3 US-09-949-016-132042	Sequence 132042, A
72	18	0.5	601	3 US-09-949-016-174245	Sequence 174245, A
73	18	0.5	601	3 US-09-949-016-174246	Sequence 174246, A
74	18	0.5	601	3 US-09-949-016-174437	Sequence 174437, A
75	18	0.5	601	3 US-09-949-016-174438	Sequence 174438, A
76	18	0.5	601	3 US-09-949-016-182124	Sequence 182124, A
77	18	0.5	601	3 US-09-949-016-182125	Sequence 182125, A
78	18	0.5	601	3 US-09-949-016-182126	Sequence 182126, A
79	18	0.5	601	3 US-09-949-016-194845	Sequence 194845, A
80	18	0.5	601	3 US-09-949-016-194846	Sequence 194846, A
81	18	0.5	601	3 US-09-949-016-195915	Sequence 195915, A
82	18	0.5	601	3 US-09-949-002-6210	Sequence 6210, Ap
83	18	0.5	601	3 US-09-949-002-6211	Sequence 6211, Ap
84	18	0.5	601	3 US-09-949-002-6212	Sequence 6212, Ap
85	18	0.5	601	3 US-09-949-002-8725	Sequence 8725, Ap
86	18	0.5	601	3 US-09-949-002-10274	Sequence 10274, A
87	18	0.5	601	3 US-09-949-002-10275	Sequence 10275, A
88	18	0.5	601	3 US-09-949-002-10276	Sequence 10276, A
89	18	0.5	601	3 US-09-248-796A-6341	Sequence 6341, Ap
90	18	0.5	687	3 US-09-735-271-1001	Sequence 1001, Ap
91	18	0.5	700	3 US-09-735-271-1002	Sequence 1002, Ap
92	18	0.5	705	3 US-09-107-532A-1163	Sequence 1163, Ap
93	18	0.5	858	3 US-09-270-767-13041	Sequence 13041, A
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98	18	0.5	987	3	US-09-583-110-1328	Sequence 1328, Ap	171	18	0.5	97195	3	US-09-949-016-12212	Sequence 12212, A
99	18	0.5	1005	3	US-09-107-433-1494	Sequence 1494, Ap	172	18	0.5	97196	3	US-09-949-016-16971	Sequence 16971, A
100	18	0.5	1026	3	US-09-248-796A-1755	Sequence 1755, Ap	173	18	0.5	97221	3	US-09-949-016-12755	Sequence 12755, A
101	18	0.5	1560	3	US-09-900-237-27	Sequence 27, Appl	174	18	0.5	97227	3	US-09-949-016-15255	Sequence 15255, A
102	18	0.5	1878	3	US-09-134-000C-667	Sequence 667, App	175	18	0.5	121427	3	US-09-949-016-11950	Sequence 11950, A
103	18	0.5	2513	3	US-09-710-279-2861	Sequence 2861, Ap	176	18	0.5	121433	3	US-09-949-016-13230	Sequence 13230, A
104	18	0.5	2513	3	US-10-131-827-8881	Sequence 8881, Ap	177	18	0.5	128237	3	US-09-949-016-16674	Sequence 16674, A
105	18	0.5	2651	2	US-08-786-164-5	Sequence 5, Appl1	178	18	0.5	128237	3	US-09-949-016-16675	Sequence 16675, A
106	18	0.5	2651	3	US-09-953-318-19	Sequence 19, Appl1	179	18	0.5	128658	3	US-09-949-016-17195	Sequence 17195, A
107	18	0.5	2685	3	US-08-362-522-21	Sequence 21, Appl1	180	18	0.5	128899	3	US-09-949-016-14684	Sequence 14684, A
108	18	0.5	2714	3	US-09-562-930-5	Sequence 5, Appl1	181	18	0.5	131860	3	US-09-949-016-11777	Sequence 11777, A
109	18	0.5	2754	2	US-08-196-989B-1	Sequence 1, Appl1	182	18	0.5	140925	3	US-09-949-002-730	Sequence 730, App
110	18	0.5	2754	2	US-08-760-936-1	Sequence 1, Appl1	183	18	0.5	140982	3	US-09-949-016-16295	Sequence 16295, A
111	18	0.5	2754	3	US-09-225-024-1	Sequence 1, Appl1	184	18	0.5	149822	3	US-09-949-016-16151	Sequence 16151, A
112	18	0.5	2764	3	US-08-961-527-240	Sequence 240, App	185	18	0.5	146428	3	US-09-949-016-12620	Sequence 12620, A
113	18	0.5	3151	3	US-09-710-279-3476	Sequence 3476, Ap	186	18	0.5	146438	3	US-09-949-016-12081	Sequence 12081, A
114	18	0.5	3349	3	US-09-710-279-4168	Sequence 4168, Ap	187	18	0.5	148156	3	US-09-949-016-11776	Sequence 11776, A
115	18	0.5	3363	3	US-09-830-230A-12	Sequence 12, Appl1	188	18	0.5	163181	3	US-09-949-016-13730	Sequence 13730, A
116	18	0.5	3441	3	US-09-830-230A-11	Sequence 11, Appl1	189	18	0.5	197336	3	US-09-949-016-12881	Sequence 12881, A
117	18	0.5	3463	3	US-09-189-462-3	Sequence 3, Appl1	190	18	0.5	197336	3	US-09-949-016-14376	Sequence 14376, A
118	18	0.5	3463	3	US-09-863-040-3	Sequence 29, Appl1	191	18	0.5	197337	3	US-09-949-002-574	Sequence 574, App
119	18	0.5	3626	3	US-09-900-237-29	Sequence 29, Appl1	192	18	0.5	203631	3	US-09-949-002-738	Sequence 738, App
120	18	0.5	3884	3	US-09-562-930-10	Sequence 10, Appl1	193	18	0.5	209631	3	US-09-949-002-802	Sequence 802, App
121	18	0.5	3992	3	US-09-944-807-9	Sequence 9, Appl1	194	18	0.5	211049	3	US-09-949-016-15770	Sequence 15770, A
122	18	0.5	4614	2	US-08-325-267A-1	Sequence 1, Appl1	195	18	0.5	221958	3	US-09-949-016-12173	Sequence 12173, A
123	18	0.5	4614	3	US-09-487-558B-103	Sequence 103, App	196	18	0.5	221966	3	US-09-949-016-15498	Sequence 15498, A
124	18	0.5	7096	3	US-09-665-493B-3	Sequence 3, Appl1	197	18	0.5	232887	3	US-09-949-002-687	Sequence 687, App
125	18	0.5	7890	3	US-09-949-016-11951	Sequence 11951, A	198	18	0.5	232888	3	US-09-949-016-17272	Sequence 17272, A
126	18	0.5	7890	3	US-09-949-016-11356	Sequence 11356, A	199	18	0.5	232888	3	US-09-949-002-841	Sequence 841, App
127	18	0.5	16600	3	US-09-949-016-13332	Sequence 13332, A	200	18	0.5	233064	3	US-09-949-016-15390	Sequence 15390, A
128	18	0.5	16600	3	US-09-949-016-13333	Sequence 13333, A	201	18	0.5	236341	3	US-09-949-016-13978	Sequence 13978, A
129	18	0.5	18568	3	US-09-949-016-16963	Sequence 16963, A	202	18	0.5	251672	3	US-09-949-016-17296	Sequence 17296, A
130	18	0.5	19389	3	US-09-949-016-15113	Sequence 15113, A	203	18	0.5	251682	3	US-09-949-016-11973	Sequence 11973, A
131	18	0.5	20303	3	US-09-902-540-1183	Sequence 1183, Ap	204	18	0.5	389504	3	US-09-949-016-11774	Sequence 11774, A
132	18	0.5	20468	3	US-09-949-016-15462	Sequence 15462, A	205	18	0.5	390416	3	US-09-949-016-16923	Sequence 16923, A
133	18	0.5	20468	3	US-09-949-016-15463	Sequence 15463, A	206	18	0.5	422592	3	US-09-949-016-14182	Sequence 14182, A
134	18	0.5	20661	3	US-09-949-016-13326	Sequence 13326, A	207	18	0.5	784019	3	US-09-949-016-14033	Sequence 14033, A
135	18	0.5	20661	3	US-09-949-016-13327	Sequence 13327, A	208	18	0.5	828152	3	US-09-949-016-12777	Sequence 12777, A
136	18	0.5	20661	3	US-09-949-016-13328	Sequence 13328, A	209	17	0.5	828152	3	US-09-396-186G-79369	Sequence 79369, A
137	18	0.5	20661	3	US-09-949-016-13329	Sequence 13329, A	210	17	0.5	48	3	US-09-345-882-59	Sequence 59, Appl1
138	18	0.5	20661	3	US-09-949-016-13330	Sequence 13330, A	211	17	0.5	48	3	US-10-071-179-59	Sequence 59, Appl1
139	18	0.5	20661	3	US-09-949-016-13331	Sequence 13331, A	212	17	0.5	50	3	US-10-131-827-3709	Sequence 3709, App
140	18	0.5	20681	3	US-09-949-016-14596	Sequence 14596, A	213	17	0.5	136	3	US-09-513-999C-15023	Sequence 15023, A
141	18	0.5	20681	3	US-09-949-016-14597	Sequence 14597, A	214	17	0.5	150	3	US-09-513-999C-19576	Sequence 19576, A
142	18	0.5	20681	3	US-09-949-016-14598	Sequence 14598, A	215	17	0.5	192	3	US-09-248-786A-11054	Sequence 11054, A
143	18	0.5	20681	3	US-09-949-016-14599	Sequence 14599, A	216	17	0.5	222	3	US-09-543-681A-1216	Sequence 1216, Ap
144	18	0.5	20681	3	US-09-949-016-14600	Sequence 14600, A	217	17	0.5	260	3	US-09-172-711-46	Sequence 46, Appl1
145	18	0.5	20681	3	US-09-949-016-14601	Sequence 14601, A	218	17	0.5	275	3	US-09-313-294A-213	Sequence 213, App
146	18	0.5	21893	3	US-09-949-016-14607	Sequence 16407, A	219	17	0.5	316	3	US-09-809-665A-162	Sequence 162, App
147	18	0.5	25235	3	US-10-164-230-2	Sequence 2, Appl1	220	17	0.5	325	3	US-09-023-655-193	Sequence 193, App
148	18	0.5	35100	2	US-08-306-691B-19	Sequence 19, Appl1	221	17	0.5	349	3	US-09-641-638-414	Sequence 414, App
149	18	0.5	35100	6	PCT-US93-06251-19	Sequence 19, Appl1	222	17	0.5	349	3	US-09-641-638-415	Sequence 415, App
150	18	0.5	37475	3	US-09-949-016-11299	Sequence 12299, A	223	17	0.5	349	3	US-10-170-097-414	Sequence 414, App
151	18	0.5	37492	3	US-09-949-016-13198	Sequence 13198, A	224	17	0.5	349	3	US-10-170-097-415	Sequence 415, App
152	18	0.5	38261	3	US-09-949-016-13802	Sequence 13802, A	225	17	0.5	374	3	US-09-621-976-10977	Sequence 10977, A
153	18	0.5	41322	3	US-10-024-396-13	Sequence 13, Appl1	226	17	0.5	450	3	US-09-702-705-106	Sequence 106, App
154	18	0.5	45762	3	US-09-949-016-16551	Sequence 16551, A	227	17	0.5	450	3	US-09-736-487-106	Sequence 106, App
155	18	0.5	49603	3	US-09-949-016-13706	Sequence 13706, A	228	17	0.5	450	3	US-09-614-124B-106	Sequence 106, App
156	18	0.5	51110	3	US-09-949-016-12069	Sequence 12069, A	229	17	0.5	450	3	US-09-671-325-106	Sequence 106, App
157	18	0.5	51121	3	US-09-949-016-15724	Sequence 15724, A	230	17	0.5	450	3	US-09-589-184-106	Sequence 106, App
158	18	0.5	53722	3	US-09-949-016-12077	Sequence 12077, A	231	17	0.5	450	3	US-09-658-824-106	Sequence 106, App
159	18	0.5	54711	3	US-09-949-016-17489	Sequence 17489, A	232	17	0.5	450	3	US-10-017-754-106	Sequence 106, App
160	18	0.5	62636	3	US-09-949-016-15464	Sequence 15464, A	233	17	0.5	450	3	US-09-651-553-106	Sequence 106, App
161	18	0.5	62636	3	US-09-949-016-15465	Sequence 15465, A	234	17	0.5	450	3	US-09-519-642-106	Sequence 106, App
162	18	0.5	69442	3	US-09-949-016-15339	Sequence 15339, A	235	17	0.5	453	3	US-09-328-352-1420	Sequence 1420, Ap
163	18	0.5	74545	3	US-09-949-002-606	Sequence 606, App	236	17	0.5	474	3	US-09-513-999C-31998	Sequence 31968, A
164	18	0.5	76985	3	US-09-949-016-12416	Sequence 12416, A	237	17	0.5	489	3	US-09-270-767-8754	Sequence 8754, Ap
165	18	0.5	76985	3	US-09-949-016-13120	Sequence 12416, A	238	17	0.5	489	3	US-09-270-767-8754	Sequence 8754, Ap
166	18	0.5	77661	3	US-09-949-016-13770	Sequence 12770, A	239	17	0.5	496	3	US-09-621-976-6388	Sequence 2087, Ap
167	18	0.5	77661	3	US-09-949-016-13751	Sequence 13751, A	240	17	0.5	499	3	US-09-270-767-6388	Sequence 6388, Ap
168	18	0.5	90472	3	US-09-949-016-14038	Sequence 14038, A	241	17	0.5	499	3	US-09-270-767-21670	Sequence 21670, A
169	18	0.5	96739	3	US-09-949-016-15606	Sequence 15606, A	242	17	0.5	519	3	US-08	

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245	17	0.5	601	3	US-09-949-016-22168	Sequence 22168, A	318	17	0.5	601	3	US-09-949-016-206562	Sequence 206562,
246	17	0.5	601	3	US-09-949-016-25421	Sequence 25421, A	319	17	0.5	611	3	US-09-328-111-375	Sequence 375, App
247	17	0.5	601	3	US-09-949-016-30093	Sequence 30093, A	320	17	0.5	621	3	US-09-248-796A-7780	Sequence 2780, Ap
C 248	17	0.5	601	3	US-09-949-016-32154	Sequence 32154, A	C 321	17	0.5	634	3	US-09-830-230A-598	Sequence 598, App
249	17	0.5	601	3	US-09-949-016-32781	Sequence 32781, A	322	17	0.5	644	3	US-10-002-344A-91	Sequence 91, App1
250	17	0.5	601	3	US-09-949-016-32840	Sequence 32840, A	323	17	0.5	651	3	US-09-270-767-5407	Sequence 5407, Ap
251	17	0.5	601	3	US-09-949-016-36318	Sequence 36318, A	324	17	0.5	651	3	US-09-270-767-20689	Sequence 20689, A
252	17	0.5	601	3	US-09-949-016-36319	Sequence 36319, A	325	17	0.5	672	3	US-09-270-767-9935	Sequence 9935, Ap
C 253	17	0.5	601	3	US-09-949-016-36320	Sequence 36320, A	C 326	17	0.5	714	3	US-09-830-230A-597	Sequence 597, App
C 254	17	0.5	601	3	US-09-949-016-44229	Sequence 44229, A	C 327	17	0.5	752	3	US-08-936-166A-151	Sequence 151, App
C 255	17	0.5	601	3	US-09-949-016-48736	Sequence 48736, A	C 328	17	0.5	788	3	US-09-328-475C-126	Sequence 126, App
256	17	0.5	601	3	US-09-949-016-50698	Sequence 50698, A	C 329	17	0.5	798	3	US-09-540-226-1365	Sequence 1365, Ap
257	17	0.5	601	3	US-09-949-016-50757	Sequence 50757, A	C 330	17	0.5	822	3	US-09-533-553-79	Sequence 79, App1
C 258	17	0.5	601	3	US-09-949-016-57185	Sequence 57185, A	C 331	17	0.5	832	3	US-09-270-767-5414	Sequence 5414, Ap
C 259	17	0.5	601	3	US-09-949-016-60788	Sequence 60788, A	C 332	17	0.5	832	3	US-09-270-767-20696	Sequence 20696, A
C 260	17	0.5	601	3	US-09-949-016-62158	Sequence 62158, A	C 333	17	0.5	840	3	US-09-902-540-7277	Sequence 7277, Ap
C 261	17	0.5	601	3	US-09-949-016-62159	Sequence 62159, A	C 334	17	0.5	864	3	US-09-252-991A-12026	Sequence 12026, A
C 262	17	0.5	601	3	US-09-949-016-62160	Sequence 62160, A	C 335	17	0.5	870	3	US-09-252-991A-11957	Sequence 11957, A
263	17	0.5	601	3	US-09-949-016-65776	Sequence 65776, A	C 336	17	0.5	917	3	US-08-956-171E-552	Sequence 552, App
C 264	17	0.5	601	3	US-09-949-016-67624	Sequence 67624, A	C 337	17	0.5	917	3	US-08-781-986A-552	Sequence 552, App
C 265	17	0.5	601	3	US-09-949-016-71389	Sequence 71389, A	C 338	17	0.5	920	2	US-08-299-849B-22	Sequence 22, App1
C 266	17	0.5	601	3	US-09-949-016-76674	Sequence 76674, A	C 339	17	0.5	920	2	US-08-142-368A-22	Sequence 22, App1
C 267	17	0.5	601	3	US-09-949-016-76692	Sequence 76692, A	C 340	17	0.5	920	3	US-08-967-727-22	Sequence 22, App1
268	17	0.5	601	3	US-09-949-016-76854	Sequence 76854, A	C 341	17	0.5	920	3	US-08-037-230D-22	Sequence 22, App1
C 269	17	0.5	601	3	US-09-949-016-78511	Sequence 78511, A	C 342	17	0.5	920	3	US-09-583-850-22	Sequence 22, App1
C 270	17	0.5	601	3	US-09-949-016-78693	Sequence 78693, A	C 343	17	0.5	920	3	US-09-579-197-22	Sequence 22, App1
C 271	17	0.5	601	3	US-09-949-016-82472	Sequence 82472, A	C 344	17	0.5	920	3	US-09-404-028-22	Sequence 22, App1
272	17	0.5	601	3	US-09-949-016-86595	Sequence 86595, A	C 345	17	0.5	920	3	US-09-312-464-22	Sequence 22, App1
273	17	0.5	601	3	US-09-949-016-86596	Sequence 86596, A	C 346	17	0.5	920	3	US-09-583-846A-22	Sequence 22, App1
274	17	0.5	601	3	US-09-949-016-86597	Sequence 86597, A	C 347	17	0.5	924	3	US-09-252-991A-12055	Sequence 12055, A
C 275	17	0.5	601	3	US-09-949-016-87416	Sequence 87416, A	C 348	17	0.5	936	3	US-09-248-796A-773	Sequence 773, App
C 276	17	0.5	601	3	US-09-949-016-88848	Sequence 88848, A	C 349	17	0.5	992	3	US-09-221-017B-770	Sequence 770, App
277	17	0.5	601	3	US-09-949-016-116494	Sequence 116494, A	C 350	17	0.5	1004	3	US-09-328-335C-266	Sequence 2366, Ap
C 278	17	0.5	601	3	US-09-949-016-116512	Sequence 116512, A	C 351	17	0.5	1025	3	US-09-328-475C-85	Sequence 85, App1
C 279	17	0.5	601	3	US-09-949-016-116536	Sequence 116536, A	C 352	17	0.5	1068	3	US-09-252-991A-5923	Sequence 5923, Ap
C 280	17	0.5	601	3	US-09-949-016-117707	Sequence 117707, A	C 353	17	0.5	1083	3	US-09-902-540-3164	Sequence 3164, Ap
C 281	17	0.5	601	3	US-09-949-016-120251	Sequence 120251, A	C 354	17	0.5	1095	3	US-09-252-991A-5981	Sequence 5981, Ap
C 282	17	0.5	601	3	US-09-949-016-128518	Sequence 128518, A	C 355	17	0.5	1125	3	US-09-949-016-4444	Sequence 4444, Ap
C 283	17	0.5	601	3	US-09-949-016-130278	Sequence 130278, A	C 356	17	0.5	1128	3	US-08-795-477B-11	Sequence 1, App1
284	17	0.5	601	3	US-09-949-016-137213	Sequence 137213, A	C 357	17	0.5	1128	3	US-09-439-856-1	Sequence 1, App1
285	17	0.5	601	3	US-09-949-016-139673	Sequence 139673, A	C 358	17	0.5	1145	9	5510472-1	Patent No. 5510472
C 286	17	0.5	601	3	US-09-949-016-139844	Sequence 139844, A	C 359	17	0.5	1200	3	US-09-252-991A-5964	Sequence 5964, Ap
287	17	0.5	601	3	US-09-949-016-151223	Sequence 151223, A	C 360	17	0.5	1203	3	US-09-889-746-1	Sequence 1, App1
288	17	0.5	601	3	US-09-949-016-151724	Sequence 151724, A	C 361	17	0.5	1242	3	US-09-248-796A-352	Sequence 352, App
289	17	0.5	601	3	US-09-949-016-151725	Sequence 151725, A	C 362	17	0.5	1316	3	US-09-270-767-2481	Sequence 2481, Ap
290	17	0.5	601	3	US-09-949-016-152749	Sequence 152749, A	C 363	17	0.5	1316	3	US-09-270-767-17763	Sequence 17763, A
291	17	0.5	601	3	US-09-949-016-156443	Sequence 156443, A	C 364	17	0.5	1326	3	US-09-107-532A-519	Sequence 519, App
C 292	17	0.5	601	3	US-09-949-016-157887	Sequence 157887, A	C 365	17	0.5	1464	3	US-09-188-930-255	Sequence 255, App
C 293	17	0.5	601	3	US-09-949-016-162110	Sequence 162110, A	C 366	17	0.5	1464	3	US-09-312-288C-255	Sequence 255, App
294	17	0.5	601	3	US-09-949-016-163288	Sequence 163288, A	C 367	17	0.5	1473	3	US-09-134-001C-673	Sequence 673, App
295	17	0.5	601	3	US-09-949-016-163289	Sequence 163289, A	C 368	17	0.5	1482	3	US-09-489-039A-6690	Sequence 6690, Ap
C 296	17	0.5	601	3	US-09-949-016-163290	Sequence 163290, A	C 369	17	0.5	1494	3	US-09-543-681A-2754	Sequence 2754, Ap
C 297	17	0.5	601	3	US-09-949-016-166312	Sequence 166312, A	C 370	17	0.5	1499	3	US-09-902-540-6248	Sequence 6248, Ap
C 298	17	0.5	601	3	US-09-949-016-167864	Sequence 167864, A	C 371	17	0.5	1501	3	US-09-902-540-343	Sequence 343, App
C 299	17	0.5	601	3	US-09-949-016-167909	Sequence 167909, A	C 372	17	0.5	1510	3	US-09-902-540-343	Sequence 343, App
C 300	17	0.5	601	3	US-09-949-016-174091	Sequence 174091, A	C 373	17	0.5	1515	3	US-09-620-312D-142	Sequence 142, App
C 301	17	0.5	601	3	US-09-949-016-174092	Sequence 174092, A	C 374	17	0.5	1534	2	US-09-252-991A-5909	Sequence 5909, App
C 302	17	0.5	601	3	US-09-949-016-174096	Sequence 174096, A	C 375	17	0.5	1534	3	US-08-592-126-97	Sequence 97, App1
C 303	17	0.5	601	3	US-09-949-016-177620	Sequence 177620, A	C 376	17	0.5	1590	3	US-09-168-559-97	Sequence 97, App1
C 304	17	0.5	601	3	US-09-949-016-184504	Sequence 184504, A	C 377	17	0.5	1633	3	US-09-248-796A-6687	Sequence 6687, Ap
C 305	17	0.5	601	3	US-09-949-016-184948	Sequence 184948, A	C 378	17	0.5	1633	3	US-09-188-930-73	Sequence 73, App1
C 306	17	0.5	601	3	US-09-949-016-184949	Sequence 184949, A	C 379	17	0.5	1635	3	US-09-713-273A-9	Sequence 9, App1
C 307	17	0.5	601	3	US-09-949-016-184950	Sequence 184950, A	C 380	17	0.5	1644	3	US-09-312-288C-73	Sequence 73, App1
C 308	17	0.5	601	3	US-09-949-016-184951	Sequence 184951, A	C 381	17	0.5	1657	3	US-08-858-207A-70	Sequence 70, App1
C 309	17	0.5	601	3	US-09-949-016-184952	Sequence 184952, A	C 382	17	0.5	1657	3	US-09-533-559-878	Sequence 878, App
C 310	17	0.5	601	3	US-09-949-016-185103	Sequence 185103, A	C 383	17	0.5	1693	3	US-09-925-842B-36	Sequence 36, App1
C 311	17	0.5	601	3	US-09-949-016-185104	Sequence 185104, A	C 384	17	0.5	1700	3	5169835-3	Patent No. 5169835
C 312	17	0.5	601	3	US-09-949-016-185105	Sequence 185105, A	C 385	17	0.5	1770	3	US-09-672-785-7	Sequence 7, App1
C 313	17	0.5	601	3	US-09-949-016-185106	Sequence 185106, A	C 386	17	0.5	1786	3	US-09-614-221A-386	Sequence 386, App
C 314	17	0.5	601	3	US-09-949-016-185107	Sequence 185107, A	C 387	17	0.5	1794	3	US-09-902-540-8279	Sequence 8279, Ap
C 315	17	0.5	601	3	US-09-949-016-203480	Sequence 203480, A	C 388	17	0.5	1842	3	US-10-104-047-1581	Sequence 1581, Ap
C 316	17	0.5	601	3	US-09-949-016-203481	Sequence 203481, A	C 389	17	0.5	1859	3	US-09-248-796A-6661	Sequence 6661, Ap
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330	17	0.5	1874	3	US-09-023-655-891	Sequence 891, App	463	17	0.5	7488	3	US-08-475-886-3	Sequence 3, App11
331	17	0.5	1881	3	US-09-235-246-2	Sequence 2, App11	464	17	0.5	7488	3	US-09-653-499-3	Sequence 3, App11
332	17	0.5	1940	3	US-09-965-599-1	Sequence 1, App1	465	17	0.5	7488	3	US-10-135-988-3	Sequence 3, App11
333	17	0.5	1950	3	US-10-104-047-1078	Sequence 1078, Ap	466	17	0.5	7493	3	US-08-475-886-1	Sequence 1, App11
334	17	0.5	1971	3	US-09-942-336A-2	Sequence 2, App1	467	17	0.5	7493	3	US-08-397-232-1	Sequence 1, App11
335	17	0.5	1971	3	US-09-270-767-14150	Sequence 14150, A	468	17	0.5	7493	3	US-09-171-387-1	Sequence 1, App11
336	17	0.5	2010	3	US-09-878-755-3	Sequence 3, App1	469	17	0.5	7493	3	US-09-653-499-1	Sequence 1, App11
337	17	0.5	2040	3	US-09-248-796A-11850	Sequence 11850, A	470	17	0.5	7493	3	US-10-135-988-1	Sequence 1, App11
338	17	0.5	2118	3	US-09-252-991A-5605	Sequence 5605, Ap	471	17	0.5	7997	3	US-09-949-016-15828	Sequence 15828, A
339	17	0.5	2143	3	US-09-990-613A-35	Sequence 35, App1	472	17	0.5	8252	3	US-09-949-016-13201	Sequence 13201, A
340	17	0.5	2217	3	US-10-104-047-1712	Sequence 1712, Ap	473	17	0.5	8596	3	US-09-949-016-14393	Sequence 14393, A
341	17	0.5	2238	3	US-09-540-236-314	Sequence 314, App	474	17	0.5	8797	3	US-09-949-016-16186	Sequence 16186, A
342	17	0.5	2329	3	US-08-961-083-85	Sequence 85, App1	475	17	0.5	9471	3	US-09-949-016-15837	Sequence 15837, A
343	17	0.5	2329	3	US-09-536-784-85	Sequence 85, App1	476	17	0.5	9471	3	US-09-949-016-15838	Sequence 15838, A
344	17	0.5	2329	3	US-09-765-271-85	Sequence 85, App1	477	17	0.5	10013	3	US-09-949-016-16474	Sequence 16474, A
345	17	0.5	2329	3	US-09-765-272A-85	Sequence 85, App1	478	17	0.5	10053	3	US-09-949-016-17485	Sequence 17485, A
346	17	0.5	2351	3	US-09-949-016-2328	Sequence 2928, Ap	479	17	0.5	10424	3	US-09-902-840-1015	Sequence 1015, Ap
347	17	0.5	2352	2	US-08-889-909A-21	Sequence 21, App1	480	17	0.5	10917	3	US-08-926-842B-11	Sequence 11, App11
348	17	0.5	2352	3	US-09-156-163A-21	Sequence 21, App1	481	17	0.5	11459	3	US-09-462-136-7	Sequence 7, App11
349	17	0.5	2352	3	US-09-982-308B-21	Sequence 21, App1	482	17	0.5	13359	3	US-09-949-016-17004	Sequence 17004, A
340	17	0.5	2411	3	US-09-446-301A-15	Sequence 15, App1	483	17	0.5	12847	2	US-08-550-715-1	Sequence 1, App11
341	17	0.5	2411	3	US-09-099-932-47	Sequence 47, App1	484	17	0.5	13198	3	US-09-949-016-16425	Sequence 16425, A
342	17	0.5	2411	3	US-10-392-970-47	Sequence 47, App1	485	17	0.5	11126	3	US-09-949-016-15171	Sequence 15171, A
343	17	0.5	2526	3	US-08-669-408B-1	Sequence 1, App11	486	17	0.5	13069	3	US-09-949-016-12886	Sequence 12886, A
344	17	0.5	2529	2	US-08-724-774B-3	Sequence 3, App11	487	17	0.5	15363	3	US-08-961-527-139	Sequence 139, App
345	17	0.5	2559	3	US-09-089-595-3	Sequence 3, App11	488	17	0.5	15598	3	US-08-956-171B-82	Sequence 82, App1
346	17	0.5	2559	3	US-09-382-855-3	Sequence 3, App11	489	17	0.5	15598	3	US-08-781-986A-82	Sequence 82, App1
347	17	0.5	2559	3	US-09-183-714B-3	Sequence 3, App11	490	17	0.5	15157	3	US-09-949-016-11943	Sequence 11943, A
348	17	0.5	2559	3	US-09-642-281-3	Sequence 3, App11	491	17	0.5	15196	3	US-09-949-016-15126	Sequence 15126, A
349	17	0.5	2559	3	US-09-589-717-3	Sequence 3, App11	492	17	0.5	18864	3	US-09-949-016-12119	Sequence 12119, A
340	17	0.5	2569	3	US-10-104-047-1237	Sequence 1237, Ap	493	17	0.5	18864	3	US-09-949-016-15558	Sequence 15558, A
341	17	0.5	2707	3	US-09-949-016-4095	Sequence 4095, Ap	494	17	0.5	18203	3	US-09-949-016-15519	Sequence 15519, A
342	17	0.5	2707	3	US-09-949-016-4096	Sequence 4096, Ap	495	17	0.5	19207	3	US-09-949-016-11974	Sequence 11974, A
343	17	0.5	2723	3	US-10-104-047-392	Sequence 392, App	496	17	0.5	19210	3	US-09-949-016-12129	Sequence 12129, A
344	17	0.5	2746	2	US-08-576-165-3	Sequence 3, App11	497	17	0.5	20093	3	US-09-949-016-15207	Sequence 15207, A
345	17	0.5	2757	2	US-08-627-254C-26	Sequence 26, App1	498	17	0.5	20468	3	US-09-949-016-15463	Sequence 15463, A
346	17	0.5	3145	3	US-10-104-047-167	Sequence 167, App	499	17	0.5	22184	3	US-09-949-016-15463	Sequence 15463, A
347	17	0.5	3236	3	US-08-961-527-222	Sequence 222, App	500	17	0.5	20875	3	US-09-949-016-15860	Sequence 15860, A
348	17	0.5	3453	3	US-10-163-214-5	Sequence 5, App11	501	17	0.5	21196	3	US-09-949-016-14670	Sequence 14670, A
349	17	0.5	3510	3	US-09-056-105-16	Sequence 16, App1	502	17	0.5	21455	3	US-09-596-002-12	Sequence 12, App1
340	17	0.5	3538	3	US-09-902-540-686	Sequence 686, App	503	17	0.5	22155	3	US-09-949-016-614	Sequence 61, App
341	17	0.5	3557	3	US-10-104-047-352	Sequence 352, App	504	17	0.5	22184	3	US-09-949-002-713	Sequence 713, App
342	17	0.5	3943	3	US-09-573-080A-163	Sequence 163, App	505	17	0.5	22773	3	US-09-990-016-13399	Sequence 13399, A
343	17	0.5	4012	3	US-08-956-171E-47	Sequence 47, App1	506	17	0.5	22786	3	US-09-949-016-16421	Sequence 16421, A
344	17	0.5	4012	3	US-08-781-986A-32	Sequence 32, App1	507	17	0.5	23569	3	US-09-949-016-12153	Sequence 12153, A
345	17	0.5	4176	3	US-09-990-613A-42	Sequence 42, App1	508	17	0.5	23569	3	US-09-949-016-15351	Sequence 15351, A
346	17	0.5	4189	3	US-09-584-585-5	Sequence 5, App11	509	17	0.5	25419	3	US-09-949-016-15476	Sequence 15476, A
347	17	0.5	4488	3	US-08-956-171E-228	Sequence 228, App	510	17	0.5	25419	3	US-09-949-016-15477	Sequence 15477, A
348	17	0.5	4488	3	US-08-781-986A-228	Sequence 228, App	511	17	0.5	25769	3	US-09-949-016-14934	Sequence 14934, A
349	17	0.5	4576	3	US-09-713-273A-17	Sequence 17, App1	512	17	0.5	25434	3	US-09-949-016-15858	Sequence 15858, A
340	17	0.5	4612	3	US-08-960-048-2	Sequence 2, App11	513	17	0.5	26671	3	US-09-949-016-12229	Sequence 12229, A
341	17	0.5	4612	3	US-09-838-586-2	Sequence 2, App11	514	17	0.5	26671	3	US-09-949-016-17105	Sequence 17105, A
342	17	0.5	4643	3	US-09-436-874-1	Sequence 1, App11	515	17	0.5	26742	3	US-09-949-016-15650	Sequence 15650, A
343	17	0.5	4980	3	US-09-487-558B-117	Sequence 117, App	516	17	0.5	32573	3	US-09-949-016-13359	Sequence 13359, A
344	17	0.5	5117	3	US-09-774-528-438	Sequence 438, App	517	17	0.5	33155	3	US-09-949-016-16421	Sequence 16421, A
345	17	0.5	5117	3	US-10-120-988-438	Sequence 438, App	518	17	0.5	33155	3	US-09-949-016-16421	Sequence 16421, A
346	17	0.5	5232	3	US-09-212-971-3	Sequence 3, App11	519	17	0.5	33478	3	US-09-949-016-13615	Sequence 13615, A
347	17	0.5	5232	3	US-08-800-929A-3	Sequence 3, App11	520	17	0.5	33478	3	US-09-949-016-14933	Sequence 14933, A
348	17	0.5	5232	3	US-09-617-053A-3	Sequence 3, App11	521	17	0.5	33580	3	US-09-949-016-11336	Sequence 11336, A
349	17	0.5	5583	3	US-09-512-283C-312	Sequence 312, App	522	17	0.5	37292	3	US-09-949-016-15382	Sequence 15382, A
340	17	0.5	5802	3	US-09-949-016-13346	Sequence 13346, A	523	17	0.5	37799	3	US-09-949-016-12503	Sequence 12503, A
341	17	0.5	5816	3	US-09-220-641-4	Sequence 4, App11	524	17	0.5	37799	3	US-09-949-016-14263	Sequence 14263, A
342	17	0.5	6421	3	US-09-949-016-15765	Sequence 15765, A	525	17	0.5	37996	3	US-09-949-016-16472	Sequence 16472, A
343	17	0.5	6519	3	US-09-583-110-2605	Sequence 2605, Ap	526	17	0.5	38575	3	US-09-949-016-17304	Sequence 17304, A
344	17	0.5	6527	3	US-09-492-308A-3	Sequence 3, App11	527	17	0.5	38805	3	US-09-949-016-19332	Sequence 19332, A
345	17	0.5	6545	6	PCT-US95-13749-3	Sequence 3, App11	528	17	0.5	39699	3	US-09-949-016-17381	Sequence 17381, A
346	17	0.5	6702	3	US-09-769-787-209	Sequence 209, App	529	17	0.5	42246	3	US-09-949-016-17008	Sequence 17008, A
347	17	0.5	6717	3	US-09-107-433-1903	Sequence 1903, Ap	530	17	0.5	44019	3	US-09-949-016-19002	Sequence 19002, A
348	17	0.5	6898	3	US-09-902-540-862	Sequence 862, App	531	17	0.5	44653	3	US-09-949-016-11944	Sequence 11944, A
349	17	0.5	7486	3	US-08-475-886-5	Sequence 5, App11	532	17	0.5	44653	3	US-09-949-016-15690	Sequence 15690, A
340	17	0.5	7486	3	US-08-397-232-3	Sequence 3, App11	533	17	0.5	46885	3	US-09-949-016-13848	Sequence 13848, A
341	17	0.5	7486	3	US-09-653-499-5	Sequence 5, App11	534	17	0.5	46899	2	US-08-471-119A-1	Sequence 1, App11
342	17	0.5	7486	3	US-10-135-988-5	Sequence 5, App11	535	17	0.5	47375	3	US-09-949-016-15420	Sequence 15420, A





682	17	0.5	235064	3	US-09-949-016-15390	Sequence 15390, A	C 755	16	0.5	76	3	US-09-633-653-6	Sequence 6, Appl1
C 683	17	0.5	236341	3	US-09-949-016-13978	Sequence 13978, A	756	16	0.5	116	2	US-07-634-278-86	Sequence 96, Appl1
684	17	0.5	237863	3	US-09-949-016-13404	Sequence 13404, A	757	16	0.5	116	2	US-08-477-728-86	Sequence 96, Appl1
C 685	17	0.5	260286	3	US-09-949-016-17037	Sequence 17037, A	758	16	0.5	116	2	US-08-474-040-86	Sequence 96, Appl1
C 686	17	0.5	260293	3	US-09-949-016-12106	Sequence 12106, A	759	16	0.5	116	2	US-08-474-200-86	Sequence 96, Appl1
C 687	17	0.5	269223	3	US-09-949-002-41	Sequence 41, Appl1	760	16	0.5	116	2	US-08-484-537-86	Sequence 96, Appl1
688	17	0.5	276687	3	US-09-949-016-13840	Sequence 13840, A	C 761	16	0.5	150	3	US-09-513-999C-35174	Sequence 35174, A
689	17	0.5	301828	3	US-09-949-016-13969	Sequence 13969, A	C 762	16	0.5	154	3	US-09-513-999C-32995	Sequence 32995, A
C 690	17	0.5	312957	3	US-09-949-001-31	Sequence 31, Appl1	763	16	0.5	182	3	US-09-621-976-753	Sequence 753, App
C 691	17	0.5	312972	3	US-09-949-001-34	Sequence 34, Appl1	764	16	0.5	186	3	US-09-513-999C-18069	Sequence 18069, A
C 692	17	0.5	314798	3	US-09-949-016-15539	Sequence 15539, A	765	16	0.5	192	3	US-09-134-000C-434	Sequence 434, App
C 693	17	0.5	317366	3	US-09-949-016-16001	Sequence 16001, A	766	16	0.5	198	3	US-09-107-532A-2820	Sequence 2820, App
694	17	0.5	330890	3	US-09-949-016-14720	Sequence 14720, A	C 767	16	0.5	205	3	US-09-453-702B-81	Sequence 81, Appl1
695	17	0.5	339753	3	US-09-949-016-14573	Sequence 14573, A	C 768	16	0.5	205	3	US-10-114-170-81	Sequence 81, Appl1
696	17	0.5	339753	3	US-09-949-016-14574	Sequence 14574, A	C 769	16	0.5	207	3	US-09-270-767-18497	Sequence 28497, A
697	17	0.5	421491	3	US-09-949-016-12805	Sequence 12805, A	C 770	16	0.5	211	3	US-09-513-999C-36086	Sequence 36086, A
698	17	0.5	421494	3	US-09-949-016-14060	Sequence 14060, A	C 771	16	0.5	215	3	US-09-513-999C-499	Sequence 499, App
C 699	17	0.5	462589	3	US-09-949-016-12900	Sequence 12900, A	C 772	16	0.5	222	3	US-09-513-999C-9439	Sequence 9439, App
C 700	17	0.5	476044	3	US-09-949-016-119412	Sequence 12412, A	773	16	0.5	222	3	US-09-513-999C-25330	Sequence 25330, A
701	17	0.5	481115	3	US-09-949-016-11904	Sequence 11940, A	774	16	0.5	236	3	US-09-513-999C-35307	Sequence 35307, A
C 702	17	0.5	580073	3	US-08-545-528D-1	Sequence 1, Appl1	775	16	0.5	237	3	US-09-540-236-1021	Sequence 1021, App
C 703	17	0.5	636591	3	US-09-949-016-11808	Sequence 11808, A	C 776	16	0.5	240	3	US-09-248-786A-10043	Sequence 10043, A
C 704	17	0.5	636591	3	US-09-949-016-13388	Sequence 13388, A	C 777	16	0.5	242	3	US-09-513-999C-31270	Sequence 31270, A
C 705	17	0.5	640681	3	US-09-790-988-1	Sequence 1, Appl1	C 778	16	0.5	249	3	US-09-248-786A-9937	Sequence 9937, App
C 706	17	0.5	678533	3	US-09-949-016-14577	Sequence 14577, A	C 779	16	0.5	252	3	US-09-270-767-1954	Sequence 1954, App
C 707	17	0.5	678533	3	US-09-949-016-14578	Sequence 14578, A	C 780	16	0.5	252	3	US-09-270-767-17236	Sequence 17236, A
C 708	17	0.5	784019	3	US-09-949-016-14033	Sequence 14033, A	C 781	16	0.5	258	3	US-09-513-999C-16618	Sequence 16618, A
709	17	0.5	786431	3	US-09-751-389-3	Sequence 3, Appl1	782	16	0.5	267	3	US-09-313-294A-1239	Sequence 1239, App
710	17	0.5	818128	3	US-09-949-016-14546	Sequence 14546, A	783	16	0.5	271	3	US-09-222-575-50	Sequence 50, Appl1
711	17	0.5	818128	3	US-09-949-016-14547	Sequence 14547, A	784	16	0.5	271	3	US-09-389-681-50	Sequence 50, Appl1
712	17	0.5	818128	3	US-09-949-016-14548	Sequence 14548, A	785	16	0.5	271	3	US-09-620-405B-50	Sequence 50, Appl1
713	17	0.5	818128	3	US-09-949-016-14549	Sequence 14549, A	786	16	0.5	271	3	US-09-339-338-50	Sequence 50, Appl1
714	17	0.5	818128	3	US-09-949-016-14550	Sequence 14550, A	787	16	0.5	271	3	US-09-433-862B-50	Sequence 50, Appl1
715	17	0.5	818128	3	US-09-949-016-14551	Sequence 14551, A	788	16	0.5	271	3	US-09-604-287A-50	Sequence 50, Appl1
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## ALIGNMENTS

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RESULT 1
US-09-949-016-16073/C
; Sequence 16073, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16073
; LENGTH: 385136
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(385136)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16073
```

```
Query Match      0.6%; Score 21; DB 3; Length 385136;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2633 ATTGCTTCTCAAGGAAAT 2653
      |||
Db      384213 ATTGCTTCTCAAGGAAAT 384193
```

```
RESULT 2
US-09-949-016-35113
; Sequence 35113, Application US/09949016
```

```
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35113
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35113
```

```
Query Match      0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      148 AAGACTATTTTGTGTTTTT 167
      |||
Db      387 AAGACTATTTTGTGTTTTT 406
```

```
RESULT 3
US-09-949-016-35114
; Sequence 35114, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35114
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35114
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```
Query Match      0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      148 AAGACTATTTTGTGTTTTT 167
      |||
Db      392 AAGACTATTTTGTGTTTTT 411
```

```
RESULT 4
US-09-949-016-35115
; Sequence 35115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35115
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-35115

Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      148 AAGAGCTATTTTGTGTTTTT 167
      |||||
Db      559 AAGAGCTATTTTGTGTTTTT 578

RESULT 5
US-09-949-016-142318
/ Sequence 142318, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 142318
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-142318

Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      148 AAGAGCTATTTTGTGTTTTT 167
      |||||
Db      387 AAGAGCTATTTTGTGTTTTT 406

RESULT 6
US-09-949-016-142319
/ Sequence 142319, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
```

```
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 142319
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-142319

Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      148 AAGAGCTATTTTGTGTTTTT 167
      |||||
Db      392 AAGAGCTATTTTGTGTTTTT 411

RESULT 7
US-09-949-016-142320
/ Sequence 142320, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 142320
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-142320

Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      148 AAGAGCTATTTTGTGTTTTT 167
      |||||
Db      559 AAGAGCTATTTTGTGTTTTT 578

RESULT 8
US-09-949-016-161496
/ Sequence 161496, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
```

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 161496  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-161496

Query Match 0.6%; Score 20; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 AATATATATATATTTTTCAC 55  
DB 138 AATATATATATATTTTTCAC 157

RESULT 9  
US-08-617-785-5  
Sequence 5, Application US/08617785E  
Patent No. 6228610  
GENERAL INFORMATION:  
APPLICANT: Flor, Peter J.  
APPLICANT: Kuhn, Rainer  
APPLICANT: Lindaur, Kristen  
APPLICANT: Puttner, Irene  
APPLICANT: Knopfel, Thomas

TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,  
TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds

FILE REFERENCE: 4-19679/A/PCT  
CURRENT APPLICATION NUMBER: US/08/617,785E  
EARLIER FILING DATE: 1996-03-19  
EARLIER APPLICATION NUMBER: PCT/EP94/02991  
EARLIER FILING DATE: 1994-09-07  
EARLIER APPLICATION NUMBER: EPO 9416553.7  
EARLIER FILING DATE: 1994-08-19  
EARLIER APPLICATION NUMBER: EPO 93810663.0  
EARLIER FILING DATE: 1993-09-20  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5

LENGTH: 1399  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(270)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (920)..(1090)  
OTHER INFORMATION: Nucleotides designated as n could be a or g or c  
OTHER INFORMATION: or t/u  
US-08-617-785-5

Query Match 0.6%; Score 20; DB 3; Length 1399;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1201 CATGGAACCATGAGAGGA 1220  
DB 283 CATGGAACCATGAGAGGA 302

RESULT 10  
US-09-817-464-5  
Sequence 5, Application US/09817464  
Patent No. 6515107  
GENERAL INFORMATION:  
APPLICANT: Flor, Peter J.  
APPLICANT: Kuhn, Rainer  
APPLICANT: Lindaur, Kristen  
APPLICANT: Puttner, Irene  
APPLICANT: Knopfel, Thomas  
TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,

TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds  
FILE REFERENCE: 4-19679/A/PCT  
CURRENT APPLICATION NUMBER: US/09/817,464  
CURRENT FILING DATE: 2001-03-26  
EARLIER APPLICATION NUMBER: US/08/617,785  
EARLIER FILING DATE: 1996-03-19  
EARLIER APPLICATION NUMBER: EPO 9416553.7  
EARLIER FILING DATE: 1994-08-19  
EARLIER APPLICATION NUMBER: EPO 93810663.0  
EARLIER FILING DATE: 1993-09-20  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 1399  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(270)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (920)..(1090)  
OTHER INFORMATION: Nucleotides designated as n could be a or g or c  
OTHER INFORMATION: or t/u  
US-09-817-464-5

Query Match 0.6%; Score 20; DB 3; Length 1399;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1201 CATGGAACCATGAGAGGA 1220  
DB 283 CATGGAACCATGAGAGGA 302

RESULT 11  
US-07-977-434-11/c  
Sequence 11, Application US/07977434  
Patent No. 5466591  
GENERAL INFORMATION:  
APPLICANT: Geland, David H.  
APPLICANT: Abramson, Richard D.  
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7  
SOFTWARE: WordPerfect 2.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,434  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,490  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,466  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,213  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 523,394  
FILING DATE: 15-MAY-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Luann Caeer  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: Case No. 546591 8753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2972  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2679 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Thermosipho africanus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2676  
US-07-977-434-11

Query Match 0.6%; Score 20; DB 2; Length 2679;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3181 AATAATCTTGAATGTCTT 3200  
Db 550 AATAATCTTGAATGTCTT 531

RESULT 12  
US-08-458-819-11/c  
Sequence 11, Application US/08458819  
Patent No. 5795762  
GENERAL INFORMATION:  
APPLICANT: Gelfand, David H.  
APPLICANT: Abramson, Richard D.  
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASIS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
ZIP: 07110-1199

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7  
SOFTWARE: WordPerfect 2.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,819  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/977,434  
FILING DATE: 23-FEB-1993  
APPLICATION NUMBER: US 590,490  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,466  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,213  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 523,394  
FILING DATE: 15-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Luann Caeer  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: Case No. 5795762 8753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2972  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2679 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Thermosipho africanus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2676  
US-08-458-819-11

Query Match 0.6%; Score 20; DB 2; Length 2679;

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3181 AATACTTTGAATTGTTCT 3200  
Db 550 AATACTTTGAATTGTTCT 531

## RESULT 13

PCT-US91-07035-11/c  
Sequence 11, Application PC/TUS9107035  
GENERAL INFORMATION:  
APPLICANT: Gelifand, David H.  
APPLICANT: Abramson, Richard D.  
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cetus Corporation  
STREET: 1400 Fifty-third Street  
CITY: Emeryville  
STATE: California  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/07035  
CLASSIFICATION: 435  
FILING DATE: 19910930  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,490  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,466  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,213  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 523,394  
FILING DATE: 15-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Sias Ph.D., Stacey R.

REGISTRATION NUMBER: 32,630  
REFERENCE/DOCKET NUMBER: Case No. 2580  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-420-3300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2679 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Thermosipho africanus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2676  
PCT-US91-07035-11

Query Match 0.6%; Score 20; DB 6; Length 2679;

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3181 AATACTTTGAATTGTTCT 3200  
Db 550 AATACTTTGAATTGTTCT 531

## RESULT 14

US-09-016-434-1118  
Sequence 11B, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Selhammer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 845-4166  
TELEFAX: (650) 855-0555  
INFORMATION FOR SEQ ID NO: 1118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3021 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:



LIBRARY: GENBANK  
CLONE: 91370110  
US-09-016-434-1118

Query Match 0.6%; Score 20; DB 3; Length 3021;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1201 CATGGAACCATGAGAGAGA 1220  
Db 2999 CATGGAACCATGAGAGAGA 3018

## RESULT 15

US-08-617-785-3  
Sequence 3, Application US/08617785E

Patent No. 6228610  
GENERAL INFORMATION:

APPLICANT: Flot, Peter J.

APPLICANT: Kuhn, Ranier

APPLICANT: Landaer, Kristen

APPLICANT: Puttner, Irene

APPLICANT: Knopfel, Thomas

TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,  
HMR6, HMR7) and Related DNA Compounds

FILE REFERENCE: 4-19679/A/PCT

CURRENT APPLICATION NUMBER: US/08/617,785E

EARLIER FILING DATE: 1996-03-19

EARLIER APPLICATION NUMBER: PCT/EP94/02991

EARLIER FILING DATE: 1994-09-07

EARLIER APPLICATION NUMBER: EPO 9416553.7

EARLIER FILING DATE: 1994-08-19

EARLIER APPLICATION NUMBER: EPO 93810663.0

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 3804

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(2604)

FEATURE:

NAME/KEY: unsure

LOCATION: (3325)..(3495)

OTHER INFORMATION: nucleotides designated as n could be a or g or c

OTHER INFORMATION: or t/u

US-08-617-785-3

Query Match

Best Local Similarity 0.6%; Score 20; DB 3; Length 3804;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1201 CATGGAACCATGAGAGAGA 1220

Db 2688 CATGGAACCATGAGAGAGA 2707

Search completed: January 14, 2006, 04:38:47

Job time : 601 secs

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2006, 11:43:25 : Search time 1892 Seconds  
(without alignments)  
11730.141 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaccacaagaagtcctcct.....tactatargacataatcaat 3330

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 333246308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Listing first 1000 summaries

Database :

N Geneseq 21:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3330	100.0	3330	9	ACCS7946	ACCS7946 Human int
2	3330	100.0	3330	10	ADA14840	ADA14840 Human int
3	2476	74.4	2887	9	ACCS7947	ACCS7947 Human int
4	2476	74.4	2887	10	ADA14842	ADA14842 Human int
5	2095	62.9	3263	3	AAA46205	AAA46205 CDNA enco
6	2094	62.9	3261	9	ACCS7960	ACCS7960 Human int
7	2094	62.9	3261	10	ADA14866	ADA14866 Human int
8	1992	59.8	2966	3	AAA46328	AAA46328 Interphot
9	1503	45.1	2244	3	AAA46329	AAA46329 Interphot
10	1503	45.1	2244	9	ACCS7948	ACCS7948 Human int
11	1503	45.1	2244	10	ADA14844	ADA14844 Human int
12	1937	5.9	1858	3	AAA46327	AAA46327 Exon 1 an
13	1937	5.9	1858	9	ACCS7949	ACCS7949 Human int
14	1937	5.9	1858	10	ADA14846	ADA14846 Human int
15	112	3.4	555	3	AAA46204	AAA46204 CDNA enco
16	112	3.4	555	9	ACCS7953	ACCS7953 Monkey in
17	112	3.4	555	10	ADA14853	ADA14853 Monkey in
18	60	1.8	60	6	ABN43651	ABN43651 Human spl
19	32	1.0	1726	9	ACCS7951	ACCS7951 Mouse int

20	32	1.0	1726	10	ADA14849	ADA14849 Mouse int
21	32	1.0	3206	3	AAA46309	AAA46309 CDNA enco
22	32	1.0	3668	9	ACCS7950	ACCS7950 Mouse int
23	32	1.0	3668	10	ADA14847	ADA14847 Mouse int
24	27	0.8	27	3	AAA46239	AAA46239 Primer IP
25	24	0.7	1321	9	ACCS7952	ACCS7952 Mouse int
26	24	0.7	1321	10	ADA14851	ADA14851 Mouse int
27	23	0.7	19127	10	ADH13788	ADH13788 Prostate
28	22	0.7	22	3	AAA46219	AAA46219 Primer IP
29	22	0.7	22	3	AAA46229	AAA46229 Primer IP
30	22	0.7	22	3	AAA46237	AAA46237 Primer IP
31	22	0.7	22	3	AAA46236	AAA46236 Primer IP
32	22	0.7	22	3	AAA46209	AAA46209 Primer IP
33	22	0.7	22	3	AAA46221	AAA46221 Primer IP
34	22	0.7	22	3	AAA46227	AAA46227 Primer IP
35	22	0.7	22	13	ADR74360	ADR74360 Allele sp
36	22	0.7	636	3	ACCS4136	ACCS4136 Arabidops
37	22	0.7	3760	12	ADO63322	ADO63322 Novel hum
38	22	0.7	56330	14	AD213264	AD213264 Murine ca
39	21	0.6	21	3	AAA46212	AAA46212 Primer IP
40	21	0.6	21	3	AAA46224	AAA46224 Primer IP
41	21	0.6	21	3	AAA46230	AAA46230 Primer IP
42	21	0.6	21	3	AAA46238	AAA46238 Primer IP
43	21	0.6	21	3	AAA46242	AAA46242 Primer IP
44	21	0.6	22	13	ADR74359	ADR74359 Allele sp
45	20	0.6	20	3	AAA46213	AAA46213 Primer IP
46	20	0.6	20	3	AAA46218	AAA46218 Primer IP
47	20	0.6	20	3	AAA46240	AAA46240 Primer IP
48	20	0.6	20	3	AAA46241	AAA46241 Primer IP
49	20	0.6	20	3	AAA46216	AAA46216 Primer IP
50	20	0.6	20	3	AAA46222	AAA46222 Primer IP
51	20	0.6	20	3	AAA46220	AAA46220 Primer IP
52	20	0.6	20	3	AAA46232	AAA46232 Primer IP
53	20	0.6	20	3	AAA46211	AAA46211 Primer IP
54	20	0.6	20	3	AAA46225	AAA46225 Primer IP
55	20	0.6	20	3	AAA46226	AAA46226 Primer IP
56	20	0.6	20	3	AAA46215	AAA46215 Primer IP
57	20	0.6	20	3	AAA46234	AAA46234 Primer IP
58	20	0.6	20	3	AAA46210	AAA46210 Primer IP
59	20	0.6	20	3	AAA46233	AAA46233 Primer IP
60	20	0.6	20	3	AAA46228	AAA46228 Primer IP
61	20	0.6	181	12	ACH94178	ACH94178 Human gen
62	20	0.6	320	5	AD176679	AD176679 Human ova
63	20	0.6	320	5	AD1770353	AD1770353 Human ova
64	20	0.6	466	5	AD141915	AD141915 Human ova
65	20	0.6	484	4	AAK78636	AAK78636 Human imm
66	20	0.6	486	4	AA12761	AA12761 Human bre
67	20	0.6	529	5	AD141887	AD141887 Human gen
68	20	0.6	541	12	ACH80478	ACH80478 Human gen
69	20	0.6	550	4	AA12760	AA12760 Human bre
70	20	0.6	560	5	AD176651	AD176651 Human ova
71	20	0.6	560	5	AD1770323	AD1770323 Human ova
72	20	0.6	678	4	AA121632	AA121632 Human bre
73	20	0.6	759	4	AA121631	AA121631 Human bre
74	20	0.6	812	6	ABN98966	ABN98966 Arabidops
75	20	0.6	822	11	ACN82898	ACN82898 Breast ca
76	20	0.6	878	11	ACN82899	ACN82899 Breast ca
77	20	0.6	887	5	AD162470	AD162470 Human ova
78	20	0.6	887	11	ACN90927	ACN90927 Breast ca
79	20	0.6	1206	9	ADB89678	ADB89678 Altiolococ
80	20	0.6	1206	9	ADB89676	ADB89676 Altiolococ
81	20	0.6	1290	6	ABQ41841	ABQ41841 Oligonuc
82	20	0.6	1290	6	ABQ41840	ABQ41840 Oligonuc
83	20	0.6	1291	6	ABQ41862	ABQ41862 Oligonuc
84	20	0.6	1291	6	ABQ41863	ABQ41863 Oligonuc
85	20	0.6	1399	6	ABQ89344	ABQ89344 Human mgl
86	20	0.6	1716	8	ADA68600	ADA68600 Arabidops
87	20	0.6	2000	8	ADJ71441	ADJ71441 Rice gene
88	20	0.6	2000	12	ADJ41616	ADJ41616 Plant CDN
89	20	0.6	2265	2	AAQ24332	AAQ24332 Mutant th
90	20	0.6	2403	2	AAQ24331	AAQ24331 Mutant th
91	20	0.6	2568	2	AAQ28937	AAQ28937 Encodes T
92	20	0.6	2571	2	AAQ24330	AAQ24330 Mutant th

C 93	20	0.6	2679	2	AAQ24329	166	19	0.6	1827	8	ADA69720	Ad69720 Rice gene
C 94	20	0.6	2679	2	AAQ28936	167	19	0.6	1989	6	AB231841	Ab231841 Candida a
C 95	20	0.6	2944	14	AD267602	168	19	0.6	2272	13	ACN49013	Acn49013 Tumour-ab
C 96	20	0.6	2958	12	AD063132	169	19	0.6	2352	12	ADO19451	Ado19451 Human PRO
C 97	20	0.6	3021	10	ACH56520	170	19	0.6	2390	7	ADM73142	Adm73142 Human kid
C 98	20	0.6	3021	12	AD156316	171	19	0.6	2390	7	ADM41996	Adm41996 CDNA elev
C 99	20	0.6	3804	2	AAQ89343	172	19	0.6	2403	13	ADT44287	Adt44287 Bacteriail
C 100	20	0.6	4286	2	AAQ23917	173	19	0.6	2501	14	ADV98050	Adv98050 Bifulfile
C 101	20	0.6	4312	8	AB242695	174	19	0.6	2960	4	AA161185	Aa161185 Human pol
C 102	20	0.6	4312	14	AB242695	175	19	0.6	2970	11	ABD17294	Abd17294 Pseudomon
C 103	20	0.6	6446	4	AA546327	176	19	0.6	3077	8	AB210215	Ab210215 Haematopo
C 104	20	0.6	15714	6	AB133172	177	19	0.6	3077	8	AB210215	Ab210215 Haematopo
C 105	20	0.6	15714	6	AB133172	178	19	0.6	3077	13	AD589641	Ad589641 Oligonuci
C 106	20	0.6	23668	6	ABA97921	179	19	0.6	3077	13	AD589367	Ad589367 Oligonuci
C 107	20	0.6	41199	12	ADO97629	180	19	0.6	3293	4	AA159399	Aa159399 Human pol
C 108	20	0.6	56587	11	ACN44972	181	19	0.6	4023	6	ABN79892	Abn79892 Fungal ZB
C 109	20	0.6	76600	12	AD079402	182	19	0.6	5013	8	AB210197	Ab210197 Haematopo
C 110	20	0.6	80268	13	ABD32951	183	19	0.6	5312	6	AB1332196	Ab1332196 Human lmm
C 111	20	0.6	84495	6	AA820588	184	19	0.6	5559	4	AB133423	Ab133423 Human lmm
C 112	20	0.6	107543	13	ABD33524	185	19	0.6	5645	4	AB103410	Ab103410 Drosophi1
C 113	20	0.6	107543	13	ABD33524	186	19	0.6	5888	14	AEA18088	Aea18088 Converterd
C 114	20	0.6	155350	9	ABD12064	187	19	0.6	5981	6	AB133763	Ab133763 Human lmm
C 115	20	0.6	191127	10	ADH13788	188	19	0.6	5997	6	ABK31311	Abk31311 Signal tr
C 116	20	0.6	256157	11	ACN44650	189	19	0.6	5997	6	AB170286	Ab170286 Chemical1
C 117	20	0.6	256157	11	ABD33570	190	19	0.6	5997	6	AA561211	Aa561211 Human gen
C 118	20	0.6	349999	13	ADC87010	191	19	0.6	6077	6	AB133854	Ab133854 Human lmm
C 119	19	0.6	19	3	AAA46217	192	19	0.6	6077	6	AB133246	Ab133246 Human lmm
C 120	19	0.6	19	3	AAA46223	193	19	0.6	6077	10	ADB54295	Adb54295 Pretreace
C 121	19	0.6	19	13	ADR74361	194	19	0.6	6077	10	ADB54167	Adb54167 Pretreace
C 122	19	0.6	105	14	AD284238	195	19	0.6	6077	10	AD584201	Ad584201 Human lym
C 123	19	0.6	233	3	AAAC02941	196	19	0.6	6077	10	AD584125	Ad584125 Human lym
C 124	19	0.6	365	5	ABV00754	197	19	0.6	6123	6	AB133036	Ab133036 Human lmm
C 125	19	0.6	390	4	AAK81838	198	19	0.6	6381	6	AB133267	Ab133267 Human lmm
C 126	19	0.6	390	4	AAK81837	199	19	0.6	6381	6	AB134519	Ab134519 Human lmm
C 127	19	0.6	391	5	ABV09923	200	19	0.6	6381	6	AB170244	Ab170244 Human met
C 128	19	0.6	410	4	AA111273	201	19	0.6	6381	7	ADS99780	Ad999780 Complemen
C 129	19	0.6	410	4	ABA52935	202	19	0.6	6923	6	ABK31297	Abk31297 Signal tr
C 130	19	0.6	410	4	AA132539	203	19	0.6	6923	6	AB170276	Ab170276 Chemical1
C 131	19	0.6	410	4	ABA42506	204	19	0.6	6923	6	AA561199	Aa561199 Human gen
C 132	19	0.6	410	4	ABA22714	205	19	0.6	7089	4	AA545362	Aa545362 Chemical1
C 133	19	0.6	410	4	AAK26666	206	19	0.6	7089	6	ABK28197	Abk28197 DNA trans
C 134	19	0.6	410	4	AAK01185	207	19	0.6	7659	6	AB1332189	Ab1332189 Human lmm
C 135	19	0.6	410	5	AB526236	208	19	0.6	7969	4	AA546679	Aa546679 Tumour su
C 136	19	0.6	410	5	AA101188	209	19	0.6	7969	4	ABQ67037	Abq67037 Human ang
C 137	19	0.6	410	5	AB501238	210	19	0.6	8049	6	AB134037	Ab134037 Human ang
C 138	19	0.6	432	5	ABV40065	211	19	0.6	8143	6	AB133896	Ab133896 Human lmm
C 139	19	0.6	432	5	ABV31097	212	19	0.6	8253	6	AAK87351	Aa87351 Human lmm
C 140	19	0.6	459	9	ACH21683	213	19	0.6	8693	6	AB133511	Ab133511 Human lmm
C 141	19	0.6	462	8	ACH34788	214	19	0.6	8693	6	ABK33985	Abk33985 Human DNA
C 142	19	0.6	466	3	AAAC08042	215	19	0.6	8693	8	ADA20373	Ada20373 Prostate
C 143	19	0.6	507	9	ACH45446	216	19	0.6	8693	8	ADA84180	Ada84180 Human ren
C 144	19	0.6	510	5	AAH55798	217	19	0.6	8998	6	AB133706	Ab133706 Human lmm
C 145	19	0.6	519	12	ACH67788	218	19	0.6	10122	4	AAK87363	Aa87363 Human lmm
C 146	19	0.6	586	5	ABV53772	219	19	0.6	11029	4	AA546413	Aa546413 Tumour su
C 147	19	0.6	653	8	AB254059	220	19	0.6	11029	13	AD589587	Ad589587 Oligonuci
C 148	19	0.6	658	13	ADX45988	221	19	0.6	11029	13	AD589287	Ad589287 Oligonuci
C 149	19	0.6	700	4	AAH93220	222	19	0.6	11187	6	ABK28451	Abk28451 DNA trans
C 150	19	0.6	788	4	AAH22397	223	19	0.6	11327	4	AA546432	Aa546432 Tumour su
C 151	19	0.6	812	4	AAH31915	224	19	0.6	11484	4	AAK87360	Aa87360 Human lmm
C 152	19	0.6	837	11	ABD17268	225	19	0.6	11497	4	AAK87362	Aa87362 Human lmm
C 153	19	0.6	1140	8	AB242111	226	19	0.6	11729	6	AB132894	Ab132894 Human lmm
C 154	19	0.6	1140	8	ADA68619	227	19	0.6	12017	6	AB558302	Ab558302 Novel hum
C 155	19	0.6	1158	11	ABD17216	228	19	0.6	13712	6	AB133531	Ab133531 Human lmm
C 156	19	0.6	1281	8	AAH84581	229	19	0.6	15295	10	ABX77181	Abx77181 Genomic D
C 157	19	0.6	1281	8	ACA18828	230	19	0.6	15536	6	AAK87354	Aa87354 Human lmm
C 158	19	0.6	1301	2	AAK077172	231	19	0.6	15954	4	AAK31495	AaK31495 Signal tr
C 159	19	0.6	1395	3	AAK1836	232	19	0.6	15954	6	AB170468	Ab170468 Chemical1
C 160	19	0.6	1405	4	AA605994	233	19	0.6	17069	4	AAK83892	AaK83892 Human lmm
C 161	19	0.6	1682	3	AAAC50162	234	19	0.6	17069	4	AAK80906	AaK80906 Human lmm
C 162	19	0.6	1686	4	AAK94503	235	19	0.6	17703	6	ABK39953	Abk39953 Human che
C 163	19	0.6	1686	12	ADL31319	236	19	0.6	17893	6	AB133364	Ab133364 Human lmm
C 164	19	0.6	1693	3	AAK49610	237	19	0.6	18133	6	ABK40017	Abk40017 Human che
C 165	19	0.6	1761	3	AAAC35476	238	19	0.6	18133	6	AB132940	Ab132940 Human lmm

239	19	0.6	18318	6	AB133948	Ab133948 Human imm	c 312	18	0.5	557	4	AB834444	Ab834444 Human liv
240	19	0.6	21354	4	AA646815	AA646815 Tumour su	c 313	18	0.5	563	13	ADX32352	Adx32352 Plant ful
241	19	0.6	23576	11	ACN44056	ACN44056 Mouse gen	c 314	18	0.5	572	13	ADQ52113	Adq52113 Novel can
c 242	19	0.6	23899	4	ABL10362	ABL10362 Drosophil	c 315	18	0.5	582	8	ACA43169	ACA43169 Prokaryot
243	19	0.6	26997	4	AA646748	AA646748 Tumour su	c 316	18	0.5	601	14	AB833029	Ab833029 Human DNA
244	19	0.6	27781	10	AA6467186	AA6467186 Genomic D	c 317	18	0.5	601	14	AB833028	Ab833028 Human DNA
245	19	0.6	34769	4	AA646774	AA646774 Tumour su	c 318	18	0.5	603	6	AB187588	Ab187588 Human ova
246	19	0.6	38045	9	AA656159	AA656159 Human sal	c 319	18	0.5	603	6	AB187588	Ab187588 Human ova
c 247	19	0.6	42353	12	ADQ97403	Adq97403 Human can	c 320	18	0.5	603	13	ADL71883	Adl71883 Streptoco
c 248	19	0.6	50002	11	ACN44510	ACN44510 Human gen	c 321	18	0.5	613	14	ACL55549	ACL55549 Human col
c 249	19	0.6	50657	13	ABD33455	ABd33455 Murine ca	c 322	18	0.5	629	13	AD554578	Ad554578 Bacterial
c 250	19	0.6	52001	12	ADP67076	ADp67076 Human mit	c 322	18	0.5	634	13	ADQ50687	Adq50687 Novel can
c 251	19	0.6	56840	13	ABD33123	ABd33123 Murine mit	c 323	18	0.5	642	6	AB134378	Ab134378 Human imm
c 252	19	0.6	70000	12	ADQ53477	AdJ53477 Human ffp	c 324	18	0.5	651	8	ACA33378	ACA33378 Prokaryot
c 253	19	0.6	73102	12	ADQ97888	Adq97888 Human can	c 325	18	0.5	663	13	ADR603298	Adr603298 Cotton cd
c 254	19	0.6	74828	12	ADQ97982	Adq97982 Human can	c 326	18	0.5	696	3	AAA01677	AAa01677 Human col
c 255	19	0.6	95050	14	ADX98574	Adx98574 Human can	c 327	18	0.5	700	4	AAH92989	AAh92989 Human inf
256	19	0.6	107602	6	AAK9657	AAk9657 DNA of th	c 328	18	0.5	700	4	AAH92990	AAh92990 Human inf
257	19	0.6	107612	6	AB154503	Ab154503 Human PAC	c 329	18	0.5	702	13	ADS63940	Ad63940 Bacterial
258	19	0.6	110000	12	ADO79173_3	ADO79173_3 Continuation (4 of	c 330	18	0.5	702	13	ADS63567	Ad63567 Bacterial
c 259	19	0.6	110000	13	ABD32921_5	ABD32921_5 Continuation (6 of	c 331	18	0.5	702	13	ADS64306	Ad64306 Bacterial
c 260	19	0.6	114693	8	AA048308	AA048308 Human tra	c 332	18	0.5	705	10	ADC91536	Adc91536 E. faeciu
c 261	19	0.6	118384	14	ABX56555	ABx56555 Human aut	c 333	18	0.5	754	5	AAA01699	AAa01699 Human col
262	19	0.6	186854	14	ADX38909	Adx38909 Vaccinia	c 334	18	0.5	760	5	AA668975	AA668975 DNA encod
263	19	0.6	203654	10	ABX16034	ABx16034 Human gen	c 335	18	0.5	779	13	ADS60372	AdS60372 Bacterial
c 264	19	0.6	254396	12	ADQ97557	Adq97557 Human can	c 336	18	0.5	813	5	ABV20296	ABv20296 Human pro
c 265	19	0.6	254396	12	ADQ97557	Adq97557 Human can	c 337	18	0.5	813	5	ABV26128	ABv26128 Human pro
c 266	19	0.6	304905	11	ADP75180	ADp75180 Human Bnd	c 338	18	0.5	821	5	AAH43681	AAh43681 PRKAG 5'
c 267	18	0.5	18	3	AAA46235	AAA46235 Primer IP	c 339	18	0.5	922	11	ACL33366	ACL33366 Rice abio
c 268	18	0.5	21	6	ABX20909	ABx20909 Candida a	c 340	18	0.5	942	13	ADR61574	Adr61574 Cotton cd
269	18	0.5	181	8	ABX52569	ABx52569 Bovine ES	c 341	18	0.5	987	13	ADK44813	ADk44813 Streptoco
269	18	0.5	208	10	ADB75819	ADb75819 Tomato pl	c 342	18	0.5	989	4	AB115359	AB115359 Drosophil
270	18	0.5	218	18	ADK11796	ADk11796 Breast ca	c 343	18	0.5	990	11	ACL29844	ACL29844 Rice abio
271	18	0.5	250	8	ABX39542	ABx39542 Bovine ES	c 344	18	0.5	1005	13	ADR29859	ADR29859 Novel S.
272	18	0.5	321	14	ABE65558	ABe65558 Rice geno	c 345	18	0.5	1005	14	AEA56729	AEa56729 Streptoco
c 273	18	0.5	338	3	AA050043	AA050043 Human sec	c 346	18	0.5	1049	12	ADJ57800	ADj57800 Marker ge
c 274	18	0.5	366	12	ADP92064	ADp92064 Cotton ex	c 347	18	0.5	1071	4	AAK82249	AAk82249 Human imm
c 275	18	0.5	368	4	AA635433	AA635433 Human car	c 348	18	0.5	1071	4	AAK82250	AAk82250 Human imm
c 276	18	0.5	368	10	AD645512	AD645512 Human car	c 349	18	0.5	1119	6	AAQ68953	AAq68953 Libetia
c 277	18	0.5	368	13	ADJ06930	ADj06930 Human can	c 350	18	0.5	1122	13	ADX63999	Adx63999 Plant ful
c 278	18	0.5	391	13	ADU12681	ADu12681 Solid tum	c 351	18	0.5	1133	13	ADL14453	ADl14453 Plant ful
c 279	18	0.5	435	5	ABV09588	ABv09588 Human pro	c 352	18	0.5	1140	13	AD551059	AD551059 Bacterial
c 280	18	0.5	435	6	ABK16475	ABk16475 Gram posi	c 353	18	0.5	1147	6	ABN85215	ABn85215 Human bsr
c 281	18	0.5	439	6	AB187546	AB187546 Human ova	c 354	18	0.5	1160	3	AA040798	AA040798 Arabidops
c 282	18	0.5	453	4	AAK31399	AAk31399 Human bon	c 355	18	0.5	1205	13	AD082395	AD082395 Plant ful
c 283	18	0.5	453	4	AAK05774	AAK05774 Human bra	c 356	18	0.5	1210	3	AA038668	AA038668 Arabidops
c 284	18	0.5	453	4	AB831080	AB831080 Human liv	c 357	18	0.5	1218	3	AA050372	AA050372 Arabidops
c 285	18	0.5	453	6	AB806152	AB806152 Human gen	c 358	18	0.5	1267	12	AD024399	AD024399 Human bof
c 286	18	0.5	464	4	AAK89758	AAk89758 Human dig	c 359	18	0.5	1290	11	ADM29267	Adm29267 Human nov
c 287	18	0.5	464	5	AA631792	AA631792 Human liv	c 360	18	0.5	1290	11	ADM29269	Adm29269 Human nov
c 288	18	0.5	464	6	ABN90147	ABn90147 Human liv	c 361	18	0.5	1290	11	ADM29263	Adm29263 Human nov
c 289	18	0.5	464	11	ADJ14914	ADj14914 Human liv	c 362	18	0.5	1290	11	ADM29265	Adm29265 Human nov
c 290	18	0.5	465	5	ABV30764	ABv30764 Human pro	c 363	18	0.5	1290	13	ADX29870	ADx29870 Plant ful
c 291	18	0.5	465	5	ABV39732	ABv39732 Human pro	c 364	18	0.5	1313	3	AA033202	AA033202 Arabidops
c 292	18	0.5	474	12	ADP92561	ADp92561 Cotton ex	c 365	18	0.5	1317	3	AA049582	AA049582 Arabidops
c 293	18	0.5	486	4	AAK91075	AAk91075 Human dig	c 366	18	0.5	1317	5	AAH48067	AAh48067 Murine HS
c 294	18	0.5	486	4	AAK91076	AAk91076 Human dig	c 367	18	0.5	1323	3	AA033454	AA033454 Arabidops
c 295	18	0.5	486	5	AA632111	AA632111 Human liv	c 368	18	0.5	1373	3	AA033158	AA033158 Arabidops
c 296	18	0.5	486	5	AA632110	AA632110 Human liv	c 369	18	0.5	1374	3	AA037991	AA037991 Arabidops
c 297	18	0.5	486	6	ABN90465	ABn90465 Human liv	c 370	18	0.5	1467	2	AAH84962	AAh84962 Human sec
c 298	18	0.5	486	6	ABN90466	ABn90466 Human liv	c 371	18	0.5	1467	8	ACD18888	ACd18888 Novel hum
c 299	18	0.5	486	11	ADJ15379	ADj15379 Human liv	c 372	18	0.5	1467	12	ADG78279	ADg78279 Human sec
c 300	18	0.5	486	11	ADJ15378	ADj15378 Human liv	c 373	18	0.5	1467	12	ADN60570	ADn60570 Human sec
c 301	18	0.5	516	9	ADB10513	ADB10513 Allolococ	c 374	18	0.5	1492	10	ADBS6401	ADb58401 Toxicycl
c 302	18	0.5	526	3	AA080687	AA080687 Human sec	c 375	18	0.5	1492	10	ADBS5979	ADb552979 Primary r
c 303	18	0.5	530	3	AA069766	AA069766 Human bre	c 376	18	0.5	1547	3	AA052821	AA052821 Arabidops
c 304	18	0.5	547	8	AB218242	AB218242 Group tti	c 377	18	0.5	1549	3	AA054728	AA054728 Arabidops
c 305	18	0.5	550	2	AA043492	AA043492 ATM gene	c 378	18	0.5	1560	2	AA057071	AA057071 AGB-modif
c 306	18	0.5	556	10	AA057644	AA057644 ATM genom	c 379	18	0.5	1619	13	ABE64996	ABe64996 Rice geno
c 307	18	0.5	556	10	AA057644	AA057644 ATM genom	c 380	18	0.5	1619	13	AD447354	AD447354 Bacterial
c 308	18	0.5	557	4	ABA60504	ABa60504 Human foe	c 381	18	0.5	1631	10	ADDE6257	ADd62557 Rat gene
c 309	18	0.5	557	4	AA140391	AA140391 Probe #90	c 382	18	0.5	1631	10	ADDA7951	ADd47951 Rat gene
c 310	18	0.5	557	4	AAK34671	AAk34671 Human bon	c 383	18	0.5	1682	13	ADX09152	ADx09152 Plant ful
c 311	18	0.5	557	4	AAK08784	AAk08784 Human bra	c 384	18	0.5	1694	10	ADL08420	ADl08420 Human can

C 385	18	0.5	1703	13	ACN37975	Acn37975 Tumour-as	458	18	0.5	3685	12	ADH48399	Adh48399 Human KRP
C 386	18	0.5	1797	12	ADN73888	Adn73888 Thale cre	459	18	0.5	3868	12	ADO26905	Ado26905 cDNA encod
C 387	18	0.5	1878	10	ADH82782	Adh82782 Enterococ	C 460	18	0.5	3884	14	ADM11286	Adm11286 Adenovitra
C 388	18	0.5	1887	4	AAO08357	Aao08357 Human sec	C 461	18	0.5	3885	4	AAO08357	Aao08357 Adenovitra
C 389	18	0.5	1887	4	AAO08357	Aao08357 Human sec	C 462	18	0.5	3984	13	ACN38296	Acn38296 Tumour-as
C 390	18	0.5	1887	8	ABZ73671	Abz73671 Human sec	C 463	18	0.5	3985	12	ADQ19494	Adq19494 Human sof
C 391	18	0.5	1887	8	ABZ73671	Abz73671 Secreted	C 464	18	0.5	3985	12	ADO71658	Ado71658 Nucleotid
C 392	18	0.5	1887	10	ABZ67293	Abz67293 Human sec	C 465	18	0.5	3985	14	ABE31948	Abi31948 Macrophag
C 393	18	0.5	1887	10	ABZ67293	Abz67293 Human sec	C 466	18	0.5	3985	13	ADO39079	Ado39079 Human SNP
C 394	18	0.5	1936	14	ABE3136	Abi3136 Soybean v	C 467	18	0.5	3992	5	AAO79666	Aao79666 DNA encod
C 395	18	0.5	1954	4	AAK73118	Aak73118 Human imm	C 468	18	0.5	3992	6	AAV94301	Avv94301 Breast ca
C 396	18	0.5	1954	4	AAK73118	Aak73118 Human imm	C 469	18	0.5	3992	6	ABK48105	Abk48105 Human mac
C 397	18	0.5	1954	4	AAK73112	Aak73112 Human imm	C 470	18	0.5	3992	8	ACA89951	Acc89951 Gene dif
C 398	18	0.5	1954	4	AAK73112	Aak73112 Human imm	C 471	18	0.5	3992	11	ADP61619	Adp61619 Leukemia
C 399	18	0.5	2000	6	ABK87589	Abk87589 Human imm	C 472	18	0.5	3992	11	ADM29259	Adm29259 Human nov
C 400	18	0.5	2033	13	ADP60774	Adp60774 Plant ful	C 473	18	0.5	3992	13	ADR83438	Adr83438 Human c-f
C 401	18	0.5	2070	2	AAO82873	Aao82873 Human ST3	C 474	18	0.5	3993	13	ADQ39080	Adq39080 Human SNP
C 402	18	0.5	2106	8	ACA32918	Acca32918 Prokaryot	C 475	18	0.5	4008	6	ABZ35433	Abz35433 Human gen
C 403	18	0.5	2119	4	AAH15612	Aah15612 Human cDN	C 476	18	0.5	4240	12	ADQ23697	Adq23697 Human sof
C 404	18	0.5	2184	4	AAH53734	Aah53734 S. epider	C 477	18	0.5	4298	6	ABK34853	Abk34853 Human cDN
C 405	18	0.5	2184	13	ADR06752	Adr06752 Full leng	C 478	18	0.5	4418	8	ABZ74665	Abz74665 Secreted
C 406	18	0.5	2262	13	ADR85692	Adr85692 Aspergill	C 479	18	0.5	4418	10	ABZ68187	Abz68187 Human bec
C 407	18	0.5	2238	2	AAO04774	Aao04774 Recombina	C 480	18	0.5	4528	6	ABA93713	Abag93713 Human cel
C 408	18	0.5	2241	2	AAK13993	Aak13993 H. pylori	C 481	18	0.5	4614	3	AAQ71390	Aaq71390 Yeast 4.7
C 409	18	0.5	2342	8	ABT42828	Abt42828 Human neu	C 482	18	0.5	4614	3	AAQ95422	Aaq95422 S. cerevi
C 410	18	0.5	2370	13	ADR85105	Adr85105 Aspergill	C 483	18	0.5	4614	13	ADS46655	Adsg46655 Bacteriat
C 411	18	0.5	2469	4	ABL24070	Abi24070 Drosophil	C 484	18	0.5	4618	12	ADN97094	Adn97094 Cnra60RF
C 412	18	0.5	2513	10	ADD14768	Add14768 Human arc	C 485	18	0.5	4713	8	ABZ74667	Abz74667 Secreted
C 413	18	0.5	2517	13	ABD33000	Abd33000 Human can	C 486	18	0.5	4713	10	ABZ68189	Abz68189 Human bec
C 414	18	0.5	2600	13	ABX67360	Abx67360 Plant ful	C 487	18	0.5	4863	8	ADA71084	Ada71084 Rice gene
C 415	18	0.5	2621	3	AAV1894	Aav1894 B. cereus	C 488	18	0.5	5218	4	ABL17253	Abi17253 Drosophil
C 416	18	0.5	2651	2	AAQ74268	Aaq74268 SVEGF-RI	C 489	18	0.5	5218	6	ABL33267	Abi33267 Human imm
C 417	18	0.5	2651	8	ACC86724	Acc86724 Human sol	C 490	18	0.5	5274	4	ABL28894	Abi28894 Drosophil
C 418	18	0.5	2651	10	ADP23254	Adp23254 Human sVE	C 491	18	0.5	5336	6	ABL34098	Abi34098 Human imm
C 419	18	0.5	2651	13	ADSI1642	Adsi1642 Nucleotid	C 492	18	0.5	5394	6	ABQ71024	Abq71024 Listeria
C 420	18	0.5	2685	2	AAQ67360	Aaq67360 S. cerevi	C 493	18	0.5	5497	4	ABL04596	Abi04596 Drosophil
C 421	18	0.5	2685	4	AAQ54029	Aaq54029 Floculat	C 494	18	0.5	5613	13	ADR32196	Adr32196 Yeast FLO
C 422	18	0.5	2714	4	AAAC89167	Aaac89167 Rat p-HYD	C 495	18	0.5	5664	12	ADP87474	Adp87474 S. cerevi
C 423	18	0.5	2714	14	ADM11281	Adm11281 Rat cance	C 496	18	0.5	5669	6	ABK31998	Abk31998 Human DNA
C 424	18	0.5	2718	4	ABL22293	Abi22293 Drosophil	C 497	18	0.5	5669	6	ABL92327	Abi92327 Chemical
C 425	18	0.5	2728	13	ABD33002	Abd33002 Human can	C 498	18	0.5	5669	8	ADA20381	Ada20381 Prostata
C 426	18	0.5	2754	2	AAV758505	Aav758505 H218 cDNA	C 499	18	0.5	5669	8	ADA84188	Ada84188 Human ren
C 427	18	0.5	2754	2	AAV84039	Aav84039 DNA encod	C 500	18	0.5	6112	6	ABL32472	Abi32472 Human imm
C 428	18	0.5	2754	2	AAV84039	Aav84039 DNA encod	C 501	18	0.5	6112	6	AAAD28374	Aaad28374 Human che
C 429	18	0.5	2754	8	ABO81032	Abob81032 Rat Endot	C 502	18	0.5	6290	6	ABL33047	Abi33047 Human imm
C 430	18	0.5	2754	9	ACA862453	Acca862453 Human eph	C 503	18	0.5	6390	5	AAO79665	Aao79665 DNA encod
C 431	18	0.5	2764	2	AAV52373	Aav52373 Streptoco	C 504	18	0.5	6390	5	AAO84936	Aao84936 DNA encod
C 432	18	0.5	2794	6	AAV43935	Aav43935 Human pho	C 505	18	0.5	6409	4	AAO46495	Aao46495 Tumour su
C 433	18	0.5	2844	1	AAV71250	Aav71250 Sequence	C 506	18	0.5	6568	3	AAO59383	Aao59383 DNA encod
C 434	18	0.5	2911	10	ADG32692	Adg32692 Human DNA	C 507	18	0.5	6568	6	ABN95037	Abn95037 Gene #153
C 435	18	0.5	2919	14	ADV42426	Adv42426 Human pcy	C 508	18	0.5	6568	14	ADX05782	Adx05782 Cyclin-de
C 436	18	0.5	2920	11	ADM29261	Adm29261 Human nov	C 509	18	0.5	6568	14	ADY14991	Ady14991 DNA encod
C 437	18	0.5	2920	11	ADM29261	Adm29261 Human nov	C 510	18	0.5	6662	11	ACN90392	Acn90392 Breast ca
C 438	18	0.5	3038	4	AAK73101	Aak73101 Human imm	C 511	18	0.5	6662	11	ADZ49341	Adz49341 Inebilin B
C 439	18	0.5	3038	4	AAK87570	Aak87570 Human imm	C 512	18	0.5	6758	13	ADU50726	Adu50726 Aspergill
C 440	18	0.5	3038	8	ABZ74681	Abz74681 Secreted	C 513	18	0.5	7000	6	ABZ35229	Abz35229 Human gen
C 441	18	0.5	3102	10	ABZ68203	Abz68203 Human sec	C 514	18	0.5	7016	10	ADH75540	Adh75540 Prostata
C 442	18	0.5	3102	4	ABL15358	Abi15358 Drosophil	C 515	18	0.5	7096	3	AAO75629	Aao75629 Nucleotid
C 443	18	0.5	3152	4	AAH54112	Aah54112 S. epider	C 516	18	0.5	7096	6	AAO39241	Aao39241 PD10-SPIC
C 444	18	0.5	3152	4	ABL28895	Abi28895 Drosophil	C 517	18	0.5	7134	6	ABL32482	Abi32482 Human imm
C 445	18	0.5	3152	4	AAH54804	Aah54804 S. epider	C 518	18	0.5	7477	11	ADOS68219	Ados68219 Hepatic
C 446	18	0.5	3250	6	ABV75523	Abv75523 Programme	C 519	18	0.5	7664	6	ABL49384	Abi49384 Human pool
C 447	18	0.5	3261	5	ABV22603	Abv22603 Human pro	C 520	18	0.5	7781	6	ABL33168	Abi33168 Human imm
C 448	18	0.5	3261	5	ABV21408	Abv21408 Human pro	C 521	18	0.5	7812	2	AAK12962	Aak12962 Enterococ
C 449	18	0.5	3261	5	ABV27226	Abv27226 Human pro	C 522	18	0.5	7812	2	AAK12962	Aak12962 Enterococ
C 450	18	0.5	3261	5	ABV28425	Abv28425 Human pro	C 523	18	0.5	8056	8	ABZ10246	Abz10246 Haematopo
C 451	18	0.5	3262	11	ACN91415	Acn91415 Breast ca	C 524	18	0.5	8130	4	ABL22932	Abi22932 Drosophil
C 452	18	0.5	3297	13	ADU08112	Adu08112 S. cerevis	C 525	18	0.5	8370	13	ADH84518	Adh84518 Aspergill
C 453	18	0.5	3297	13	ADU08112	Adu08112 Baker's y	C 526	18	0.5	8687	4	ABL17252	Abi17252 Drosophil
C 454	18	0.5	3363	2	AAK61475	Aak61475 B. burgdo	C 527	18	0.5	8923	4	AAK87591	Aak87591 Human imm
C 455	18	0.5	3441	2	AAK61475	Aak61475 B. burgdo	C 528	18	0.5	8923	8	ABZ74669	Abz74669 Secreted
C 456	18	0.5	3445	13	ADX14414	Adx14414 Plant ful	C 529	18	0.5	8923	10	ABZ68191	Abz68191 Human sec
C 457	18	0.5	3463	2	AAK76755	Aak76755 Candida R	C 530	18	0.5	9100	10	ADP50313	Adp50313 Human prk

531	18	0.5	9524	6	ABK3993	Abk3993 Human che	604	18	0.5	4938	14	AD212650	Ad212650 Murine ca
532	18	0.5	9524	6	ABL32838	Abi12838 Human imm	605	18	0.5	52479	9	ADA02795	Ada02795 Mouse Thf
533	18	0.5	11370	4	ABL10066	Abi10066 Drosophill	606	18	0.5	52479	10	ADB72533	ADB72533 Mouse Thf
534	18	0.5	11872	4	AAK94027	Aak94027 Human imm	607	18	0.5	52479	10	ADC85275	ADC85275 Mouse Thf
535	18	0.5	11872	4	AAK66893	Aak66893 Human imm	608	18	0.5	52479	12	ADM74390	ADM74390 Murine ca
536	18	0.5	12660	4	ABLO8874	Abi08874 Drosophill	609	18	0.5	54169	11	ACN44838	ACN44838 Human gen
537	18	0.5	13076	13	ADS89651	Ad889651 Oligonuc1	610	18	0.5	54929	11	ACN44396	ACN44396 Mouse gen
538	18	0.5	13216	4	AAK73092	Aak73092 Human imm	611	18	0.5	55050	6	AB075680	Ab075680 Human SBR
539	18	0.5	13216	4	AAK87561	Aak87561 Human imm	612	18	0.5	55829	13	ABD33512	ABD33512 Human can
540	18	0.5	13216	8	ABZ74661	Abz74661 Secreted	613	18	0.5	56290	4	ABU22618	AbU22618 Drosophill
541	18	0.5	13216	10	ABZ68183	Abz68183 Human sec	614	18	0.5	58262	14	AD213229	AD213229 Human can
542	18	0.5	13249	6	ABU32117	AbU32117 Human imm	615	18	0.5	59846	14	AD213300	AD213300 Murine ca
543	18	0.5	13249	6	ABK31177	Abk31177 Signal tr	616	18	0.5	60935	13	ACN37224	ACN37224 Human per
544	18	0.5	13249	6	ABL70132	AbL70132 Chemicall	617	18	0.5	61020	4	AMS46788	AmS46788 Tumour su
545	18	0.5	14304	6	ABK69840	Abk69840 Human sec	618	18	0.5	70215	11	ACN43992	ACN43992 Mouse gen
546	18	0.5	14617	5	ABAI9132	Abai9132 Human sec	619	18	0.5	73100	14	AD242280	Ad242280 Human end
547	18	0.5	14627	5	ABAI9130	Abai9130 Human ner	620	18	0.5	76644	12	ADQ97602	AdQ97602 Mouse can
548	18	0.5	15400	12	ADH23303	AdH23303 Novel hum	621	18	0.5	78056	8	ABV99701	AbV99701 Bovine BS
549	18	0.5	15400	13	ADT91775	Adt91775 Human kin	622	18	0.5	78082	12	ADO97968	AdO97968 Human can
550	18	0.5	15765	5	ABAI8276	Abai8276 Human ner	623	18	0.5	78925	3	ACB89888	AcB89888 Human FN
551	18	0.5	15765	5	ABAI9009	Abai9009 Human ner	624	18	0.5	86804	12	ADQ97700	AdQ97700 Mouse can
552	18	0.5	15765	5	ABAI7911	Abai7911 Human ner	625	18	0.5	87878	9	ADA02576	Ada02576 Human PKB
553	18	0.5	15765	5	ABAI8250	Abai8250 Human ner	626	18	0.5	87878	10	ADB72314	ADB72314 Human PKB
554	18	0.5	15941	6	AAD39443	Aad39443 Soybean E	627	18	0.5	87878	10	ADB95824	ADb95824 Human PKB
555	18	0.5	15941	6	AAD39447	Aad39447 Soybean E	628	18	0.5	88398	13	ADT55150	Adt55150 Nucleotid
556	18	0.5	16720	6	ABU32414	AbU32414 Human imm	629	18	0.5	94781	13	ABD32711	ABD32711 Mouse can
557	18	0.5	16720	6	ABU61118	Abu61118 Human gen	630	18	0.5	96594	10	ADE95974	AdE95974 Human SYK
558	18	0.5	18154	6	ABU32255	AbU32255 Human imm	631	18	0.5	96595	9	ADA02726	Ada02726 Human SYK
559	18	0.5	20303	14	ACL64720	AcL64720 M. xanthu	632	18	0.5	96595	10	ADB72464	ADB72464 Human RAS
560	18	0.5	20391	8	AAK87545	Aak87545 Human sec	633	18	0.5	96596	9	ADA02564	Ada02564 Human RAS
561	18	0.5	20391	8	ABZ74668	Abz74668 Secreted	634	18	0.5	96596	10	ADB72302	ADB72302 Human RAS
562	18	0.5	20391	8	ABZ68190	Abz68190 Human sec	635	18	0.5	96596	10	ADB95812	ADB95812 Human RAS
563	18	0.5	24218	4	AAK87556	Aak87556 Human imm	636	18	0.5	106398	13	ABD33432	ABD33432 Human can
564	18	0.5	24218	4	AAK73088	Aak73088 Human imm	637	18	0.5	106398	13	ADP67034	ADp67034 Human can
565	18	0.5	24218	4	AAK71828	AaK71828 Human imm	638	18	0.5	107310	14	ADZ13456	ADz13456 Human can
566	18	0.5	24218	8	AAI62935	Aai62935 Human gen	639	18	0.5	109306	6	ABK94411	AbK94411 DNA encod
567	18	0.5	24218	8	ABZ74664	Abz74664 Secreted	640	18	0.5	109306	12	ADL08112	AdL08112 Human gen
568	18	0.5	24218	10	ABZ68186	Abz68186 Human sec	641	18	0.5	110000	2	AAK20248_00	AaK20248 Borrelia
569	18	0.5	25235	4	AAH45310	Aah45310 Human SBR	642	18	0.5	110000	6	ABH90521_04	AbH90521_04 Continuation (5 of
570	18	0.5	26000	9	ADU58250	Aad58250 Human PK	643	18	0.5	110000	6	ABG69245_17	AbG69245_17 Continuation (18 o
571	18	0.5	28126	14	AD215682	Ad215682 Murine ca	644	18	0.5	110000	9	ACH03408_0	AcH03408 Genomic D
572	18	0.5	28397	12	ADO59407	AdO59407 Human can	645	18	0.5	110000	9	ADB12064_11	AdB12064_11 Continuation (12 o
573	18	0.5	30724	8	ABZ74670	Abz74670 Secreted	646	18	0.5	110000	10	ADF77343_06	AdF77343_06 Continuation (17 of
574	18	0.5	30724	10	ABZ68192	Abz68192 Human sec	647	18	0.5	110000	10	ABSS6454_03	ABsS6454_03 Continuation (4 of
575	18	0.5	31412	6	ABQ75595	Abq75595 Sheep FRP	648	18	0.5	110000	11	ADM27081_05	AdM27081_05 Continuation (6 of
576	18	0.5	31412	6	ABV99702	Abv99702 Sheep SBR	649	18	0.5	110000	12	ADN46845_11	ADn46845_11 Continuation (12 o
577	18	0.5	31702	8	ABO67190	AbO67190 Listeria	650	18	0.5	110000	12	ADN47591_08	ADn47591_08 Continuation (9 of
578	18	0.5	32073	13	ABD32944	AbD32944 Mouse can	651	18	0.5	110000	12	ADN46123_11	ADn46123_11 Continuation (12 o
579	18	0.5	32190	4	AAI62927	Aai62927 Human gen	652	18	0.5	110000	12	ADN46123_11	ADn46123_11 Continuation (12 o
580	18	0.5	32349	4	AAI62932	Aai62932 Human gen	653	18	0.5	110000	12	ADN47209_08	ADn47209_08 Continuation (9 of
581	18	0.5	35100	2	AAV20441	Aav20441 Human c-f	654	18	0.5	110000	12	ADN47209_09	ADn47209_09 Continuation (10 o
582	18	0.5	35465	4	AAFS4723	AafS4723 Nucleotid	655	18	0.5	110000	12	ADN46464_11	ADn46464_11 Continuation (12 o
583	18	0.5	35465	8	ABT17380	Abt17380 Human IG	656	18	0.5	110000	12	ADN47960_08	ADn47960_08 Continuation (9 of
584	18	0.5	36991	8	ABT17382	Abt17382 Human IG	657	18	0.5	110000	12	ADN47960_09	ADn47960_09 Continuation (10 o
585	18	0.5	38258	6	AA898633	AA898633 DNA encod	658	18	0.5	110000	14	ADZ13631_2	ADz13631_2 Continuation (3 of
586	18	0.5	39068	4	AAK71820	Aak71820 Human imm	659	18	0.5	110000	14	ADZ13620_2	ADz13620_2 Continuation (3 of
587	18	0.5	39068	4	AAK85294	Aak85294 Human imm	660	18	0.5	110000	14	AEA61160_2	AEa61160_2 Continuation (3 of
588	18	0.5	39068	4	AAK73078	Aak73078 Human imm	661	18	0.5	110000	14	AEA61120_0	AEa61120_0 Continuation (5 of
589	18	0.5	39068	4	AAK87544	Aak87544 Human imm	662	18	0.5	110000	14	AEA39175_04	AEa39175_04 Continuation (6 of
590	18	0.5	39068	4	AAK87544	Aak87544 Human imm	663	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
591	18	0.5	39068	10	ABZ74662	Abz74662 Secreted	664	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
592	18	0.5	39110	4	AAK73087	Aak73087 Human sec	665	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
593	18	0.5	39110	4	AAK73087	Aak73087 Human imm	666	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
594	18	0.5	39110	4	AAK71825	Aak71825 Human imm	667	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
595	18	0.5	39110	4	AAK87555	Aak87555 Human imm	668	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
596	18	0.5	39110	10	ABZ74663	Abz74663 Secreted	669	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
597	18	0.5	39110	10	ABZ68185	Abz68185 Human sec	670	18	0.5	110000	14	AEA39175_05	AEa39175_05 Continuation (6 of
598	18	0.5	45300	4	AAK62633	AaK62633 Human CD3	671	18	0.5	115829	6	ABU34175	AbU34175 Human imm
599	18	0.5	45300	4	AAK87547	Aak87547 Human imm	672	18	0.5	115829	12	ABD33448	ABD33448 Human can
600	18	0.5	45300	8	AAK73079	Aak73079 Human imm	673	18	0.5	124987	13	ADP03055	ADp03055 Human hou
601	18	0.5	45300	8	ABZ74666	Abz74666 Secreted	674	18	0.5	124990	13	ADS88553	AdS88553 Human hou
602	18	0.5	46374	12	ABZ68188	Abz68188 Human sec	675	18	0.5	134525	2	AAU04525	AaU04525 Total bas
603	18	0.5	48469	11	ACN44802	Acn44802 Human gen	676	18	0.5	145068	13	ABD33090	ABD33090 Murine ca

C 677	18	0.5	146547	8	ABZ80817	Abz80817 Human pho	750	17	0.5	268	4	AA147932	AA147932 Probe #16
C 678	18	0.5	147300	12	ADP45593	ADP45593 Human Rho	751	17	0.5	268	4	ABA49797	ABA49797 Human bre
C 679	18	0.5	147700	14	ADX98570	Adx98570 Human gua	752	17	0.5	268	4	AAK41870	AAK41870 Human hon
C 680	18	0.5	150351	13	ABD33360	Abd333360 Murine ca	753	17	0.5	268	4	ABS41473	ABS41473 Human liv
C 681	18	0.5	151826	3	AAE22291	AAE22291 BAC conta	754	17	0.5	268	4	ABS41473	ABS41473 Human liv
C 682	18	0.5	155074	6	ABN85735	Abn85735 Human gen	755	17	0.5	272	6	ABN21569	ABN21569 Human gen
C 683	18	0.5	158091	12	ADL08119	Adl08119 Human gen	756	17	0.5	275	10	ABX81753	ABX81753 Corn ear-
C 684	18	0.5	158091	14	ABE45166	ABE45166 Human FAT	757	17	0.5	285	5	ABV59673	ABV59673 Human pro
C 685	18	0.5	157537	6	ABK83571	Abk83571 Human CDN	758	17	0.5	287	5	ADL44105	ADL44105 Human ova
C 686	18	0.5	157537	10	ADL13596	ADL13596 Osteocarth	759	17	0.5	291	11	ACL30508	ACL30508 Rice abio
C 687	18	0.5	175737	12	ADQ18934	Adq18934 Human sof	760	17	0.5	291	14	ACL57908	ACL57908 Human col
C 688	18	0.5	178024	12	ADQ97721	Adq97721 Human can	761	17	0.5	300	2	AAZ14424	AAZ14424 Human gen
C 689	18	0.5	180385	10	ADL13931	Adl13931 Osteocarth	762	17	0.5	300	11	ACL26400	ACL26400 Rice abio
C 690	18	0.5	185035	8	ABT10147	ABT10147 Human bre	763	17	0.5	301	5	ABV19728	ABV19728 Human pro
C 691	18	0.5	185035	8	ACA64951	ACA64951 Human PEN	764	17	0.5	306	6	ABN79228	ABN79228 Human ORF
C 692	18	0.5	185035	12	ADQ20284	Adq20284 Human sof	765	17	0.5	315	6	ABN21500	ABN21500 Human ORF
C 693	18	0.5	194534	12	ADQ97481	Adq97481 Human can	766	17	0.5	316	6	AAE79669	AAE79669 Vitulence
C 694	18	0.5	198849	14	ADZ13007	Adz13007 Human can	767	17	0.5	316	6	ABQ83546	ABQ83546 Actinobac
C 695	18	0.5	200000	12	ADQ47192	Adq47192 DNA seque	768	17	0.5	318	5	ABV49495	ABV49495 Human pro
C 696	18	0.5	207542	14	ABE33385	ABE33385 Human gen	769	17	0.5	322	4	AAI35250	AAI35250 Human mus
C 697	18	0.5	207557	14	ABE33371	ABE33371 Human gen	770	17	0.5	322	8	ABX58238	ABX58238 CDNA enco
C 698	18	0.5	210204	12	ADQ18927	Adq18927 Human bof	771	17	0.5	322	12	ADJ27965	ADJ27965 Human mus
C 699	18	0.5	225734	12	ADQ59377	Adq59377 Human can	772	17	0.5	323	3	AAA43370	AAA43370 Rat secro
C 700	18	0.5	225734	14	ADZ1617	Adz1617 Murine ca	773	17	0.5	323	3	AAA43384	AAA43384 Rat secro
C 701	18	0.5	237961	6	ABQ80552	ABQ80552 Human Can	774	17	0.5	323	3	AAA43358	AAA43358 Rat secro
C 702	18	0.5	243335	13	ABE44735	ABE44735 L. pneumo	775	17	0.5	323	3	AAA43378	AAA43378 Rat secro
C 703	18	0.5	245531	13	ABD33022	ABD33022 Human can	776	17	0.5	323	3	AAA43389	AAA43389 Rat secro
C 704	18	0.5	247682	12	ADL08109	ADL08109 Human gen	777	17	0.5	323	3	AAA43349	AAA43349 Rat secro
C 705	18	0.5	256294	13	ABD33020	ABD33020 Mouse can	778	17	0.5	323	3	AAA43354	AAA43354 Rat secro
C 706	18	0.5	262090	12	ADQ59207	Adq59207 MSI-H car	779	17	0.5	323	4	AA849350	AA849350 Staphyloc
C 707	18	0.5	263853	14	ABE339171	ABE339171 L. pneumo	780	17	0.5	323	4	AA850705	AA850705 Staphyloc
C 708	18	0.5	272022	12	ADQ97126	Adq97126 Human can	781	17	0.5	323	8	ACA16627	ACA16627 Prokaryot
C 709	18	0.5	276820	11	ADP75188	ADP75188 Human ADA	782	17	0.5	323	8	ACA17976	ACA17976 Prokaryot
C 710	18	0.5	295844	14	ABE335721	ABE335721 L. pneumo	783	17	0.5	324	8	ABX55032	ABX55032 Bovine BS
C 711	18	0.5	298667	14	ABE335173	ABE335173 L. pneumo	784	17	0.5	325	11	ADJ30867	ADJ30867 Human CDN
C 712	18	0.5	299598	12	ADQ59380	Adq59380 Human can	785	17	0.5	325	13	ADU13769	ADU13769 Solid tum
C 713	18	0.5	302603	11	ADP75187	ADP75187 Human End	786	17	0.5	325	13	AD882934	AD882934 Human lym
C 714	17	0.5	19	14	AAA46231	AAA46231 Primer IP	787	17	0.5	325	14	ABE53355	ABE53355 Human pro
C 715	17	0.5	17	14	ADX86859	ADX86859 XIAP targ	788	17	0.5	334	6	ABN94010	ABN94010 Gene #508
C 716	17	0.5	19	14	ADX86392	ADX86392 XIAP targ	789	17	0.5	337	4	AAI25559	AAI25559 Probe #15
C 717	17	0.5	30	12	ADP45758	ADP45758 PCR prime	790	17	0.5	337	4	ABA71764	ABA71764 Human foe
C 718	17	0.5	30	14	ADX98816	Adx98816 PCR prime	791	17	0.5	337	4	AAI52097	AAI52097 Probe #20
C 719	17	0.5	41	6	ABL49873	ABL49873 Human CHD	792	17	0.5	337	4	ABA37850	ABA37850 Probe #16
C 720	17	0.5	48	3	AAZ87022	AAZ87022 RBP-7 bta	793	17	0.5	337	4	AAK46190	AAK46190 Human bon
C 721	17	0.5	50	6	ABZ03718	Abz03718 Human leu	794	17	0.5	337	4	AAK20131	AAK20131 Human bra
C 722	17	0.5	50	12	ADP10090	ADP10090 50-mer OL	795	17	0.5	337	4	ABE45909	ABE45909 Human liv
C 723	17	0.5	51	12	ADQ27378	ADQ27378 DNA encod	796	17	0.5	337	6	ABE20501	ABE20501 Human gen
C 724	17	0.5	60	6	ABN44357	ABN44357 Human spl	797	17	0.5	339	12	ADH13000	ADH13000 Franc18el
C 725	17	0.5	60	6	ABN49549	ABn49549 Human spl	798	17	0.5	341	6	ABN18493	ABn18493 Human ORF
C 726	17	0.5	60	6	ABN38571	Abn38571 Human spl	799	17	0.5	346	12	ADL87958	ADL87958 DNA up-re
C 727	17	0.5	65	6	ABE26411	ABe26411 Candida e	800	17	0.5	346	12	ADL87958	ADL87958 DNA up-re
C 728	17	0.5	65	6	ABN30749	Abn30749 Rat splic	801	17	0.5	348	5	ADT74147	ADT74147 Human ova
C 729	17	0.5	121	11	ADZ42654	ADZ42654 Human gen	802	17	0.5	348	5	ADT67769	ADT67769 Human ova
C 730	17	0.5	136	3	AAE10948	AAE10948 Human sec	803	17	0.5	349	3	AAE57780	AAE57780 AArchidon
C 731	17	0.5	139	12	ADQ13254	ADQ13254 SNP targ	804	17	0.5	349	3	AAE57781	AAE57781 AArchidon
C 732	17	0.5	150	3	AAE15501	AAE15501 Human sec	805	17	0.5	355	2	AAE19541	AAE19541 Human gen
C 733	17	0.5	160	4	AAI49682	AAI49682 Probe #18	806	17	0.5	357	6	ABN21456	ABN21456 Human ORF
C 734	17	0.5	160	4	ABE43284	ABe43284 Human liv	807	17	0.5	362	13	ADX32022	ADX32022 Plant ful
C 735	17	0.5	163	2	AAH86503	AAh86503 Human bin	808	17	0.5	363	2	AAE90012	AAE90012 Heavy cha
C 736	17	0.5	184	12	ADQ34461	ADQ34461 Human SLI	809	17	0.5	363	8	ABE219123	ABE219123 Group IIT
C 737	17	0.5	184	12	ADQ34456	ADQ34456 Human SLI	810	17	0.5	363	10	ADDA49856	ADDA49856 Human lun
C 738	17	0.5	184	12	ADQ34962	ADQ34962 Human KCh	811	17	0.5	371	4	AAK72391	AAK72391 Human lmm
C 739	17	0.5	190	4	AAE49885	AAe49885 Staphyloc	812	17	0.5	382	14	ADV65849	ADV65849 S. manson
C 740	17	0.5	190	8	ACA177130	ACA177130 Prokaryot	813	17	0.5	386	4	AAI36661	AAI36661 Probe #52
C 741	17	0.5	192	3	AAA41608	AAA41608 Human sec	814	17	0.5	386	4	ABE330298	ABE330298 Human liv
C 742	17	0.5	193	14	AAE15582	AAE15582 Human col	815	17	0.5	389	4	AAH36551	AAH36551 Human col
C 743	17	0.5	222	10	ADFO0931	ADFO0931 Bacterial	816	17	0.5	390	14	ADMO6538	ADMO6538 Human gen
C 744	17	0.5	237	6	ABE182449	ABe182449 Human ova	817	17	0.5	400	5	ABV15452	ABV15452 Human pro
C 745	17	0.5	260	6	AAI10194	AAI10194 Rat liver	818	17	0.5	404	9	ACH49561	ACH49561 Human leu
C 746	17	0.5	260	6	ABN61428	ABn61428 Human can	819	17	0.5	411	4	AAI191179	AAI191179 Human pol
C 747	17	0.5	267	11	ACL30358	ACL30358 Rice abio	820	17	0.5	413	9	ACH18324	ACH18324 Human adu
C 748	17	0.5	268	4	AAI22638	AAI22638 Probe #12	821	17	0.5	414	5	ADL39384	ADL39384 Human ova
C 749	17	0.5	268	4	ABA67715	ABa67715 Human foe	822	17	0.5	416	4	AAI87910	AAI87910 Human pol



C 823	17	0.5	421	4	AA110104	Ad110104	Probe #37	C 896	17	0.5	487	5	AD175478	Ad175478	Human ova
C 824	17	0.5	421	4	ABA51733	Ab51733	Human foe	C 897	17	0.5	487	5	AD169131	Ad169131	Human ova
C 825	17	0.5	421	4	AA131350	Ad131350	Probe #36	C 898	17	0.5	489	10	ADD32608	Add32608	Human mit
C 826	17	0.5	421	4	ABA21566	Ab21566	Probe #32	C 899	17	0.5	492	13	ACN51874	Acn51874	Cotton an
C 827	17	0.5	421	4	AAK25480	Aak25480	Human bon	C 900	17	0.5	493	5	ADL42259	Adl42259	Human ova
C 828	17	0.5	421	4	AAK00043	Aak00043	Human bra	C 901	17	0.5	494	10	ADBE1808	Adeb1808	Arabidops
C 829	17	0.5	421	4	AB825047	Ab825047	Human liv	C 902	17	0.5	497	4	AAH13080	Aah13080	Human CDN
C 830	17	0.5	421	4	AA100045	Ad100045	Probe #36	C 903	17	0.5	501	12	ACH73415	Ach73415	Human gen
C 831	17	0.5	421	6	AB800046	Ab800046	Human gen	C 904	17	0.5	501	13	ACN61671	Acn61671	Cotton gy
C 832	17	0.5	422	10	ACD96340	Adc96340	Human col	C 905	17	0.5	502	4	AAK11861	Aak11861	Human bra
C 833	17	0.5	426	6	ABN66455	Abn66455	Streptoco	C 906	17	0.5	503	12	ACH67625	Ach67625	Human gen
C 834	17	0.5	427	13	ADR12306	Adr12306	Human int	C 907	17	0.5	507	8	ABE25183	Abe25183	Aspergill
C 835	17	0.5	429	13	ADV85075	Adv85075	Streptoco	C 908	17	0.5	507	10	ADBE1482	Adeb1482	Arabidops
C 836	17	0.5	431	4	AA183653	Ad183653	Human pol	C 909	17	0.5	514	12	ACH74082	Ach74082	Human gen
C 837	17	0.5	432	4	AA119400	Ad119400	Probe #93	C 910	17	0.5	520	13	ACF86022	Acf86022	Human SIR
C 838	17	0.5	432	4	ABA64412	Ab64412	Human foe	C 911	17	0.5	522	14	ACLS7968	Acl57968	Human col
C 839	17	0.5	432	4	AA144588	Ad144588	Probe #13	C 912	17	0.5	523	4	ABL17905	Ab117905	Drosophi
C 840	17	0.5	432	4	ABA46550	Ab46550	Human bre	C 913	17	0.5	524	10	ABX57600	Abx57600	Arabidops
C 841	17	0.5	432	4	ABA31553	Ab31553	Probe #10	C 914	17	0.5	525	6	ABO57413	Ab057413	Human col
C 842	17	0.5	432	4	AAK38600	Aak38600	Human bon	C 915	17	0.5	527	5	ABO57942	Ab057942	Human pro
C 843	17	0.5	432	4	AAK12871	Aak12871	Human bra	C 916	17	0.5	533	5	ABV50889	Abv50889	Human pro
C 844	17	0.5	432	4	AB838163	Ab838163	Human 11v	C 917	17	0.5	535	6	ABT04093	Abt04093	Human ova
C 845	17	0.5	432	5	AA105125	Ad105125	Probe #51	C 918	17	0.5	544	13	AD055873	Ad055873	Novel can
C 846	17	0.5	432	6	AB812666	Ab812666	Human gen	C 919	17	0.5	545	12	ACH76165	Ach76165	Human gen
C 847	17	0.5	433	12	ADP72208	Adp72208	Renal tox	C 920	17	0.5	546	13	ACN48501	Acn48501	Cotton pr
C 848	17	0.5	438	4	AA105689	Ad105689	Human rep	C 921	17	0.5	548	5	ADL63068	Adl63068	Human ova
C 849	17	0.5	439	4	AAK58152	Aak58152	Human imm	C 922	17	0.5	548	5	ADL40714	Adl40714	Human ova
C 850	17	0.5	442	5	ABV45285	Abv45285	Human pro	C 923	17	0.5	552	5	ADL40202	Adl40202	Human ova
C 851	17	0.5	442	5	ABV36244	Abv36244	Human pro	C 924	17	0.5	554	4	AAH10428	Aah10428	Human CDN
C 852	17	0.5	442	13	ACF82958	Acf82958	Human SIR	C 925	17	0.5	555	5	AD174965	Ad174965	Human ova
C 853	17	0.5	444	5	ADL36991	Adl36991	Human ova	C 926	17	0.5	555	5	AD168601	Ad168601	Human ova
C 854	17	0.5	444	5	AD171840	Ad171840	Human ova	C 927	17	0.5	559	5	ADL43375	Adl43375	Human ova
C 855	17	0.5	447	4	AA113410	Ad113410	Probe #33	C 928	17	0.5	561	5	AA571903	Aa571903	DNA encod
C 856	17	0.5	447	4	ABA55107	Ab55107	Human foe	C 929	17	0.5	561	10	ADD34185	Add34185	Human CDN
C 857	17	0.5	447	4	AA134765	Ad134765	Probe #34	C 930	17	0.5	562	10	ADBE1808	Adeb1808	Human CDN
C 858	17	0.5	447	4	ABA44652	Ab44652	Human bon	C 931	17	0.5	568	13	ACN48146	Acn48146	Cotton pr
C 859	17	0.5	447	4	AAK248821	Aak248821	Human bon	C 932	17	0.5	571	10	ADBE6113	Adbe6113	Human bre
C 860	17	0.5	447	6	AB828432	Ab828432	Human 11v	C 933	17	0.5	571	10	ADBE6113	Adbe6113	Human bre
C 861	17	0.5	447	6	AB803352	Ab803352	Human gen	C 934	17	0.5	577	12	ACH69161	Ach69161	Human gen
C 862	17	0.5	450	5	AAK68188	Aak68188	Human 11v	C 935	17	0.5	578	13	ACN62634	Acn62634	Cotton de
C 863	17	0.5	450	6	ABK38099	Abk38099	Human 11v	C 936	17	0.5	581	6	ABO31274	Ab031274	Oligonuc
C 864	17	0.5	450	8	ACA10428	Ac10428	CDNA enc	C 937	17	0.5	581	6	ABO31275	Ab031275	Oligonuc
C 865	17	0.5	450	8	ABX99379	Abx99379	Human 11v	C 938	17	0.5	581	13	ACN49342	Acn49342	Cotton pr
C 866	17	0.5	450	10	ADB6754	Adb6754	Lung can	C 939	17	0.5	582	4	AA122914	Aal122914	Human bre
C 867	17	0.5	450	10	ADG79128	Adg79128	Toxicity-	C 940	17	0.5	585	5	ABV51371	Abv51371	Human pro
C 868	17	0.5	450	12	ADH45625	Adh45625	Calcineur	C 941	17	0.5	587	6	ABK53364	Abk53364	Human eov
C 869	17	0.5	450	12	ADE72162	Ade72162	Human 11v	C 942	17	0.5	588	5	ADL45469	Adl45469	Human ova
C 870	17	0.5	450	13	ADJ19544	Adj19544	Human 11v	C 943	17	0.5	588	10	ACA54561	Ac54561	Human NF-
C 871	17	0.5	453	9	AD330133	Ad330133	DNA encod	C 944	17	0.5	588	11	ADM44803	Adm44803	Insect re
C 872	17	0.5	453	13	ADQ56548	Adq56548	Novel can	C 945	17	0.5	588	14	ADU83038	Adu83038	Human NFK
C 873	17	0.5	455	4	AAK72077	Aak72077	Human imm	C 946	17	0.5	592	5	ABV58450	Abv58450	Human pro
C 874	17	0.5	456	4	AAK72076	Aak72076	Human imm	C 947	17	0.5	592	10	ADD34186	Add34186	Mouse mit
C 875	17	0.5	457	6	ABV96272	Abv96272	Human pan	C 948	17	0.5	599	4	AA162757	Aa162757	Human CDN
C 876	17	0.5	457	14	ABE70406	Abe70406	Interleuk	C 949	17	0.5	599	5	ABA11361	Ab11361	Human ner
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C 878	17	0.5	464	13	ADQ52374	Adq52374	Novel can	C 951	17	0.5	601	14	ABE33022	Aeb33022	Human DNA
C 879	17	0.5	465	9	ACH27966	Ach27966	Human adu	C 952	17	0.5	604	13	ADRE0993	Adre0993	Human CD
C 880	17	0.5	468	6	ABN12903	Abn12903	Human ORF	C 953	17	0.5	606	11	ADM45358	Adm45358	Insect re
C 881	17	0.5	471	6	ABN19253	Abn19253	Human end	C 954	17	0.5	607	12	ACH92148	Ach92148	Human gen
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C 885	17	0.5	474	3	AAK27893	Aak27893	Human foe	C 958	17	0.5	614	5	ADL17542	Adl17542	Human ova
C 886	17	0.5	478	4	ACH40050	Ach40050	Human foe	C 959	17	0.5	615	13	AD050677	Ad050677	Novel can
C 887	17	0.5	479	4	AA549351	Aa549351	Staphyloc	C 960	17	0.5	621	6	ABK34787	Abk34787	Human CDN
C 888	17	0.5	479	4	AA549357	Aa549357	Staphyloc	C 961	17	0.5	621	10	ACD93366	Acd93366	Human col
C 889	17	0.5	479	8	ACA16579	Ac16579	Prokaryot	C 962	17	0.5	626	13	ADQ54276	Adq54276	Novel can
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C 894	17	0.5	482	6	ABN84615	Abn84615	Anti-Stre	C 967	17	0.5	634	13	ACN46424	Acn46424	Cotton pr
C 895	17	0.5	485	13	ACN51695	Acn51695	Cotton an	C 968	17	0.5	635	13	ACN46424	Acn46424	Cotton pr

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969 17 0.5 636 13 ACN52158 Acn52158 Cotton an
C 970 17 0.5 639 5 AAS67088 Aas67088 Aspergill
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C 978 17 0.5 662 13 ADJ07103 Adj07103 Human car
C 979 17 0.5 667 5 AAB64922 Aab64922 Human sec
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C 984 17 0.5 693 10 ADK65610 Adk65610 Murine de
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C 987 17 0.5 714 2 AAX61769 Aax61769 B. burgdo
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C 998 17 0.5 730 10 ADA55885 Ada55885 Gene enclo
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## ALIGNMENTS

```
RESULT 1
ACCS7946
ID ACCS7946 standard; cDNA; 3330 BP.
AC
ACCS7946;
XX
XX 11-AUG-2003 (first entry)
XX
DE Human Interphotoreceptor matrix IPM 150, isoform A, cDNA.
XX
XX Human; Interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX
XX receptor; ophthalmological; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 131..2586
XX FT /*tag= a
XX FT /product= "IPM 150"
XX FT /transl_except= (pos:668..756,aa:Thr-Asp)
XX FT sig_peptide 131..150
XX FT /*tag= b
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XX WO2003039346-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-US036090.
XX
XX 08-NOV-2001; 2001US-00077270.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-441440/41.
XX
XX
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DR P-PSDB; ABR42342.
XX
XX New Interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX
XX Claim 1; Page 77; 105pp; English.
XX
XX The present sequence is that of cDNA encoding isoform A of novel human
XX Interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 6q13-q15, a region that also contains loci for
XX progressive bilateral chorioretinal atrophy, autosomal dominant Stargardt's
XX -like macular dystrophy, North Carolina macular dystrophy and Salla
XX disease. Members of the IPMC gene family have been identified in humans,
XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
XX Subfamilies are designated IPM 150 (or IPM61) and IPM 200 (or IPM62). The
XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
XX antibodies that specifically bind the polypeptides, and vectors
XX comprising the polynucleotides. A claimed method of treating or
XX preventing photoreceptor death or retinal detachment involves
XX administering an IPMC polynucleotide, polypeptide or antibody. Also
XX claimed is a method for identifying a compound capable of modulating IPMC
XX gene expression
XX
XX Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 3330; DB 9; Length 3330;
XX Best Local Similarity 100.0%; Freq. No. 0;
XX Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 TAAACCAAGAGGTTATCTCTCAATCATCTGGTATCATATATATATATTTTTCACATTTTC
XX 1 TAAACCAAGAGGTTATCTCTCAATCATCTGGTATCATATATATATATTTTTCACATTTTC
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XX 61 TGTACTTTTAAATGAGATTGAGTTGTTCTGTGATTGTTATCAGAAATTCAGATGCAC 120
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XX 121 AAAAGCCAGAAATGATTTGGAAACTAGAAAGCTAATTTTGGATTTTTCCTCA 180
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XX 601 AATAAACAGAGAAATTTCCCTGACAGAAAAGATGAATATCTGACAGAGAACATTTGGG 660
XX
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DB 3301 GGCGAAGTTGTACTATGACATATCAAT 3330

RESULT 2
ADA14840
ID ADA14840 standard; cDNA; 3330 BP.
XX
XX ADA14840;
AC
XX
XX
DT 06-NOV-2003 (first entry)
DB
XX
XX Human interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX
XX 88; gene; human; IPMC 150 isoform A; gene therapy;
XX
XX interphotoreceptor matrix component; IPMC; ocular disorder;
XX
XX macular degeneration; photoreceptor death; retinal detachment.
OS
XX Homo sapiens.
XX
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XX Key Location/Qualifiers
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PF 08-NOV-2001; 2001US-00007270.
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XX 29-OCT-1998; 98US-00183972.
PR 29-OCT-1999; 99US-00430195.
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XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-238235/23.
DR P-PSDB; ADA14841.
XX
XX New isolated or recombinant interphotoreceptor matrix component
PT polynucleotide and polypeptide, useful for diagnosing, preventing,
PT treating or prognosticating ocular disorders, e.g. macular degeneration
PT or retinal detachment.
XX
XX Claim 3; Page 29-30; 76pp; English.
XX
XX The invention relates to an isolated or recombinant interphotoreceptor
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC gene operatively linked to the IPMC polynucleotide. The IPMC
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC preventing, treating or prognosticating ocular disorders, e.g. macular
CC degeneration, photoreceptor death or retinal detachment. They are also
CC useful for identifying a compound capable of modulating IPMC gene
CC expression in a cell. The present sequence represents cDNA encoding human
CC interphotoreceptor matrix component, IPMC, 150 isoform A.
XX
XX Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;
SQ
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Query Match 100.0%; Score 3330; DB 10; Length 3330;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATTTTTCACATTTC 60
DB 1 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATTTTTCACATTTC 60
QY 61 TGTACTTTTATGAGATTTGAGGTTGTTCTGTGATTTGTTATGAAATTAACAATGAC 120
DB 61 TGTACTTTTATGAGATTTGAGGTTGTTCTGTGATTTGTTATGAAATTAACAATGAC 120
QY 121 AAAAGCCAGATGTTATTTGGAAACTAGAAAGCTATTTTGTGTTTGGATTTTCTCCA 180
DB 121 AAAAGCCAGATGTTATTTGGAAACTAGAAAGCTATTTTGTGTTTGGATTTTCTCCA 180
QY 181 AGTTCAAGAAACCAAGATATCTCATATACATATACATTTCTGAAACTTAAGACATAGA 240
DB 181 AGTTCAAGAAACCAAGATATCTCATATACATATACATTTCTGAAACTTAAGACATAGA 240
QY 241 CAATCCCCCAAGAAATGAAACAAGTAAAGTAAAGAAATGTAACAATGTCAACTAT 300
DB 241 CAATCCCCCAAGAAATGAAACAAGTAAAGTAAAGAAATGTAACAATGTCAACTAT 300
QY 301 GAGAGCAATATTCATTTTGGCAAGCATGCAACAAAAGATCCGATTTTCCCAAGCGG 360
DB 301 GAGAGCAATATTCATTTTGGCAAGCATGCAACAAAAGATCCGATTTTCCCAAGCGG 360
QY 361 GATTAAAGTCTGTCCACAGAGATCCATGAAACAGATTTTGAACAGTCTTCAAGTTATTA 420
DB 361 GATTAAAGTCTGTCCACAGAGATCCATGAAACAGATTTTGAACAGTCTTCAAGTTATTA 420
QY 421 TAGATTGAGAGTGTCTCAGAAAGCATATGGAAGCATATCGATCTTTCTGGATCGAT 480
DB 421 TAGATTGAGAGTGTCTCAGAAAGCATATGGAAGCATATCGATCTTTCTGGATCGAT 480
QY 481 CCTGACACAGGGGAATATCAGAGACTGGCTCAGCATCTGCCAGCAGAGAGACTTGTGCT 540
DB 481 CCTGACACAGGGGAATATCAGAGACTGGCTCAGCATCTGCCAGCAGAGAGACTTGTGCT 540
QY 541 CTTGACATTTGGAATAAACTTCAGCAATTCACAGAGACCTGGATCTTCTCCAGCAGAG 600
```

Db 541 CTTTGACATTTGAAAAAATTGAGCAATTCACAGAGCACTGGACTCTTCCAGAGAG 600  
Qy 601 AATTAACAGAGAGATTTCCTCGACAGAAAAGATGAATATCTGCAGAGAGACATTGG 660  
Db 601 AATTAACAGAGAGATTTCCTCGACAGAAAAGATGAATATCTGCAGAGAGACATTGG 660  
Qy 661 AGAGCTGGTGAACCATTTGTCACTTCAACAGAACTCAATTTGAAAGATTGGGCAAT 720  
Db 661 AGAGCTGGTGAACCATTTGTCACTTCAACAGAACTCAATTTGAAAGATTGGGCAAT 720  
Qy 721 ATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTTGCCAACGTCCTCACTTGGGCT 780  
Db 721 ATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTTGCCAACGTCCTCACTTGGGCT 780  
Qy 781 TTCCCTCTCACTCTCTGATGACACCTCTCTCATATGAATTTCTGATTAATACCTCAAGAC 840  
Db 781 TTCCCTCTCACTCTCTGATGACACCTCTCTCATATGAATTTCTGATTAATACCTCAAGAC 840  
Qy 841 ACCAAGATGCTTACACAGAAAGAGAAAGAAATTCGCTGTGTGGAGGAGCAGGGGTG 900  
Db 841 ACCAAGATGCTTACACAGAAAGAGAAAGAAATTCGCTGTGTGGAGGAGCAGGGGTG 900  
Qy 901 GAGCTCAGCGTCTCTGTGTAAACAGAAAGTTCAAGCAGAGCTCGCTGACTCCAGTCC 960  
Db 901 GAGCTCAGCGTCTCTGTGTAAACAGAAAGTTCAAGCAGAGCTCGCTGACTCCAGTCC 960  
Qy 961 CCAATATTACAGAGAGCTTACAGAGAAAGTCCAACTTCAGATGCAGAAAGATTTAAGAA 1020  
Db 961 CCAATATTACAGAGAGCTTACAGAGAAAGTCCAACTTCAGATGCAGAAAGATTTAAGAA 1020  
Qy 1021 CTTTCCAGGATTTCAAAAAATTCATGTGTATGATTTAGACCAAGAAAGAAAAAGTGGC 1080  
Db 1021 CTTTCCAGGATTTCAAAAAATTCATGTGTATGATTTAGACCAAGAAAGAAAAAGTGGC 1080  
Qy 1081 TCAAGCTCCACAGAGATGCACTTACGGGCATCTTTAAGAGACAGTGCAGAGCAAAA 1140  
Db 1081 TCAAGCTCCACAGAGATGCACTTACGGGCATCTTTAAGAGACAGTGCAGAGCAAAA 1140  
Qy 1141 AGCCCTGCAAGTGAACCTCTGTCTTTTGAATCCAAAGAAATTTGAAGTGAAGTCTAT 1200  
Db 1141 AGCCCTGCAAGTGAACCTCTGTCTTTTGAATCCAAAGAAATTTGAAGTGAAGTCTAT 1200  
Qy 1201 CATGGAACCATGAGAGAGAGACAGCAACAGAAATTTATCTCAACAGCTACAGACTCAAA 1260  
Db 1201 CATGGAACCATGAGAGAGAGACAGCAACAGAAATTTATCTCAACAGCTACAGACTCAAA 1260  
Qy 1261 AGGCTGATCAGAAAGCACTAAGAGAAAGCAATCTTTGATGTGGGAGCAATTCAGTTTC 1320  
Db 1261 AGGCTGATCAGAAAGCACTAAGAGAAAGCAATCTTTGATGTGGGAGCAATTCAGTTTC 1320  
Qy 1321 ACTGATGAATTTGCTGGATCACTGCGCAGCTTTTGGTCTTGACACCCAAATCAAGGCTGCC 1380  
Db 1321 ACTGATGAATTTGCTGGATCACTGCGCAGCTTTTGGTCTTGACACCCAAATCAAGGCTGCC 1380  
Qy 1381 AATCTTTTGTCTGTATTAACAGAGATGCTACTTTGAGTCCAGAACTTCTCTGTGAA 1440  
Db 1381 AATCTTTTGTCTGTATTAACAGAGATGCTACTTTGAGTCCAGAACTTCTCTGTGAA 1440  
Qy 1441 CCCCAAGCTTGAAGAGTGAACGAGAGAGAGAGATGCTACCTGACACTTCTTGGTCTCCA 1500  
Db 1441 CCCCAAGCTTGAAGAGTGAACGAGAGAGAGAGATGCTACCTGACACTTCTTGGTCTCCA 1500  
Qy 1501 CCTGTATAGGCTCTACCTCTCTGTCAAGAGTCCACTTTCTTTATGAGCATCAAGCATC 1560  
Db 1501 CCTGTATAGGCTCTACCTCTCTGTCAAGAGTCCACTTTCTTTATGAGCATCAAGCATC 1560  
Qy 1561 TTCTCTCTGATCTGATCAAGGACACAGATACATAGGCCATCTGACAGACATGCTAAT 1620  
Db 1561 TTCTCTCTGATCTGATCAAGGACACAGATACATAGGCCATCTGACAGACATGCTAAT 1620  
Qy 1621 CCAAGGCTCAACCATCCCAAGTGAATTTCTGCAATCAGGCAATGGCTCTGGGAAT 1680  
Db 1621 CCAAGGCTCAACCATCCCAAGTGAATTTCTGCAATCAGGCAATGGCTCTGGGAAT 1680

Db 1681 TCAATTCACCTGCACTTTCAATGATACAGCCGATCAAGTCAAGTGGCGAAGATATGTC 1740  
Qy 1681 TCAATTCACCTGCACTTTCAATGATACAGCCGATCAAGTCAAGTGGCGAAGATATGTC 1740  
Db 1681 TCAATTCACCTGCACTTTCAATGATACAGCCGATCAAGTCAAGTGGCGAAGATATGTC 1740  
Qy 1741 AGACCTTAAGAAATGGAATGATCTGTCTGACATCTCCCGCCCATCTAGGATCAAGGCTC 1800  
Db 1741 AGACCTTAAGAAATGGAATGATCTGTCTGACATCTCCCGCCCATCTAGGATCAAGGCTC 1800  
Qy 1801 AGCGAATATGTTCTGTCCAGATCATTTCTTGAAGATACCACTCTCTCAGCTTAA 1860  
Db 1801 AGCGAATATGTTCTGTCCAGATCATTTCTTGAAGATACCACTCTCTCAGCTTAA 1860  
Qy 1861 CAGTATATCACCACTAGTCTATATGACCAATTCGCCCCCAAGGGCCGAGAGCTGTAGTTC 1920  
Db 1861 CAGTATATCACCACTAGTCTATATGACCAATTCGCCCCCAAGGGCCGAGAGCTGTAGTTC 1920  
Qy 1921 TTCACTGCGGTGTGTCAACATGGGCTTCTCCAAAGACCTGTTCAGAGAGCTCTCTG 1980  
Db 1921 TTCACTGCGGTGTGTCAACATGGGCTTCTCCAAAGACCTGTTCAGAGAGCTCTCTG 1980  
Qy 1981 GAGTACCGAGCTCTGAGCAACAATTCACACAGCTGTGTTCATATCTACGATCCAA 2040  
Db 1981 GAGTACCGAGCTCTGAGCAACAATTCACACAGCTGTGTTCATATCTACGATCCAA 2040  
Qy 2041 CTTACAGATTTTAAGCAACTTGAATTAATCTTAAGAAAGGAGTGTATGTAAT 2100  
Db 2041 CTTACAGATTTTAAGCAACTTGAATTAATCTTAAGAAAGGAGTGTATGTAAT 2100  
Qy 2101 AGCAAAATGAAGTTTGTCTAAGTCTGTGCGCTTAACCTTCAACAGGCTGTGACGGGCTC 2160  
Db 2101 AGCAAAATGAAGTTTGTCTAAGTCTGTGCGCTTAACCTTCAACAGGCTGTGACGGGCTC 2160  
Qy 2161 TTGAGAGATTTTGTCTGTCTGACAGCCCAACAATCTCACTGGAATTAAGACCTACTCT 2220  
Db 2161 TTGAGAGATTTTGTCTGTCTGACAGCCCAACAATCTCACTGGAATTAAGACCTACTCT 2220  
Qy 2221 CTCAACATTTGAACAGCTGATCAAGCAAGATCCCTGCAAGTTCTTGGCTCTGCGCAATTT 2280  
Db 2221 CTCAACATTTGAACAGCTGATCAAGCAAGATCCCTGCAAGTTCTTGGCTCTGCGCAATTT 2280  
Qy 2281 GCCCAATGTGTAAAGAAAGAAAGGAGCTGAGAGAGGAGTGTCTGCAAAACAGAGATAT 2340  
Db 2281 GCCCAATGTGTAAAGAAAGAAAGGAGCTGAGAGAGGAGTGTCTGCAAAACAGAGATAT 2340  
Qy 2341 GACAGCCAGGGGAGCTGAGAGGCTGTGGAACAGGCTCTGTGGCTCTGGGCAAAAGGA 2400  
Db 2341 GACAGCCAGGGGAGCTGAGAGGCTGTGGAACAGGCTCTGTGGCTCTGGGCAAAAGGA 2400  
Qy 2401 TGGAGGCTCTTCAAGGAAAGGAGCTTCATGCAAGTGGCCAGATCACTTGAATAATCA 2460  
Db 2401 TGGAGGCTCTTCAAGGAAAGGAGCTTCATGCAAGTGGCCAGATCACTTGAATAATCA 2460  
Qy 2461 GCATCAAAATCTAGTGTAAAAAGTTCCAAATCAACAAATTAACAGATTAATCACTAA 2520  
Db 2461 GCATCAAAATCTAGTGTAAAAAGTTCCAAATCAACAAATTAACAGATTAATCACTAA 2520  
Qy 2521 AGAAATTCGATTAAGTACCGTAGAATATGAGAAATTTAACCAATCAAGATTTGGAGGA 2580  
Db 2521 AGAAATTCGATTAAGTACCGTAGAATATGAGAAATTTAACCAATCAAGATTTGGAGGA 2580  
Qy 2581 AATTAATACTGAATATGATCAATTAATCACTTGGCTTCTCAAGAGATGATTTGGCT 2640  
Db 2581 AATTAATACTGAATATGATCAATTAATCACTTGGCTTCTCAAGAGATGATTTGGCT 2640  
Qy 2641 TCTCAAGAAATATGAGACAGGCAATTCATGGGCTATCAAAATCAAGATTAATCACTAA 2700  
Db 2641 TCTCAAGAAATATGAGACAGGCAATTCATGGGCTATCAAAATCAAGATTAATCACTAA 2700  
Qy 2701 CACTGAGATCAGCAACACCATATTTCAAAATTAAGAGATCATGTACTTGGCAACAG 2760  
Db 2701 CACTGAGATCAGCAACACCATATTTCAAAATTAAGAGATCATGTACTTGGCAACAG 2760

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OY 2761 TAAATTCGAAAAAAGACACTTATTATTATTAACCCCAATGCATCAGGGAAC 2820
DB 2761 TBAATTCGAAAAAAGACACTTATTATTATTAACCCCAATGCATCAGGGAAC 2820
OY 2821 AATATTTTATCTATCTTGAGATAGTCAAAATGATCATAGCAGTTGGCTTACCT 2880
DB 2821 AATATTTTATCTATCTTGAGATAGTCAAAATGATCATAGCAGTTGGCTTACCT 2880
OY 2881 TCCCTGAAAAATTTTACTCAGATCATTTGGCAACGATGACTTACTTATTTGTTAAGG 2940
DB 2881 TCCCTGAAAAATTTTACTCAGATCATTTGGCAACGATGACTTACTTATTTGTTAAGG 2940
OY 2941 ACTGAAACAATTTATTTGGGAAGAACTCTTATATGCTAGAAAGTACATTTAAAGATGA 3000
DB 2941 ACTGAAACAATTTATTTGGGAAGAACTCTTATATGCTAGAAAGTACATTTAAAGATGA 3000
OY 3001 CTACTTACGCAAGGAGATGCAAGGTCTCTTAAACGATATGTATGTGTGTAGCA 3060
DB 3001 CTACTTACGCAAGGAGATGCAAGGTCTCTTAAACGATATGTATGTGTGTAGCA 3060
OY 3061 CTGTATGATGTATATATGCTCCACACTAGCTGTATTAACAACTCAGTATTCAG 3120
DB 3061 CTGTATGATGTATATATGCTCCACACTAGCTGTATTAACAACTCAGTATTCAG 3120
OY 3121 TTATTAGGCACTAGTTTATAGCACTAGCTTATAGTATAGTATGTTGTTGCC 3180
DB 3121 TTATTAGGCACTAGTTTATAGCACTAGCTTATAGTATAGTATGTTGTTGCC 3180
OY 3181 AATTAATCTTGAATTTGTTTAAAGAACTGAGGTTGATGATACATACATGAGAAA 3240
DB 3181 AATTAATCTTGAATTTGTTTAAAGAACTGAGGTTGATGATACATACATGAGAAA 3240
OY 3241 ATCTTAATCTTGTGTTTACTTACACAAAGCTATTTTAAAGATGCTATGTTGGAGAAG 3300
DB 3241 ATCTTAATCTTGTGTTTACTTACACAAAGCTATTTTAAAGATGCTATGTTGGAGAAG 3300
OY 3301 GCGGAAGTTGTACTATATGACATTAATCAAT 3330
DB 3301 GCGGAAGTTGTACTATATGACATTAATCAAT 3330

RESULT 3
ACC57947
ID ACC57947 standard; cDNA; 2887 BP.
AC ACC57947;
AT 11-AUG-2003 (first entry)
CT
DE Human Interphotoreceptor matrix IPM 150, isoform B, cDNA.
KW Human; Interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMG;
KW receptor; ophthalmological; gene therapy; gene; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 2..2143
XX FT /*tag= a
XX FT /product= "IPM 150"
XX FT /partial
XX FT /note= "No start codon"
XX
XX MO2003039346-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002MO-US036090.
XX
XX 08-NOV-2001; 2001US-00077270.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX
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XX
PI Hageman GS, Kuehn MH;
XX
XX WPI; 2003-441440/41.
DR
XX
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX
XX Claim 1; Page 78-79; 105pp; English.
XX
XX The present sequence is that of cDNA encoding isoform B of novel human
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 6q13-q15, a region that also contains loci for
XX progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's
XX -like macular dystrophy, North Carolina macular dystrophy and Sallé
XX disease. Members of the IPMC gene family have been identified in humans,
XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
XX Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
XX antibodies that specifically bind the polypeptides, and vectors
XX comprising the polynucleotides. A claimed method of treating or
XX preventing photoreceptor death or retinal detachment involves
XX administering an IPMC polynucleotide, polypeptide or antibody. Also
XX claimed is a method for identifying a compound capable of modulating IPMC
XX gene expression
XX
XX Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;
SQ
XX
XX Query Match 74.4%; Score 2476; DB 9; Length 2887;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 2576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
OY 753 AGATGTTGCCAAGCTCTGACTTGGGCTTTCCCTCTCACTCTGATGACACCTTCTCAA 812
DB 310 AGATGTTGCCAAGCTCTGACTTGGGCTTTCCCTCTCACTCTGATGACACCTTCTCAA 369
OY 813 TGAATTTCTGATTAATCACTCAACGACACCAAGATGCTCAACAGAAAGAAACAGA 872
DB 370 TGAATTTCTGATTAATCACTCAACGACACCAAGATGCTCAACAGAAAGAAACAGA 429
OY 873 ATTCGCTGTGTGGAGAGACAGAGGTGAGCTCAGCTCTCTGTGTTAAACGAAAGTT 932
DB 430 ATTCGCTGTGTGGAGAGAGAGAGGTGAGCTCAGCTCTCTGTGTTAAACGAAAGTT 489
OY 933 CAAGCAGAGCTCGCTGACTCCCACTCCCATATTTACAGAGAGCTAGCAGAAAGTCCCA 992
DB 490 CAAGCAGAGCTCGCTGACTCCCACTCCCATATTTACAGAGAGCTAGCAGAAAGTCCCA 549
OY 993 ACTTCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAAAAAATCCATGTTAGG 1052
DB 550 ACTTCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAAAAAATCCATGTTAGG 609
OY 1053 ATTTAGACCAAAAGAAAGAAAGATGCTCAGCTCCACAGAGATGCAACTTACGGCAT 1112
DB 610 ATTTAGACCAAAAGAAAGAAAGATGCTCAGCTCCACAGAGATGCAACTTACGGCAT 669
OY 1113 CTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTACCTCTGTTGATTTC 1172
DB 670 CTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTACCTCTGTTGATTTC 729
OY 1173 CAACAAATTTGAAGTGAAGAGTCTATATGAAACCATGAGAGAGCAAGCAACAGCA 1232
DB 730 CAACAAATTTGAAGTGAAGAGTCTATATGAAACCATGAGAGAGCAAGCAACAGCA 789
OY 1233 AATCTATCTCAGCTACAGACTCTCAAAAGGCTGTACAGCAAGCACTTAGAGAAAGACA 1292
DB 790 AATCTATCTCAGCTACAGACTCTCAAAAGGCTGTATCAGAAAGCACTTAGAGAAAGACA 849
OY 1293 ATCTTGGATGTGGGAGCAATTCAGTCACTGATGAAATTCGTGATCATCTGCCAGCTT 1352
DB 850 ATCTTGGATGTGGGAGCAATTCAGTCACTGATGAAATTCGTGATCATCTGCCAGCTT 909
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QY 1353 TGGTCTGACACCCCAATCAGAGCTGCGCACATCTTTTGTGTTATTAAGAGGATGCTAC 1412  
DB 910 TGGTCTGACACCCCAATCAGAGCTGCGCACATCTTTTGTGTTATTAAGAGGATGCTAC 969  
QY 1413 TTTAGTCCAGAACTTCTCTCTGTGAAAGCCAGCTTGAGACAGTGAACGAGCAGACGA 1472  
DB 970 TTTAGTCCAGAACTTCTCTCTGTGAAAGCCAGCTTGAGACAGTGAACGAGCAGACGA 1029  
QY 1473 TGGTCTACCTGACACTTTTGTGTTCTCACTGCTATGAGCTCTTACTCTCTGTCAGAGC 1532  
DB 1030 TGGTCTACCTGACACTTTTGTGTTCTCACTGCTATGAGCTCTTACTCTCTGTCAGAGC 1089  
QY 1533 TCCACCTTTCTTATGAGCATCAAGACATCTCTGTCAGCTGATCAAGGACCAAGATAC 1592  
DB 1090 TCCACCTTTCTTATGAGCATCAAGACATCTCTGTCAGCTGATCAAGGACCAAGATAC 1149  
QY 1593 AATGGCACTGACACAGACATGCTAGTACAGAGGCTCACCATCCCAACAGTATTTTC 1652  
DB 1150 AATGGCACTGACACAGACATGCTAGTACAGAGGCTCACCATCCCAACAGTATTTTC 1209  
QY 1653 TGGCATCAGCCAACTGGCTCTGGGAAATTTCAATCCACCTGCATCTTCAAGATGACGCCG 1712  
DB 1210 TGGCATCAGCCAACTGGCTCTGGGAAATTTCAATCCACCTGCATCTTCAAGATGACGCCG 1269  
QY 1713 ATCAAGTGAAGGAGGAGATATGTTGTCAGACACTAGATGAAATGGAATCTGTCTGACAC 1772  
DB 1270 ATCAAGTGAAGGAGGAGATATGTTGTCAGACACTAGATGAAATGGAATCTGTCTGACAC 1329  
QY 1773 TCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTT 1832  
DB 1330 TCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTT 1389  
QY 1833 GAGAGATCAACTCTGTGTCTCAGCTTTACAGATATATCACCCTAGTTCTATGACCAATTC 1892  
DB 1390 GAGAGATCAACTCTGTGTCTCAGCTTTACAGATATATCACCCTAGTTCTATGACCAATTC 1449  
QY 1893 CCCCAAGGGCCGAGAGCTGGTATGTTCTTCACTGCTGCGGTGCTTAAAGGCTTCTTC 1952  
DB 1450 CCCCAAGGGCCGAGAGCTGGTATGTTCTTCACTGCTGCGGTGCTTAAAGGCTTCTTC 1509  
QY 1953 CAACGACTGTTCACACAGAGCTCTCTGAGATACAGAGCTTGAGCAACAATTCACACA 2012  
DB 1510 CAACGACTGTTCACACAGAGCTCTCTGAGATACAGAGCTTGAGCAACAATTCACACA 1569  
QY 2013 GCTGCTGTTCCATATCTACATCAATCTTACAGGATTTAAGCACTTGAATACTTAA 2072  
DB 1570 GCTGCTGTTCCATATCTACATCAATCTTACAGGATTTAAGCACTTGAATACTTAA 1629  
QY 2073 CTTCAGAAACGGGAGCTGATGTTGTAATGCAAAATGAAATTGCTAAGTCTGTGCCGTA 2132  
DB 1630 CTTCAGAAACGGGAGCTGATGTTGTAATGCAAAATGAAATTGCTAAGTCTGTGCCGTA 1689  
QY 2133 TAACTCACAAGAGCTGTGACAGGAGTCTTGAGAGATTTTCTGCTGCTGACGCCCAAA 2192  
DB 1690 TAACTCACAAGAGCTGTGACAGGAGTCTTGAGAGATTTTCTGCTGCTGACGCCCAAA 1749  
QY 2193 ACTCCACTGAAATAGACAGCTACTCTCTCAACATTGAAACAGCTGATCAAGCAGATCC 2252  
DB 1750 ACTCCACTGAAATAGACAGCTACTCTCTCAACATTGAAACAGCTGATCAAGCAGATCC 1809  
QY 2253 CTGCAAGTTCTGCTGCGCTGCGGGGAATTTGCCAATGTGTAAAGCAACGAACTGAGGA 2312  
DB 1810 CTGCAAGTTCTGCTGCGCTGCGGGGAATTTGCCAATGTGTAAAGCAACGAACTGAGGA 1869  
QY 2313 ACGGAGTGTGCTGCAACAGGATATGACAGCCAGGGGAGCTGGAAGGCTGGAACCC 2372  
DB 1870 ACGGAGTGTGCTGCAACAGGATATGACAGCCAGGGGAGCTGGAAGGCTGGAACCC 1929  
QY 2373 AAGCCTCTGTGGCCCTGGACAAAGGAATGCGAGGTCTTCAAGGAAAGGAGCTTCATG 2432  
DB 1930 AAGCCTCTGTGGCCCTGGACAAAGGAATGCGAGGTCTTCAAGGAAAGGAGCTTCATG 1989

QY 2433 CAGTTGCCAGATCACTGTGAAATCAAGCATACAAATCAAGTGTAAAAAGTTCCAAA 2492  
DB 1990 CAGTTGCCAGATCACTGTGAAATCAAGCATACAAATCAAGTGTAAAAAGTTCCAAA 2049  
QY 2493 TCAACAAAATTAACAAGTATATGTAAGAAATTTCTGAATTAAGCAGCGTAGAATATGA 2552  
DB 2050 TCAACAAAATTAACAAGTATATGTAAGAAATTTCTGAATTAAGCAGCGTAGAATATGA 2109  
QY 2553 AGAATTTAAACATCAAGATTTGGAGAGAAATTTAAACCTGAAATGTACATTTATCACT 2612  
DB 2110 AGAATTTAAACATCAAGATTTGGAGAGAAATTTAAACCTGAAATGTACATTTATCACT 2169  
QY 2613 AAGCTATCTCAAGAGATGATTTGCTCTCAAGGAAATAGGAGCAGGCATATTCAG 2672  
DB 2170 AAGCTATCTCAAGAGATGATTTGCTCTCAAGGAAATAGGAGCAGGCATATTCAG 2229  
QY 2673 GGTCAATCAAAATCCAGACATACAGTCAACATCTGAGATGAGCACACCATATTTCAAT 2732  
DB 2230 GGTCAATCAAAATCCAGACATACAGTCAACATCTGAGATGAGCACACCATATTTCAAT 2289  
QY 2733 ATGAAAGACTATGATCTTTGGCAACAGTAAATTTGAAAAAAGACACTTACTATTA 2792  
DB 2290 ATGAAAGACTATGATCTTTGGCAACAGTAAATTTGAAAAAAGACACTTACTATTA 2349  
QY 2793 TTTAAACCCCAATGCAATCAGCGAAACATATTTTACTATTTCTTGATGATATGTA 2852  
DB 2350 TTTAAACCCCAATGCAATCAGCGAAACATATTTTACTATTTCTTGATGATATGTA 2409  
QY 2853 TGATCATTAAGCCAGGTTTGCTTCCACTTCCCTGAAAAATTTTAAGTCAAGATCATTTGA 2912  
DB 2410 TGATCATTAAGCCAGGTTTGCTTCCACTTCCCTGAAAAATTTTAAGTCAAGATCATTTGA 2469  
QY 2913 ACAAGCATATGCTTACTTATTTGTTAAGGACGTGAACAATTTATGGAACAAACTCTTTA 2972  
DB 2470 ACAAGCATATGCTTACTTATTTGTTAAGGACGTGAACAATTTATGGAACAAACTCTTTA 2529  
QY 2973 TATGCTAGAAATGATTAATAAGATGACTACTTACGCGAGGAGATGCGAGTCTCTTAA 3032  
DB 2530 TATGCTAGAAATGATTAATAAGATGACTACTTACGCGAGGAGATGCGAGTCTCTTAA 2589  
QY 3033 ACGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3092  
DB 2590 ACGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2649  
QY 3093 TCTGATTAACAACAACCTCAGATTCAGTTATTTAGGACACATGTTTATAGCAACTAC 3152  
DB 2650 TCTGATTAACAACAACCTCAGATTCAGTTATTTAGGACACATGTTTATAGCAACTAC 2709  
QY 3153 TGTCTACATAGTAGACTGTTTGTGCGCAATATCTTGAATGTTCTTTAAAGAACT 3212  
DB 2710 TGTCTACATAGTAGACTGTTTGTGCGCAATATCTTGAATGTTCTTTAAAGAACT 2769  
QY 3213 GAGGTTGAGTACATATCCANTGAAAAATCTTACTTTCTGTTACTACACAAAGCTAT 3272  
DB 2770 GAGGTTGAGTACATATCCANTGAAAAATCTTACTTTCTGTTACTACACAAAGCTAT 2829  
QY 3273 TTTAAAGAAAGATGCTATGTTGGAGAGGCGCAAGTTGATATATGACATATCAAT 3330  
DB 2830 TTTAAAGAAAGATGCTATGTTGGAGAGGCGCAAGTTGATATATGACATATCAAT 2887

RESULT 4  
ADAI4842  
ID ADAI4842 standard; cDNA; 2887 BP.  
XX ADAI4842;  
AC  
XX  
XX  
DT 06-NOV-2003 (first entry)  
XX  
XX  
DE Human Interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.  
XX  
XX ss: gene; human; IPMC 150 isoform B; gene therapy;  
KM Interphotoreceptor matrix component; IPMC; ocular disorder;



KW macular degeneration; photoreceptor death; retinal detachment.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
FH CDS 5..2143  
FT /\*tag= a  
FT /partial  
FT /product= "IPMC 150 isoform B"  
FT /note= "No start codon given. Encodes residues 8-719 of  
FT {seqid:4}"  
XX US2002160954-A1.  
XX 31-OCT-2002.  
XX 08-NOV-2001; 2001US-00007270.  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
XX MPI; 2003-238235/23.  
XX P-PsDB; ADA14843.  
XX New isolated and recombinant interphotoreceptor matrix component  
XX polynucleotide and polypeptide, useful for diagnosing, preventing,  
XX treating or prognosticating ocular disorders, e.g. macular degeneration  
XX or retinal detachment.  
XX Claim 3; Page 33-34; 76pp; English.  
XX The invention relates to an isolated or recombinant interphotoreceptor  
XX matrix component (IPMC) polynucleotide. Also disclosed is a vector  
XX comprising a promoter of an interphotoreceptor matrix component (IPMC)  
XX gene operatively linked to the IPMC polynucleotide. The IPMC  
XX polynucleotides, polypeptides and antibodies are useful for diagnosing,  
XX preventing, treating or prognosticating ocular disorders, e.g. macular  
XX degeneration, photoreceptor death or retinal detachment. They are also  
XX useful for identifying a compound capable of modulating IPMC gene  
XX expression in a cell. The present sequence represents cDNA encoding human  
XX interphotoreceptor matrix component, IPMC, 150 isoform B.  
SQ Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;  
Query Match 74.4%; Score 2476; DB 10; Length 2887;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 753 AGATGTTGCCAAGCTCTCACTTGGGCTTTCCTCTCACTCTGTATGACACCTCTCTCA 812  
DB 310 AGATGTTGCCAAGCTCTCACTTGGGCTTTCCTCTCACTCTGTATGACACCTCTCTCA 369  
QY 813 TGAATTCCTCGAATTAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 872  
DB 370 TGAATTCCTCGAATTAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 429  
QY 873 ATTGCTGTGTGAGAGACAGAGGAGTGAAGTCAAGCTCTCTGTGTAAACCAAGATT 932  
DB 430 ATTGCTGTGTGAGAGACAGAGGAGTGAAGTCAAGCTCTCTGTGTAAACCAAGATT 489  
QY 933 CAAGCAGAGCTGCTGACTCCCAAGTCCCATATTAACAAGAGCTAAGCAGAAAGTCCA 992  
DB 490 CAAGCAGAGCTGCTGACTCCCAAGTCCCATATTAACAAGAGCTAAGCAGAAAGTCCA 549  
QY 993 ACTTCAGATGCAAAAGATATTTAAAGAACTTCAGAGATTCAAAAAATTCAGTGTAG 1052  
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QY 1053 ATTAGACCAAGAAAGAAAGATGCTCAAGCTCCAGAGATGCACTTACGGCCAT 1112

DB 610 ATTTAGACAAAGAAAGAAAGATGCTCAAGCTCCAGAGATGCACTTACGGCCAT 669  
QY 1113 CTTTAAAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTACCTCTGTCTTTGATTC 1172  
DB 670 CTTTAAAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTACCTCTGTCTTTGATTC 729  
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DB 790 AATCTATCTCAAGCTACAGACCTCAAAAGGCTGATCAGCAAGACACTAAGAGAAACA 849  
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DB 850 ATCTTTGATGTTGGGAGCAATTCAGTTCACTGATGAAATTCCTGATACCTGCCAGCTT 909  
QY 1353 TGGTCTGAGACCAATCAGAGCTGCCCAATCTTTTGGCTGTTTAAACAGAGATGCTAC 1412  
DB 910 TGGTCTGAGACCAATCAGAGCTGCCCAATCTTTTGGCTGTTTAAACAGAGATGCTAC 969  
QY 1413 TTTGAGTCCAGAACTTCTCTGTGTAACCCCAAGCTTGAGACAGTGAACGAGACAGA 1472  
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QY 1533 TCCACCTTCTTTTGGGATCAAGATCTTCTCTGCTGATCAAGGACCAACAGATAC 1592  
DB 1090 TCCACCTTCTTTTGGGATCAAGATCTTCTCTGCTGATCAAGGACCAACAGATAC 1149  
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DB 1570 GCTGCTGTTCTATATCTACAGATCCAACTTAAAGAGATTAAAGCACTTGAATCTTAA 1629  
QY 2073 CTTCAAGAAAGGAGTGTGATTTGAATGAAGAAATGAAGTTTGTAAAGTGTGAGCGTA 2132  
DB 1630 CTTCAAGAAAGGAGTGTGATTTGAATGAAGAAATGAAGTTTGTAAAGTGTGAGCGTA 1689  
QY 2133 TAACTTCACAAAGGCTGTGACGAGGCTTGTGAGAGATTTGTGCTGACGCCAACA 2192



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Db      1690 TAACCTCACAAAGGCTGTGCAAGGGGCTTTGAGAGATTTTCGTTCTGCTGACCCACA 1749
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Db      1750 ACTCCATCTGGAATAGACAGCTACTCTCTCAACATTGAAACCAAGCTGATCAAGCAGATCC 1809
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Db      1810 CTGCAAGTTCTTGCGCTTGCGGCGAATTTTGCCCAATGTGTAAAGAAACGACGTGAGGA 1869
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Qy      2613 AGGCTATCTCAAGAGATGATTTGCTTCTCAAGGAAATGAGACAGGCATATTGATG 2672
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Qy      2673 GGTCAATCAAAATTCAGACATACAGTCAACATGAGAAATGAGACACACATATTTCAA 2732
Db      2230 GGTCAATCAAAATTCAGACATACAGTCAACATGAGAAATGAGACACACATATTTCAA 2289
Qy      2733 ATAGAAGAGTCAATGTACTTTGGCAACCAATTAATCTGAAAAAAAAGACATTACTTA 2792
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Qy      2853 TGATCATTAAGCAGGTTGCTTCCACCTCCCGTGAATAATTTTACTCAGACATTTGCA 2912
Db      2410 TGATCATTAAGCAGGTTGCTTCCACCTCCCGTGAATAATTTTACTCAGACATTTGCA 2469
Qy      2913 ACAAGCATAGCTTACTTATTTGTTAGGACAGACAAATTTATTTGGAGCAAACTCTTT 2972
Db      2470 ACAAGCATAGCTTACTTATTTGTTAGGACAGACAAATTTATTTGGAGCAAACTCTTT 2529
Qy      2973 TATGCTAGAAAGTACATTTAAAGATGATCTTACGCGGAGATGACAGTCTCTTAA 3032
Db      2530 TATGCTAGAAAGTACATTTAAAGATGATCTTACGCGGAGATGACAGTCTCTTAA 2589
Qy      3033 ACGCATGAATGTATGATGATGAGGCACTGTAGAGAGTATATATGCTCCACACTAG 3092
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Qy      3093 TGTGATTAACACAAACCTCAGTATTCAGTTATTAAGGACACTAGTTTATACGCACTAC 3152
Db      2650 TGTGATTAACACAAACCTCAGTATTCAGTTATTAAGGACACTAGTTTATACGCACTAC 2709
Qy      3153 TGCCTTACATAGTAGACTGTTTGTGCGCAATATCTTTGAATTTGTTCTTTAAAGAACT 3212
Db      2710 TGCCTTACATAGTAGACTGTTTGTGCGCAATATCTTTGAATTTGTTCTTTAAAGAACT 2769
Qy      3213 GAGGTTCAAGATACATATACATGAAAAATCTTACTTTCTTTGTTACTACACAAAGCTAT 3272
Db      2770 GAGGTTCAAGATACATATACATGAAAAATCTTACTTTCTTTGTTACTACACAAAGCTAT 2829

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Qy      3273 TTTAAAGAGATGATGTTGGAGAGGCGGAAGTTGATATATGACATATCAT 3330
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RESULT 5
AAA46205
ID AAA46205 standard; cDNA; 3263 BP.
XX
AC AAA46205;
XX
DT 04-SBP-2000 (first entry)
XX
DE cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW chromosome 6q13-q15; ocular disease; retinal detachment;
KW choriorretinal degeneration; retinal degeneration; cone degeneration;
KW age related macular degeneration; photoreceptor degeneration;
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;
KW rod-cone dystrophy; cone-rod dystrophy; ss.
XX
OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT CDS
FT 128..244
FT /tag=a
FT /transl_except= (pos: 2411..2414, aa: Lys)
FT /product="Interphotoreceptor matrix proteoglycan IPM150"
PN WO200026367-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025440.
XX
PR 29-OCT-1998; 98US-00183972.
XX
PA (IOWA ) UNIV IOWA RES FOUNO.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2000-365616/31.
XX
P-PSDB; AAY93336.
XX
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT preventing, diagnosing and treating ocular disorders such as retinal
PT detachment and choriorretinal degeneration.
XX
PS Claim 2; Fig 3; 183pp; English.
XX
CC The present sequence encodes an interphotoreceptor matrix (IPM)
CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).
CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
CC is located on chromosome 6q13-q15, between markers CHC.GATA11P10 and
CC D6S284. The IPM proteins may be used to supplement a patient's own
CC production of the protein or to rectify alterations in their nucleic
CC acids that result in expression of an inactive protein. The IPM nucleic
CC acids may be used in this way to treat ocular diseases such as retinal
CC detachment, choriorretinal degeneration, retinal degeneration, age related
CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment
CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
CC also be used to assay for other modulators of IPM proteoglycan expression
CC and activity that may be used to treat ocular diseases. The nucleic acids
CC and proteins may also be used as diagnostic reagents to detect the
CC presence of IPM nucleic acids and their products in samples from patients
CC according to standard methodologies
XX
SQ Sequence 3263 BP; 1040 A; 721 C; 663 G; 838 T; 0 U; 1 Other;
XX
Query Match 62.9%; Score 2095; DB 3; Length 3263;

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Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2575; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

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DB 748 TGAATTTCTGATTAATACATCAACGACACCAAGATGCTTACACAGAAAGAGAAACAGA 807
OY 873 ATTGCTGTGTTGAGAGACGAGAGGTGAGCTCAAGCTTCTTCTGTAAACGAGAGTT 932
DB 808 ATTGCTGTGTTGAGAGACGAGAGGTGAGCTCAAGCTTCTTCTGTAAACGAGAGTT 867
OY 933 CAAGGACAGCTGCGTCACTCCAGTCCCATTTATACGAGAGCTAGAGAGAAAGTCCCA 992
DB 868 CAAGGACAGCTGCGTCACTCCAGTCCCATTTATACGAGAGCTAGAGAGAAAGTCCCA 927
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DB 988 ATTTAGACCAAAAGAAAGAAAGATGGCTCAAGCTTCACAGAGATGCAACTTACGGCAT 1047
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DB 1048 CTTTAAAGACACAGTGCAGAGAGCAAAAGCCCTGGAAGTGAATCTTCCTTTGATTTC 1107
OY 1173 CAACAAATTTGAAAGTGAAGAAATCTATCATGGAACATGAGAGAGAGCAACAAACAGA 1232
DB 1108 CAACAAATTTGAAAGTGAAGAAATCTATCATGGAACATGAGAGAGAGCAACAAACAGA 1167
OY 1233 AATCTATCTCAACGCTACAGACTCTCAAAAGCTGATCAGCAAAGCACTAGAGAAAGACA 1292
DB 1168 AATCTATCTCAACGCTACAGACTCTCAAAAGCTGATCAGCAAAGCACTAGAGAAAGACA 1227
OY 1293 ATCTTGAATGTGGGGACAAATTCAGTTCACTGATGAATTTGCTGATCACTCCAGCCTT 1352
DB 1228 ATCTTGAATGTGGGGACAAATTCAGTTCACTGATGAATTTGCTGATCACTCCAGCCTT 1287
OY 1353 TGGTCTGACACCCATCAGAGCTGCCACATCTTTTGTCTTATTAACAGAGATGCTAC 1412
DB 1288 TGGTCTGACACCCATCAGAGCTGCCACATCTTTTGTCTTATTAACAGAGATGCTAC 1347
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DB 1348 TTTGAGTCCAGAACTTCTCTGTTGAACCCAGCTTGAGACAGTGAACGAGACAGAGA 1407
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DB 1528 AATGCGACTGACCAATGCTAGTACAGAGGCTCACCATCCCAACAGATGATTTATTC 1587
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DB 1588 TGGAAATCAGCCAACTGGCTCTGGGAATTTCAATCCACTGCATCTTCAAGTACAGCCG 1647
OY 1713 ATCAATGAGAGTGGAGAGATATGCTCAGACACTAGATGAAATGATCTGTCTGACAC 1772
DB 1648 ATCAATGAGAGTGGAGAGATATGCTCAGACACTAGATGAAATGATCTGTCTGACAC 1707
OY 1773 TCTGCCCCATCTGAGGTACAGAGTCAAGCGAATATGTTTCTGTCCAGATCATTTCTT 1832
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DB 1708 TCTTCCCCCATCTGAGGTACAGAGCTCAGGAAATATGTTCTGTCCAGATCATTTCT 1767
OY 1893 GGAGGATACCACTCTGCTCAGGCTTACAGATATACCACTAGTCTATGACCAATGCG 1892
DB 1768 GGAGGATACCACTCTGCTCAGGCTTACAGATATACCACTAGTCTATGACCAATGCG 1827
OY 1893 CCCCAAGGCGGAGAGCTGATAGTGTCTTCAAGTCTGCGTGTGTAAACATGGCTCTC 1952
DB 1828 CCCCAAGGCGGAGAGCTGATAGTGTCTTCAAGTCTGCGTGTGTAAACATGGCTCTC 1887
OY 1953 CAACGACTGTTCAACAGAGCTCTGTGAGTACCGAGCTGTGAGCAACATTCACACA 2012
DB 1888 CAACGACTGTTCAACAGAGCTCTGTGAGTACCGAGCTGTGAGCAACATTCACACA 1947
OY 2013 GCTGCTGTTCATATCTACGATCCCATCTTAACAGATTTTAAGCACTTGAAATACTTA 2072
DB 1948 GCTGCTGTTCATATCTACGATCCCATCTTAACAGATTTTAAGCACTTGAAATACTTA 2007
OY 2073 CTTCAAGAAACGGAGTGTGATTTGTGAATAGCAAAATGAAGTTTGCTAAGTCTGTGCGTA 2132
DB 2008 CTTCAAGAAACGGAGTGTGATTTGTGAATAGCAAAATGAAGTTTGCTAAGTCTGTGCGTA 2067
OY 2133 TAACTTCAACAAAGCTGTGACAGGGCTTTGAGAGATTTTGTTCTGTGACCCCAACA 2192
DB 2068 TAACTTCAACAAAGCTGTGACAGGGCTTTGAGAGATTTTGTTCTGTGACCCCAACA 2127
OY 2193 ACTCATCTGGAATAATAGACAGTACTCTCTCAACTTGAACAGAGTATCAAGCATGCC 2252
DB 2128 ACTCATCTGGAATAATAGACAGTACTCTCTCAACTTGAACAGAGTATCAAGCATGCC 2187
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DB 2248 AGCGAGTGTGCTGCAAAACCGATATAGACACGCCAGGGAGCTGTGACAGTCTGGAACC 2307
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DB 2308 AGGCTCTGTGGCCCTTGCAACAAAGAAATGCGAGGTCTCCCAAGGAAAGGAGCTCCATG 2366
OY 2433 CAGGTTGCAAGTCACTCTGAAATCAAGCATACAAATCTAGTGTAAAAAGTTCCAAA 2492
DB 2367 C-GGTT-CGAGTCACTCGAAATCAAGCATACAAATCTAGTGTAAAAAGTTCCAAA 2424
OY 2493 TCAACAAATTAACAGGTATATGATGTAAGAAATTTCTGAATTA-CTGACCGTGAATATG 2551
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OY 2552 AAGATTTTAACCATCAAGTATGGGAAGAAATTAATACTGAAATATGTAATTAATCACT 2611
DB 2485 AAGATTTTAACCATCAAGTATGGGAAGAAATTAATACTGAAATATGTAATTAATCACT 2544
OY 2612 TAGGCTATCTCAAGAGATGATTTTGCTTCTCAAGAAATAGAGACAGGATATTCAT 2671
DB 2545 TAGGCTATCTCAAGAGATGATTTTGCTTCTCAAGAAATAGAGACAGGATATTCAT 2604
OY 2672 GGGTATCAAAAATCAGACATACAGTCAACATGGAATCAGACACACATATTTTCAA 2731
DB 2605 GGGTATCAAAAATCAGACATACAGTCAACATGGAATCAGACACACATATTTTCAA 2664
OY 2732 TATTAAGAGTCAATGCTATGCGCAACAGTAAATCTGAAAAAAGACACTTACTTAT 2791
DB 2665 TATTAAGAGTCAATGCTATGCGCAACAGTAAATCTGAAAAAAGACACTTACTTAT 2724
OY 2792 ATTTAAACCCCAATATGACATACAGCAAACTATTTTACTATCTTGTGATGATGCAAA 2851
DB 2725 ATTTAAACCCCAATATGACATACAGCAAACTATTTTACTATCTTGTGATGATGCAAA 2784
OY 2852 ATGATCATTAAGCAGGTTTGTCTTCACTTCCCTGAAAAATTTTACTCAAGATCATTTGC 2911
DB 2785 ATGATCATTAAGCAGGTTTGTCTTCACTTCCCTGAAAAATTTTACTCAAGATCATTTGC 2844
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Oy	2912	AACAAGCACTAGCTTACTTAATGTTAGGGACTGAACATTTATGGGAAGCAAACTCTT	2971
Db	2845	AACAGCACTAGCTTACTTAATGTTAGGGACTGAACATTTATGGGAAGCAAACTCTT	2904
Oy	2972	ATATGCTGAAAGTACATTTTAAAGATGACTTACCGCAGGAGATCAGGTCTCTTA	3031
Db	2905	ATATGCTGAAAGTACATTTTAAAGATGACTTACCGCAGGAGATCAGGTCTCTTA	2966
Oy	3032	AACGATTAATGTATGTATGTGTATGGCACTGTATGTATATATATGCTCCACATAC	3091
Db	2965	AACGATTAATGTATGTATGTGTATGGCACTGTATGTATATATATGCTCCACATAC	3024
Oy	3092	GTCGTATTAACACAAACCTCAGTATCTAGTTATTTAGGCACTGTATTTATACGAACTA	3151
Db	3025	GTCGTATTAACACAAACCTCAGTATCTAGTTATTTAGGCACTGTATTTATACGAACTA	3084
Oy	3152	CTGCTTACATAGTAGACTCTTTTGTGTGCAATTAATCTTTGAATGTCTTTTAAAGAAGC	3211
Db	3085	CTGCTTACATAGTAGACTCTTTTGTGTGCAATTAATCTTTGAATGTCTTTTAAAGAAGC	3144
Oy	3212	TGAGGTCAGATACACATACCATGGAATAATCTTACTTTCTGTACTACACAAAGCTA	3271
Db	3145	TGAGGTCAGATACACATACCATGGAATAATCTTACTTTCTGTACTACACAAAGCTA	3204
Oy	3272	TTTTTAAACAATGCTATGTTGGGGAAGGCGAAGTGTACTATATGACATTAATCAAT	3330
Db	3205	TTTTTAAACAATGCTATGTTGGGGAAGGCGAAGTGTACTATATGACATTAATCAAT	3263

RESULT 6  
ACC57960  
ID ACC57960 standard; cDNA; 3261 BP

DT 11-AUG-2003 (first entry)

DE Human interphotoreceptor matrix IPM 150, isoform A variant, cDNA.

KM Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
KM receptor; ophthalmological; gene therapy; gene; 88.

**OS Homo sapiens.**

FH	Key	Location/Qualifiers
FT	CDS	128. .2443
FT		/*tag= a
FT		/product= "IPM 150"

PN WO2003039346-A2.

PD 15-MAY-2003

PF 08-NOV-2002; 2002WO-US036090

PR 08-NOV-2001; 2001US-00077270

PA (IOWA ) UNIV IOWA RES FOUND.

PI Hageman GS, Kuehn MH;

DR WPI; 2003-441440/41.

XX

PT New interphotoreceptor matrix proteins and polynucleotides, useful for  
PT treating or preventing photoreceptor death or retinal detachment, or for  
PT treating ocular disorders.

PS Claim 1; Page 91-94; 105pp; English.

CC The present sequence is that of cDNA encoding a variant of isoform A of  
CC novel human interphotoreceptor matrix 150 (IPM 150), a member of the

CC newly identified interphotoreceptor matrix component (IPMC) gene family.  
CC The cDNA was isolated from a human retinal cDNA library. The IMP 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bilateral choriorretinal atrophy, autosomal dominant Steargardt's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IMPG1) and IPM 200 (or IMPG2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polynucleotides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression  
XX  
SQ Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;

Query Match	62.9%	Score 2094;	DB 9;	Length 3261;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2574;	Conservative	0;	Mismatches 0;	Indels 4;
				Gaps 4

OY		753 AGATGTTGCCACGCCTCACTTGAGCCCTTTCCTCCTCATCTCGTAGACAACCCTCTCAA	812
Dδ		688 AGATTGTGGCAACGCTCTCACTTGAGCCCTTTCCTCCTCATCTCGTAGACAACCCTCTCAA	747

QY	813	TGAATTCTCGATATACACTCAACGACACCAAGATGCTTACACAGAAAGAAACAGA	872
Db	748	TGAATTCTCGATATACACTCAACGACACCAAGATGCTTACACAGAAAGAAACAGA	807

QY	873	ATTGCTGTGTTGGAGAGCAGAGGGGTGAGCTCAGCGTCTCTCTGGTAAACCAAGATT	932
Db	808	ATTGCTGTGTTGGAGAGCAGAGGGGTGAGCTCAGCGTCTCTCTGGTAAACCAAGATT	867

QY 933 CAAGGCAGAGCTCGCTGACTGCCAGTCCCATATTATCCAGAGCTAGCAGAGAAAGTCCCA 992

Db 868 CAAGGCAGAGCTCGCTGACTGCCAGTCCCATATTATCCAGAGCTAGCAGAGAAAGTCCCA 927

QY 993 ACTTCAGATGCAGAAAGATATTTAAGAACTTCAGGATTCAAAAAATCCATGTGTAGG 105

Db 928 ACTTCAGATGCAGAAAGATATTTAAGAACTTCAGGATTCAAAAAATCCATGTGTAGG 987

Qy	1053	ATTTAGCCAAAGAAAGAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCAT	111
Dp	988	ATTTAGACCAACGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCAT	104

Dy 1113 CTTAAGACACACTGCAGAGAAGAAAGCCCTGCAAGACCTCCTGTCTTGGATTC 117  
Dc 1048 CTATTGAAGCATCATCTGCGACAAGCAAAGAACCCCCTCCAATCGCACCTCTGCTTTTTGGATTTC 119

09 1173 CAACAAATTGAAGTAGAGAGCTATCATGGAACCATGAGGAGCAAGCAACCGA 123

QY 1233 AATCTATCTCACAGCTACGACCCTAAAGGCTGATCAGCAAGCACTAGAGGAAGACA 129

1293 ATCTTTGATGTGGGACATTCAGTTCATGATGAATTCGTGGATCACTGCCACCTT 135

1353 TGGTCTTCACACCCCATCAGAGCTGCCACATCTTTTGTGTATTAACAGAGATGCTAC 1411

1413 TTTGAGTCCGAACCTTCTCTCTGTGAACCCAGCTTGAGACAGTGGACGGAGCAGACGA 1477

1473 TGGTCTACTGACATTCTGGTTCACCTGCTATGAGCCTTACTCCCTGTGAGAGC 1533

Db 1408 TGGTCTACCTGACACTTCTTGGTCTCCACCTGCTATGGCCCTTACTTCCCTGTCAAGAAGC 1467

Qy	1533	TCGACCTTTCTTATAGGATATCAAGACTTTCTCTGACTGATCAAGGACCAAGATAC	1552
Db	1468	TCGACCTTTCTTATAGGATATCAAGACTTTCTCTGACTGATCAAGGACCAAGATAC	1527
Qy	1593	AATGGCCACTACCAAGACAATAGTACTAGTCCAGGGCTCACTCCCAACAGTGAATTATTC	1652
Db	1528	AATGGCCACTACCAAGACAATAGTACTAGTACAGGGGTCACTATCCCAACAGTGAATTATTC	1587
Qy	1653	TGCAATCAGCCAACTGGCTCTGGGAATTTCAATCCACCTGCATCTTCAATGACAGCCG	1712
Db	1588	TGCAATCAGCCAACTGGCTCTGGGAATTTCAATCCACCTGCATCTTCAATGACAGCCG	1647
Qy	1713	ATCAAGTSCAGGTGGCGAAGATATGGTACAGACCTAGATGAATAATGATCTGTGCAC	1772
Db	1648	ATCAAGTSCAGGTGGCGAAGATATGGTACAGACCTAGATGAATAATGATCTGTGCAC	1707
Qy	1773	TCTGCCCCCATCTAGAGTACCAAGACTCAGGAAATATGTTTCTGTCCCAATCATTTCTT	1832
Db	1708	TCTGCCCCCATCTAGAGTACCAAGACTCAGGAAATATGTTTCTGTCCCAATCATTTCTT	1767
Qy	1833	GGAGGATACCACTCCTGTCAGACTTTACATATATACCACTAGTCTTAAGACATTGTC	1892
Db	1768	GGAGGATACCACTCCTGTCAGACTTTACATATATACCACTAGTCTTAAGACATTGTC	1827
Qy	1893	CCCCAAGGGCCGAGAGCTGATAGTTCCTTCACTGCTGCTTGTCTAATATGSCCTTCTC	1952
Db	1828	CCCCAAGGGCCGAGAGCTGATAGTTCCTTCACTGCTGCTTGTCTAATATGSCCTTCTC	1887
Qy	1953	CAAGACCTGTTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCACAATTACACA	2012
Db	1888	CAAGACCTGTTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCACAATTACACA	1947
Qy	2013	GCTGCTGGTTCCATATCTAACATCCAACTTACAGAAATTTAAGCACTTGAATACTTAA	2072
Db	1948	GCTGCTGGTTCCATATCTAACATCCAACTTACAGAAATTTAAGCACTTGAATACTTAA	2007
Qy	2073	CTTCGAAACGGAGTGTGATTTGTGAATAGCAAAATGAAGTTTGCTAAGTCTGTGCGTA	2132
Db	2008	CTTCGAAACGGAGTGTGATTTGTGAATAGCAAAATGAAGTTTGCTAAGTCTGTGCGTA	2067
Qy	2133	TAACTCTCAAGAGCTGTGACGCGGCTTTGAGAGATTTTGTTCTGTGACGCCAACA	2192
Db	2068	TAACTCTCAAGAGCTGTGACGCGGCTTTGAGAGATTTTGTTCTGTGACGCCAACA	2127
Qy	2193	ACTCCATCTGAAATATAGACAGTACTCTCTCAACATTGAAACAGCTGATCAAGCAGATCC	2252
Db	2128	ACTCCATCTGAAATATAGACAGTACTCTCTCAACATTGAAACAGCTGATCAAGCAGATCC	2187
Qy	2253	CTGCAAGTTCTTGCGCTGCGCGGGAATTTGCCAATGTGTAAAGAACGAACGAACCTGAGGA	2312
Db	2188	CTGCAAGTTCTTGCGCTGCGCGGGAATTTGCCAATGTGTAAAGAACGAACGAACCTGAGGA	2247
Qy	2313	AGCGAGTGTGCTGSCAAACAGAGTATGACAGCCAGGGGAGCTCGACGCTCGGAAC	2372
Db	2248	AGCGAGTGTGCTGSCAAACAGAGTATGACAGCCAGGGGAGCTCGACGCTCGGAAC	2307
Qy	2373	AGGCTCTGTGGCCTTGCGACAAAGAAATGCGAGGTCCTCCAGGGAAAGGAGCTCCATG	2432
Db	2308	AGGCTCTGTGGCCTTGCGACAAAGAAATGCGAGGTCCTCCAGGGAAAGGAGCTCCATG	2366
Qy	2433	CAGGTTCAGATCACTCTGAAAATCAAGCATCAAAACTAGTGTAAAGAAAGTTCCAAA	2492
Db	2367	CAGGTTCAGATCACTCTGAAAATCAAGCATCAAAACTAGTGTAAAGAAAGTTCCAAA	2423
Qy	2493	TCACAAATAATACAAAGTATACGTAAAGAAATTCGAAATTAAGTCCGTAGATAATGA	2552
Db	2424	TCACAAATAATACAAAGTATACGTAAAGAAATTCGAAATTAAGTCCGTAGATAATGA	2483
Qy	2553	AGAAATTTAACATCAAGATATGGGAAGAAATTAAGAACTGAAATGTACAAATTATCACTT	2612
Db	2484	AGAAATTTAACATCAAGATATGGGAAGAAATTAAGAACTGAAATGTACAAATTATCACTT	2543

QY	2613	AGGCTATCTCAAGAGATGATTTGGCTTCTCAAGGAAAAATGGAGAGAGCATTTTCATG	2612
Db	2514	AGGCTATCTCAAGAGATGATTTGGCTTCTCAAGGAAAAATGGAGAGAGCATTTTCATG	2603
QY	2673	GGTCATCAAAATCCAGACATACAGTCAACACTGGAATCAGACACACCATATTTCAAT	2732
Db	2604	GGTCATCAAAATCCAGACATACAGTCAACACTGGAATCAGACACACCATATTTCAAT	2663
QY	2733	ATGAGAGTCATGTACTTGGCAACAGTAAATTTGAAAAAAAAGACCTTACTTATTA	2792
Db	2664	ATGAGAGTCATGTACTTGGCAACAGTAAATTTGAAAAAAAAGACCTTACTTATTA	2723
QY	2793	TTAAAACCCCAAATGCATACGCGAAACATATTTTACTATCTTGGATGATAGTCAAAA	2852
Db	2724	TTAAAACCCCAAATGCATACGCGAAACATATTTTACTATCTTGGATGATAGTCAAAA	2783
QY	2853	TGATCATTAAGCAGATTGGCTTCCACCTCCCTGAAAATTTTACTCAAGATCATTTGCA	2912
Db	2784	TGATCATTAAGCAGATTGGCTTCCACCTCCCTGAAAATTTTACTCAAGATCATTTGCA	2843
QY	2913	ACAAGCATAGCTTACTTATTTGTTTAAAGGACTGAACAAATTTATTTGGAGCAAACTCTTAA	2972
Db	2844	ACAAGCATAGCTTACTTATTTGTTTAAAGGACTGAACAAATTTATTTGGAGCAAACTCTTAA	2903
QY	2973	TATGCTAGAAAATGATCATTTTAAAGATGATCTTACGAGGAGATAGCAGTCTCTTAA	3032
Db	2904	TATGCTAGAAAATGATCATTTTAAAGATGATCTTACGAGGAGATAGCAGTCTCTTAA	2963
QY	3033	ACGCATGAATGTATGTAGTGTGTAGGCACTGTAGTGAAGTATATATGCTCCACACTAGC	3092
Db	2964	ACGCATGAATGTATGTAGTGTGTAGGCACTGTAGTGAAGTATATATGCTCCACACTAGC	3023
QY	3093	TCTGATTAACCAAAACCTCAGTATTTCAAGTTATTAAGCACACTAGTTTATACGCACTAC	3152
Db	3024	TCTGATTAACCAAAACCTCAGTATTTCAAGTTATTAAGCACACTAGTTTATACGCACTAC	3083
QY	3153	TGCTTACATAGTACGTGTTTGTGGCAATATCTTTGAATTTGTTCTTTAAAGAAACT	3212
Db	3084	TGCTTACATAGTACGTGTTTGTGGCAATATCTTTGAATTTGTTCTTTAAAGAAACT	3143
QY	3213	GAGGTTCAAGATACATACATCGATGGAATAATCTTCTTGTACTACAAAGCTAT	3272
Db	3144	GAGGTTCAAGATACATACATCGATGGAATAATCTTCTTGTACTACAAAGCTAT	3203
QY	3273	TTTAAAGAAAGTGTATGTTGGAGAAAGGCGAAGTTGTACTATATGACATTAATCAAT	3330
Db	3204	TTTAAAGAAAGTGTATGTTGGAGAAAGGCGAAGTTGTACTATATGACATTAATCAAT	3261
RESULT 7			
ADA14866			
ID	ADA14866	standard, cDNA; 3261 BP.	
XX	ADA14866;		
AC			
DT	06-NOV-2003	(first entry)	
XX			
XX			
DE	Human cDNA encoding variant IPMC 150 isoform A.		
XX			
KM	88; gene; human; IPMC 150 isoform A; gene therapy; interphotoreceptor matrix component; IPMC; ocular disorder; macular degeneration; photoreceptor death; retinal detachment.		
XX			
OS	Homo sapiens.		
XX			
FN	Key	Location/Qualifiers	
FT	CDS	128..2443	
XX		/*tag= A	
XX		/product= "Variant IPMC 150 isoform A"	
PD	US2002160954-A1.		
XX			
XX	31-OCT-2002.		

XX 08-NOV-2001; 2001US-00007270.  
PF 29-OCT-1998; 98US-0018392.  
PR 29-OCT-1999; 99US-00430195.  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
PI MPI; 2003-238235/23.  
DR P-PSDB; ADA14667.  
XX  
XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
or retinal detachment.  
XX  
XX Claim 3; Page 63-66; 76pp; English.  
XX  
XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotide, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding  
CC variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
XX  
SQ Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;  
Query Match 62.9%; Score 2094; DB 10; Length 3261;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2574; Conservative 0; Mismatches 0; Indels 4; Gaps 4;  
QY 753 AGATGTGGCAAGCTCTCACTTGGGCTTCCCTCTCACTCTGATGACACCTCTCTCA 812  
DB 688 AGATGTGGCAAGCTCTCACTTGGGCTTCCCTCTCACTCTGATGACACCTCTCTCA 747  
QY 813 TGAATTCCTCGAATATACCTCAAGACACCAAGATGCTTACACGAAGAAGAACGA 872  
DB 748 TGAATTCCTCGAATATACCTCAAGACACCAAGATGCTTACACGAAGAAGAACGA 807  
QY 873 ATTCCTGTGTGAGAGACAGAGGTGAGCTCAGCGTCTCTGTGTAACCAAGAGTT 932  
DB 808 ATTCCTGTGTGAGAGACAGAGGTGAGCTCAGCGTCTCTGTGTAACCAAGAGTT 867  
QY 933 CAAGCAGAGCTCGTCACTCCCAAGTCCCATATTAACAGAGCTTAGAGAAAGTCCA 992  
DB 868 CAAGCAGAGCTCGTCACTCCCAAGTCCCATATTAACAGAGCTTAGAGAAAGTCCA 927  
QY 993 ACTTGAGATGCAAAAGATATTTAAAGAACTTCCAGATTCAAAATAATCAATGTAG 1052  
DB 928 ACTTGAGATGCAAAAGATATTTAAAGAACTTCCAGATTCAAAATAATCAATGTAG 987  
QY 1053 ATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCAGAGATGCACTTACGGCCAT 1112  
DB 988 ATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCAGAGATGCACTTACGGCCAT 1047  
QY 1113 CTTTAAAGACACAGTGCAGAAACAAAAGCCCTGCAAGTGAACCTCTCTTTTGATTC 1172  
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QY 1173 CAACAAATTTGAAAGTGAAGTCTATCATGGAACATGGAAGGAGGACAAACACAGA 1232  
DB 1108 CAACAAATTTGAAAGTGAAGTCTATCATGGAACATGGAAGGAGGACAAACACAGA 1167  
QY 1233 AATCTATCTCAGAGCTACAGACTCAAAAGGTGATCAGCAAGCACTAGAGGAAGACA 1292  
DB 1168 AATCTATCTCAGAGCTACAGACTCAAAAGGTGATCAGCAAGCACTAGAGGAAGACA 1227

QY 1293 AATCTTGAATGAGGAGCAATTCACTTCACTGANGAAATTGCTGATCATCTGCCACTT 1352  
DB 1228 AATCTTGAATGAGGAGCAATTCACTTCACTGANGAAATTGCTGATCATCTGCCACTT 1287  
QY 1353 TGGTCTGACACCCATCAGAGCTGCCACATCTTTGCTGTTATTAACAGAGATGCTAC 1412  
DB 1288 TGGTCTGACACCCATCAGAGCTGCCACATCTTTGCTGTTATTAACAGAGATGCTAC 1347  
QY 1413 TTTGAGTCAGAACTTCTCTGTTGAAACCCAGCTTGAGACAGTGAACGAGACAGACA 1472  
DB 1348 TTTGAGTCAGAACTTCTCTGTTGAAACCCAGCTTGAGACAGTGAACGAGACAGACA 1407  
QY 1473 TGGTCTACCTGACATCTTCTGCTCCACCTGCTATAGGCTTACTCTCTGACAGAC 1532  
DB 1408 TGGTCTACCTGACATCTTCTGCTCCACCTGCTATAGGCTTACTCTCTGACAGAC 1467  
QY 1533 TCCACCTTCTTTTATGAGATCAAGATCTTCTCTGACTGATCAAGGACACAGATAC 1592  
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QY 1593 AATGACCACTGACAGACAAATGCTATGACAGAGGCTCAACATCCACAGATTAATTC 1652  
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DB 1588 TGCATTCAGCCAACTGGCTCTGGGAATTTCAATCCACTGATCTTTCAGATGACAGCG 1647  
QY 1713 ATCAAGTCAGAGTGCAGAAATATGATGACAGACCTAGATGAATAGATCTGTGACAC 1772  
DB 1648 ATCAAGTCAGAGTGCAGAAATATGATGACAGACCTAGATGAATAGATCTGTGACAC 1707  
QY 1773 TCTTCCCATCTGAGATGACAGAGCTCAAGCAATATGTTCTGTCCAGATCATTTCTT 1832  
DB 1708 TCTTCCCATCTGAGATGACAGAGCTCAAGCAATATGTTCTGTCCAGATCATTTCTT 1767  
QY 1833 GAGAGATACCACTCTGTCTCAGCTTTACAGTATATCACCACTAGTTCTATGACATTC 1892  
DB 1768 GAGAGATACCACTCTGTCTCAGCTTTACAGTATATCACCACTAGTTCTATGACATTC 1827  
QY 1893 CCCGAAGGCGAGAGCTGTGATGTTCTTCAAGTGTGATGTTGCTTAAACATGAGCTTTC 1952  
DB 1828 CCCGAAGGCGAGAGCTGTGATGTTCTTCAAGTGTGATGTTGCTTAAACATGAGCTTTC 1887  
QY 1953 CAACGACCTGTTCAACAGAGCTCTCTGAGTACCGAGCTCTGAGCAACATTCACACA 2012  
DB 1888 CAACGACCTGTTCAACAGAGCTCTCTGAGTACCGAGCTCTGAGCAACATTCACACA 1947  
QY 2013 GCTGCTGTTCCATATCTACATCCATCTTAAGATTTTAAGCACTTGAATATCTTAA 2072  
DB 1948 GCTGCTGTTCCATATCTACATCCATCTTAAGATTTTAAGCACTTGAATATCTTAA 2007  
QY 2073 CTTGAGAAACGGGAGTGTGATTGTAATAGCAAAATGAAATTTGCTAAGTCTGTGCCGA 2132  
DB 2008 CTTGAGAAACGGGAGTGTGATTGTAATAGCAAAATGAAATTTGCTAAGTCTGTGCCGA 2067  
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DB 2068 TAACTCAACAAAGCTGTGACAGGGGCTTGGAGATTTTCGTTCTGTGACCCCAACA 2127  
QY 2193 ACTCATCTGGAATATGACAGCTACTCTCAACATTGAACAGCTGATCAAGCAGATTC 2252  
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QY 2253 CTGCAAGTTCTCGGCTCGGCGAATTTGGCCAAATGTTGAAGAAAGCAAGCACTGAGGA 2312  
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QY 2313 AGCGAGTGTGCTGCAACCAAGATATGACAGCAAGGAGGAGCTGGAACGCTGGAACC 2372  
DB 2248 AGCGAGTGTGCTGCAACCAAGATATGACAGCAAGGAGGAGCTGGAACGCTGGAACC 2307  
QY 2373 AGGCTCTGTGCGCTTGACCAAGAGATTCGAGAGTCTTCCAGGGAAGGAGCTCCATG 2432

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DB 2308 AGGCTCTGTGG-CCGGGCAAGAAAGGAGGCTCCGAGGGAAGGAGGCTCCATG 2366
QY 2433 CAGGTGGCAGATCTCTGAAAAATCAGACATACAAAATCTAGTGTAAAAAGTTCCAAA 2492
DB 2367 C-GGTT-CCAGATCACTCTGAAAAATCAGACATACAAAATCTAGTGT-AAAAATTCAAA 2423
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DB 2424 TCAACAAAATTAACAAGTATCATGTAAAGAAATCTGAATTAAGACCGTGAATATGA 2483
QY 2553 AGAATTTAACATCAAGATTGGAAAGAAATTTAAAACTGAAATGTACATTAATCACTT 2612
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QY 2673 GGTCAATCAAAATCCAGACATACAGTCAACATGAGATGACACACACATATTTCAAT 2732
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QY 2853 TGATCATAGCCAGGTTTCTTCAACCTTCCCTGAAAAATTTTACTCAGACATTTGCA 2912
DB 2784 TGATCATAGCCAGGTTTCTTCAACCTTCCCTGAAAAATTTTACTCAGACATTTGCA 2843
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DB 2904 TATGCTAGAAAGTCAATTTAAAGATGATTAACGCGAGAGATGCGAGTCTCTTA 2963
QY 3033 AGCATGATATGATAGTGTAGGACCTGATGAGTATGATATGCTCCACACTAG 3092
DB 2964 AGCATGATATGATAGTGTAGGACCTGATGAGTATGATATGCTCCACACTAG 3023
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DB 3084 TCGTTCATAGTATGATGTTTGTGCGCAATATCTTTGAATGTTCTTTAAAAAGAACT 3143
QY 3213 GAGGTCAGATACATATCAGTAAAGAAATCTTACTTCTTGTAACACAAAGCTAT 3272
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DB 3204 TTTAAAGAAAGTCTATGTTGGAGAAAGGCGAAGTTGATATATGACATATCAAT 3261

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RESULT 8
AAA46328
ID AAA46328 standard; DNA; 2966 BP.
XX
AC AAA46328;
XX
DT 04-SEP-2000 (first entry)
XX
DB Interphotoreceptor matrix proteoglycan (IPM150) splice variant.

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XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KM Chromosome 6q13-q15; ocular disease; retinal detachment;
KM Choroidretinal degeneration; retinal degeneration; cone degeneration;
KM Age related macular degeneration; photoreceptor degeneration;
KM Retinal pigment epithelium degeneration; mucopolysaccharidosis;
KM rod-cone dystrophy; cone-rod dystrophy; ss.
OS
EN Homo sapiens.
PD WO200026367-A2.
PD 11-MAY-2000.
PF 29-OCT-1999; 99WO-US0254440.
PR 29-OCT-1998; 98US-00183972.
PA (IOWA) UNIV IOWA RES FOUND.
PI Hageman GS, Kuehn MH;
DR WPI; 2000-365616/31.
XX The present sequence represents a splice variant of an interphotoreceptor
XX matrix (IPM) proteoglycan, designated IPM150. The sequence is missing
XX exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs,
XX IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome
XX 6q13-q15, between markers CHL1, GATA11F10 and D6S284. The IPM proteins may
XX be used to supplement a patient's own production of the protein or to
XX rectify alterations in their nucleic acids that result in expression of
XX an inactive protein. The IPM nucleic acids may be used in this way to
XX treat ocular diseases such as retinal detachment, choroidretinal
XX degeneration, retinal degeneration, age related macular degeneration,
XX photoreceptor degeneration, RPE (retinal pigment epithelium)
XX degeneration, cone degeneration, mucopolysaccharidosis, rod-cone
XX dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also
XX be used to assay for other modulators of IPM proteoglycan expression and
XX activity that may be used to treat ocular diseases. The nucleic acids and
XX proteins may also be used as diagnostic reagents to detect the presence
XX of IPM nucleic acids and their products in samples from patients
XX according to standard methodologies
SQ
Sequence 2966 BP; 918 A; 687 C; 624 G; 737 T; 0 U; 0 Other;
Query Match 59.8%; Score 1992; DB 3; Length 2966;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2572; Conservative 0; Mismatches 2; Indels 4; Gaps 4;
QY 753 AGATGTTGCCAAGCTCACTTGGGCTTCCCTCTCACTCTGATGACACCCCTCTCAA 812
DB 310 AGATGTTGCCAAGCTCACTTGGGCTTCCCTCTCACTCTGATGACACCCCTCTCAA 369
QY 813 TGAATTTCTGATATATCACTCAACGACACCAAGATGCTTACACAGAAAGAAACAG 872
DB 370 TGAATTTCTGATATATCACTCAACGACACCAAGATGCTTACACAGAAAGAAACAG 429
QY 873 ATTGCTGTGTTGAGAGACAGAGGTTGAGAGTCAAGCTCTCTCTGTTAAACAGAAATT 932
DB 430 ATTGCTGTGTTGAGAGACAGAGGTTGAGAGTCAAGCTCTCTCTGTTAAACAGAAATT 489
QY 933 CAAGGACAGAGCTCGTCACTCCAGTCCCAATTTACACAGAGCTTACAGAGAAAGTCCCA 992
DB 490 CAAGGACAGAGCTCGTCACTCCAGTCCCAATTTACACAGAGCTTACAGAGAAAGTCCCA 549
QY 993 ACTTCAGATGCAAAAGATATTTAAGAAATTTCCAGATTCAAAATTCATGTTAG 1052

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Db 610 ATTTAGACCAAGAAAGAAAGATGGCTTCAGAGATGCCAATTACGGCCAT 669  
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QY 1353 TGGTCTGACACCCATCAGAGCTGCCACATCTTTTGTGTTATAACAGAGATCTAC 1412  
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QY 1593 AATGGCATTGACAGACATGCTAGTACAGAGGCTCACATCCCAAGATGATTTATTC 1652  
Db 1150 AATGGCATTGACAGACATGCTAGTACAGAGGCTCACATCCCAAGATGATTTATTC 1209  
QY 1653 TGCATCAGCCAACTGGCTCTGGGAATTCACATCCACCTGCATCTTCAGATGACAGCGG 1712  
Db 1210 TGCATCAGCCAACTGGCTCTGGGAATTCACATCCACCTGCATCTTCAGATGACAGCGG 1269  
QY 1713 ATCAAGTCAGAGTGGGAGATATGCTCAGACACCTAGATGAATGATCTGTGACAC 1772  
Db 1270 ATCAAGTCAGAGTGGGAGATATGCTCAGACACCTAGATGAATGATCTGTGACAC 1329  
QY 1773 TCCCTGCCATCTGAGGTACAGAGCTCAGCAATATGTTTCTGTCCAGATCATTTCTT 1832  
Db 1330 TCCCTGCCATCTGAGGTACAGAGGCTCAGCAATATGTTTCTGTCCAGATCATTTCTT 1389  
QY 1833 GGAAGATACCACTCTCTGTCTCAGCTTTAAGATATACCACTAGTCTTATGACATTCG 1892  
Db 1390 GGAAGATACCACTCTCTGTCTCAGCTTTAAGATATACCACTAGTCTTATGACATTCG 1449  
QY 1893 CCCCAAGGGCGAGAGCTGATGTTCTTCAGTCTGAGTGTGCTTAAATGAGCCCTTCC 1952  
Db 1450 CCCCAAGGGCGAGAGCTGATGTTCTTCAGTCTGAGTGTGCTTAAATGAGCCCTTCC 1509  
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Db 1510 CAAGCACTGTTCAACAAGAGCTCTCTGAGATACCGAGCTCTGAGCACAATTCACACA 1569  
QY 2013 GCTGCTGTTCCATATCTACATCCAACTCTTACAGATTTAAGCACTTGAATACTTAA 2072  
Db 1570 GCTGCTGTTCCATATCTACATCCAACTCTTACAGATTTAAGCACTTGAATACTTAA 1629  
QY 2073 CTTTCAGAAACGGGAGTGTATGTAATGCAAAATGAAGTTGCTAGTCTGTGCGGTA 2132  
Db 1630 CTTTCAGAAACGGGAGTGTATGTAATGCAAAATGAAGTTGCTAGTCTGTGCGGTA 1689

QY 2133 TAACCTCACCAGGCTGTGACAGGGGCTTGGAGATTTTCGTTGCTGACGCCACA 2192  
Db 1690 TAACCTCACCAGGCTGTGACAGGGGCTTGGAGATTTTCGTTGCTGACGCCACA 1749  
QY 2193 ACTCCATCTGAAATATGACAGCTACTCTCAACATTTGAACAGAGCTATCAAGCAATCC 2252  
Db 1750 ACTCCATCTGAAATATGACAGCTACTCTCTCAACATTTGAACAGAGCTATCAAGCAATCC 1809  
QY 2253 CTGCAAGTCTGAGCTGTGCGGCAATTTGCCCCAATGTGTAAAGAACGAGCTGAGGA 2312  
Db 1810 CTGCAAGTCTGAGCTGTGCGGCAATTTGCCCCAATGTGTAAAGAACGAGCTGAGGA 1869  
QY 2313 AGCGAGTGTGCTGTCAACACAGATATGACACCCAGGGGAGCTGTGACGTTGGAACC 2372  
Db 1870 AGCGAGTGTGCTGTCAACACAGATATGACACCCAGGGGAGCTGTGACGTTGGAACC 1929  
QY 2373 AGGCTCTGTGCGCCGTGGCAAAAGGATGCGAGGCTCTCAGGGGAAAGGGAGCTTCATG 2432  
Db 1930 AGGCTCTGTGCGCCGTGGCAAAAGGATGCGAGGCTCTCAGGGGAAAGGGAGCTTCATG 1988  
QY 2433 CAGTTTGCAGATCACTGTGAAATCAAGCATACAAACTAGTGTAAAGTTCCAAA 2492  
Db 1989 C-GGTT-CCAGTCACTGTGAAATCAAGCATACAAACTAGTGT-AAAAGTTCCAAA 2045  
QY 2493 TCAACAAATTAACAAGTATCATGTPAAGAAATCTGAATTAAGCCGTAGAAATAGA 2552  
Db 2046 TCAACAAATTAACAAGTATCATGTPAAGAAATCTGAATTAAGCCGTAGAAATAGA 2105  
QY 2553 AGAATTTAACCTCAAGATTTGGAGAGAAATTTAAACAGAAATGTACATTAATCACTT 2612  
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QY 2673 GGTCAATCAAAATCCAGCATACATGTCACACGTGAATTCAGCAACACCATATTCMAAT 2732  
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QY 3033 ACGCATATGATATGATGTGTAGGACCTGATGAGTATATATGTCTCACAATAAG 3092  
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QY 3093 TCTGATTAACAACAACCTCAGATTAAGTATTTAGGACACATAGTTTATATAGCAATAC 3152  
Db 2646 TCTGATTAACAACAACCTCAGATTAAGTATTTAGGACACATAGTTTATATAGCAATAC 2705  
QY 3153 TGTTCATATAGTACTTTTGTGTCCAATATCTTTGAATTTGTTCTTTTAAAGAAACT 3212  
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Db      1190 TTCCAAAGAAATGGAAGAGAGATCTATCATGGAACCATGAGAGAGAGACAGAACCC 1249
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      1430 TACTTGAATCCAGAACTTCTCTCTGTTGAACCCAGCTTGAGACAGTGAACGAGACAGA 1489
      1470 GGATGGTCTACCGTACACTTCTGCTCTGATGAGCTGATGAGCTGATGAGCTGCTCTGTCAGA 1529
      1490 GGATGGTCTACCGTACACTTCTGCTCTGATGAGCTGATGAGCTGATGAGCTGCTCTGTCAGA 1548
      1530 AGCTCACCTTTCTTATGAGCATCAAGACATCTTCTCTGATGATCAAGGACACACAGA 1589
      1549 AGCTCACCTTTCTTATGAGCATCAAGACATCTTCTCTGATGATCAAGGACACACAGA 1608
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      1830 CTTGAGAGATACCACTCTGCTCTGAGCTTACAGATATACCACTAGTCTGATGACAT 1889
      1849 CTTGAGAGATACCACTCTGCTCTGAGCTTACAGATATACCACTAGTCTGATGACAT 1908
      1890 TGCCCCCAAGGGCCGAGAGCTGTAGTGTCTTCACTGCTGCGTGTGCTAAACATGCGCTT 1949
      1909 TGCCCCCAAGGGCCGAGAGCTGTAGTGTCTTCACTGCTGCGTGTGCTAAACATGCGCTT 1968
      1950 CTCACAAGACCTGTTCAACAGAGCTCTCTGAGATACCGAGCTCTGAGCAACAATTCAC 2009
      1969 CTCACAAGACCTGTTCAACAGAGCTCTCTGAGATACCGAGCTCTGAGCAACAATTCAC 2028
      2010 AAGAGCTGCTGTTCCATATCTACGATCCATCTTACAGAGATTTAAGCACTTGAATACT 2069
      2039 AAGAGCTGCTGTTCCATATCTACGATCCATCTTACAGAGATTTAAGCACTTGAATACT 2088
      2070 TAACTTCAAGAAACGGGAGTGTGATTTGTAATGACAAATGAAGTTTGTCTGCTGCGC 2129
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      2130 GTATAAAGCTCAGCAAGGCTGTGACAGGAGCTTGGAGATTTTGTCTGCTGACGCCA 2189
      2149 GTATAAAGCTCAGCAAGGCTGTGACAGGAGCTTGGAGATTTTGTCTGCTGACGCCA 2208
      2190 ACAAATCTCTGGAATATGACAGTACTCTCTC 2223
      2209 ACAAATCTCTGGAATATGACAGTACTCTCTC 2242

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RESULT 10

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ACC57948
ID ACC57948 standard; cDNA; 2244 BP.
XX
AC ACC57948;
XX
DT 11-AUG-2003 (first entry)
XX
DB Human Interphotoreceptor matrix IPM 150, isoform C, cDNA.
XX
KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW receptor; ophthalmological; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
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FT /*product= "IPM 150"
FT sig_peptide 151..210
FT /*tag= b
FT /*tag= 265..267
FT /*tag= c
FT /*note= "encodes Pro"
FT 346..348
FT /*tag= d
FT /*note= "encodes His"
XX
PN WO2003039346-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002MO-US036090.
XX
PR 08-NOV-2001; 2001US-00077270.
XX
PA (IOWA ) UNIV IOWA RES FOUNO.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2003-441440/41.
XX
DR P-PSDB; ABR42344.
XX
PT New interphotoreceptor matrix proteins and polynucleotides, useful for
PT treating or preventing photoreceptor death or retinal detachment, or for
PT treating ocular disorders.
XX
PS Claim 1; Page 79-80; 105pp; English.
XX
CC The present sequence is that of cDNA encoding isoform C of novel human
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
CC is located on chromosome 6q13-q15, a region that also contains loci for
CC progressive bilateral chorioretinal atrophy, autosomal dominant Stargardt's
CC -like macular dystrophy, North Carolina macular dystrophy and Salla
CC disease. Members of the IPMC gene family have been identified in humans,
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
CC antibodies that specifically bind the polypeptides, and vectors
CC comprising the polynucleotides. A claimed method of treating or
CC preventing photoreceptor death or retinal detachment involves
CC administering an IPMC polynucleotide, polypeptide or antibody. Also
CC claimed is a method for identifying a compound capable of modulating IPMC
CC gene expression
XX
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
XX
Query Match 45.1%; Score 1503; DB 9; Length 2244;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2123; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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90 TCTGTGATTTGTTATCAGAAATACCAATGACAGAAAGCAGAGATGTTGGAACTAGAA 149

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Db 110 TCTGTATTGTTATCAGATTACCAATGACAAAAGCCAGAAATGATTGAAACATGAA 169  
Qy 150 GAGCAATTTTGTGTTTGGATTTTCTCCAGTTCAAGAAACCAAGATATCTCATTA 209  
Db 170 GAGCAATTTTGTGTTTGGATTTTCTCCAGTTCAAGAAACCAAGATATCTCATTA 229  
Qy 210 ACAATATCATTTCTGAAACCTAAAGACATAGACATCCCCAAGAAATGAAACACTGAA 269  
Db 230 ACAATATCATTTCTGAAACCTAAAGACATAGACATCCCCAAGAAATGAAACACTGAA 289  
Qy 270 GTAATGAAAAATGTAACAAATGTCAACTATAGACGAATVTTGATTTGGCAAGCATC 329  
Db 290 GTAATGAAAAATGTAACAAATGTCAACTATAGACGAATVTTGATTTGGCAAGCATC 349  
Qy 330 GAACAAAAAGATCCGATTTTCCCAAGGGGGTTAAAGTCTGTCCACAGGAATCCATGA 389  
Db 350 GAACAAAAAGATCCGATTTTCCCAAGGGGGTTAAAGTCTGTCCACAGGAATCCATGA 409  
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Db 410 AACAGATTTTAAACAGTCTTCAAGCTTATATAGATTGAGTGTGAGAAAGCATAT 469  
Qy 450 GGGAAACATATCGGATCTTTCTGATCGATCCCTGACACAGGGGAATATCAGACTGG 509  
Db 470 GGGAAACATATCGGATCTTTCTGATCGATCCCTGACACAGGGGAATATCAGACTGG 529  
Qy 510 TCGATCTTGCACAGAGGAGACCTTGTGCTCTTTGACATTTGAAAAAACTTCAGCAT 569  
Db 530 TCGATCTTGCACAGAGGAGACCTTGTGCTCTTTGACATTTGAAAAAACTTCAGCAT 589  
Qy 570 CCCAGAGACCTGATCTTCTCCAGCAGAGAAATAAACAGAGATTTCCCTGACAGA 629  
Db 590 CCCAGAGACCTGATCTTCTCCAGCAGAGAAATAAACAGAGATTTCCCTGACAGA 649  
Qy 630 AAGATGAAATATCTGACAGAGAAACATTTGGAGAGCTGTGTAAACCATTTGATTCAT 689  
Db 650 AAGATGAAATATCTGACAGAGAAACATTTGGAGAGCTGTGTAAACCATTTGATTCAT 709  
Qy 690 CAGCAATCTACATTTCAAGACCTTGGGAGATTTCTAAGAAAACTTCAGAAAGCAAT 749  
Db 710 CAGCAATCTACATTTCAAGACCTTGGGAGATTTCTAAGAAAACTTCAGAAAGCAAT 769  
Qy 750 TCAAGATTTGCGAACAGTCTCACTTGGGCTTTCCCTCTCACTCTGATGACACCTCT 809  
Db 770 TCAAGATTTGCGAACAGTCTCACTTGGGCTTTCCCTCTCACTCTGATGACACCTCT 829  
Qy 810 CAATGAAATTTCTGATATATCACTCAACGACACCAAGATGCTTACCAAGAAAGAAAC 869  
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Qy 930 GTTCAAGGAGAGCTGCTGATCCCAAGTCCCAATTTACCAAGAGCTGACAGAAAGTC 989  
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Db 1010 CCAACTTCAGATGCAAAAGATATTTAAGAACTTCCAGATTCAAAAAATCATGTGTT 1069  
Qy 1050 AAGATTTTAAACCAAGAAAGAAAGAAATGCTCAAGCTCAACAGAGATGCAACTTACG 1109  
Db 1070 AAGATTTTAAACCAAGAAAGAAAGAAATGCTCAAGCTCAACAGAGATGCAACTTACG 1129  
Qy 1110 CATCTTTAAGAGACAGAGTGCAGAAAGCAAAAGCCCTGCAAGTGAACCTCTGTCTTTGA 1169  
Db 1130 CATCTTTAAGAGACAGAGTGCAGAAAGCAAAAGCCCTGCAAGTGAACCTCTGTCTTTGA 1189  
Qy 1170 TTCACAAAAATTTGAAAGTGAAGAGTCTATCATGGAACCATGAGAGAGACAAAGCAAC 1229  
Db 1190 TTCACAAAAATTTGAAAGTGAAGAGTCTATCATGGAACCATGAGAGAGACAAAGCAAC 1249

Qy 1230 AGAAATCTATCTCAAGCTTACAGACCTGAAAAGCTGATCAAGCAAAAGCACTAGAGGAAGA 1289  
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Qy 1350 CTTTGTCTCTGACACCCATCAAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1409  
Db 1370 CTTTGTCTCTGACACCCATCAAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1429  
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Qy 1590 TACATGAGCACTGACCAAGACAAATGCTAGTACAGAGGCTCACATCCCCACAGATTA 1649  
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Qy 1650 TTCTGCATTCAGACCACTGAGCTTGGGAATTTTCACTCACTGTGATCTTCAGATGACAG 1709  
Db 1669 TTCTGCATTCAGACCACTGAGCTTGGGAATTTTCACTCACTGTGATCTTCAGATGACAG 1728  
Qy 1710 CCGATCAAGTGAAGTGGCGAAGATATGTCAGACACCTAATGAAATGATCTGTCTGA 1769  
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Qy 1770 CACTCTGCCCCATCTGAGGTACCAAGAGCTCAGAGAAATATGTTCTGTCCAGATCATTT 1829  
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Qy 2130 GTATTAACCTCAACAAAGGCTGTGACAGGGGCTTGGAGAAATTTTGTCTGTGACGCCA 2189  
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Db 2209 ACAACTCCATCTGAAATATGACAGCTACTCTC 2242

RESULT 11  
AD14844  
ID AD14844 standard; cDNA; 2244 BP.

XX ADAl4844;  
AC  
XX 06-NOV-2003 (first entry)  
XX  
XX  
DE Human Interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.  
XX  
XX ss; gene; human; IPMC 150 isoform C; gene therapy;  
XX Interphotoreceptor matrix component; IPMC; ocular disorder;  
XX macular degeneration; photoreceptor death; retinal detachment.  
XX  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 151..747  
FT /tag= b  
FT /product= "IPMC 150 isoform C"  
FT sig\_peptide 151..200  
FT /tag= a  
FT /note= "Signal sequence"  
FT mat\_peptide 201..744  
FT /tag= c  
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FT /note= "Encodes Pro"  
FT unsure 346..348  
FT /tag= e  
FT /note= "Encodes His"  
XX  
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XX  
XX 31-OCT-2002.  
XX  
XX 08-NOV-2001; 2001US-00007270.  
XX  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Hageman GS, Kuehn MH;  
XX  
XX WPI; 2003-238235/23.  
XX P-PSDB; ADAl4845.  
XX  
XX  
XX New isolated or recombinant interphotoreceptor matrix component  
XX polynucleotide and polypeptide, useful for diagnosing, preventing,  
XX treating or prognosticating ocular disorders, e.g. macular degeneration  
XX or retinal detachment.  
XX  
XX Claim 3; Page 36-37; 76pp; English.  
XX  
XX The invention relates to an isolated or recombinant interphotoreceptor  
XX matrix component (IPMC) polynucleotide. Also disclosed is a vector  
XX comprising a promoter of an interphotoreceptor matrix component (IPMC)  
XX gene operatively linked to the IPMC polynucleotide. The IPMC  
XX polynucleotide, polypeptides and antibodies are useful for diagnosing,  
XX preventing, treating or prognosticating ocular disorders, e.g. macular  
XX degeneration, photoreceptor death or retinal detachment. They are also  
XX useful for identifying a compound capable of modulating IPMC gene  
XX expression in a cell. The present sequence represents cDNA encoding human  
XX interphotoreceptor matrix component, IPMC, 150 isoform C.  
XX  
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;

Query Match 45.1%; Score 1503; DB 10; Length 2244;  
Best Local Similarity 99.5%; Freq. No. 0;  
Matches 2123; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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DB 170 GAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAGAGAACCAAGATATCTCATTA 229  
QY 210 ACATATACCATCTGAAACTAAAGCATAGACATCCCAAGAAATGAAACAAGTAA 269  
DB 230 ACATATACCATCTGAAACTAAAGCATAGACATCCCAAGAAATGAAACAAGTAA 289  
QY 270 GTACTGAAAAATGTACAAAATGTCACTATGAGACGAATATTCGATTTGGCAAGCATC 329  
DB 290 GTACTGAAAAATGTACAAAATGTCACTATGAGACGAATATTCGATTTGGCAAGCATC 349  
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QY 1170 TTCCAACAAAATTTGAAATGAGAGAGTATCATGGAACCAATGAGAGAGCAACCAACC 1229  
DB 1190 TTCCAACAAAATTTGAAATGAGAGAGTATCATGGAACCAATGAGAGAGCAACCAACC 1249

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QY 1230 AGAAATCTATCTCAGAGCTACAGACCTCAAAGGCTGATCAGCAAGCACTAGAGGAAGA 1289
DB 1250 AGAAATCTATCTCAGAGCTACAGACCTCAAAGGCTGATCAGCAAGCACTAGAGGAAGA 1309
QY 1280 ACAATCTTTGGATGTGGGGCAATTCAGTTCACTGATGAAATTTGCTGATCATCTGCCAGC 1349
DB 1310 ACAATCTTTGGATGTGGGGCAATTCAGTTCACTGATGAAATTTGCTGATCATCTGCCAGC 1369
QY 1350 CTTTGTCTCTGACACCCCAATCAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1409
DB 1370 CTTTGTCTCTGACACCCCAATCAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1429
QY 1410 TACTTGTAGTCCAGAACTTCTCTGTGTAACCCAGCTTGAGAGAGTGAAGAGCAGAGA 1469
DB 1430 TACTTGTAGTCCAGAACTTCTCTGTGTAACCCAGCTTGAGAGAGTGAAGAGCAGAGA 1489
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DB 1490 GCATGCTCTACCTGACACTTTCTTGGTCTCCACCTGTTATGGCTCTTACTCTCTGTGAGA 1548
QY 1530 AGCTCACCTTTCTTTATGGCAATCAAGCACTTTCTCTGACCTGATCAAGGACGACAGA 1589
DB 1549 AGCTCACCTTTCTTTATGGCAATCAAGCACTTTCTCTGACCTGATCAAGGACGACAGA 1608
QY 1590 TACAATGGCACTGACAGACCAATGCTAGTACCAAGGCTCACCATCCCAACGATGATTA 1649
DB 1609 TACAATGGCACTGACAGACCAATGCTAGTACCAAGGCTCACCATCCCAACGATGATTA 1668
QY 1650 TTCTGCAATCAGCACTGGCTCTGGGAATTTTCACTCCACTGCACTTTCAGATGACAG 1709
DB 1669 TTCTGCAATCAGCACTGGCTCTGGGAATTTTCACTCCACTGCACTTTCAGATGACAG 1728
QY 1710 CCGATCAAGTGAAGGAGGAGGAGATATGGTCAAGACCACTAGATGAAATGGATCTGTGGA 1769
DB 1729 CCGATCAAGTGAAGGAGGAGGAGATATGGTCAAGACCACTAGATGAAATGGATCTGTGGA 1788
QY 1770 CACTCTGCCCCATCTGAGGTAACAGAGCTCAGCGAATATGTTTCTGTCTCCAGATCATTT 1829
DB 1789 CACTCTGCCCCATCTGAGGTAACAGAGCTCAGCGAATATGTTTCTGTCTCCAGATCATTT 1848
QY 1830 CTTTGGAGATACCACTCTGTCTCAGCTTTTACAGTATATCAACCACTAGTTCTATGACAT 1889
DB 1849 CTTTGGAGATACCACTCTGTCTCAGCTTTTACAGTATATCAACCACTAGTTCTATGACAT 1908
QY 1890 TGGCCCAAGGGGCGAGAGCTGGTAGTCTTCTCAGTCTGCGCTGGTGTCAATGAGCTT 1949
DB 1909 TGGCCCAAGGGGCGAGAGCTGGTAGTCTTCTCAGTCTGCGCTGGTGTCAATGAGCTT 1968
QY 1950 CTCGAACGACTGTTCACAGAAGCTCTCTGAGTACCGAGCTCTGAGCAACAATTCAC 2009
DB 1969 CTCGAACGACTGTTCACAGAAGCTCTCTGAGTACCGAGCTCTGAGCAACAATTCAC 2028
QY 2010 ACAGCTGCTGCTTCATATCTAGATTCATCTTACAGAGATTTTAAAGCACTTGAAATACT 2069
DB 2029 ACAGCTGCTGCTTCATATCTAGATTCATCTTACAGAGATTTTAAAGCACTTGAAATACT 2088
QY 2070 TAACTTCAGAAACGGAGGTGATGTTGTAATAGCAAAATGAAGTTGCTAAAGTCTGTGCC 2129
DB 2089 TAACTTCAGAAACGGAGGTGATGTTGTAATAGCAAAATGAAGTTGCTAAAGTCTGTGCC 2148
QY 2130 GTATTAACCTCACCAGAGCTGTGACCGGGTCTTGGAGATTTTCTTCTGTCTGACGCCA 2189
DB 2149 GTATTAACCTCACCAGAGCTGTGACCGGGTCTTGGAGATTTTCTTCTGTCTGACGCCA 2208
QY 2190 ACAACTTCATCTGGAATATGACAGCTACTCTCTC 2223
DB 2209 ACAACTTCATCTGGAATATGACAGCTACTCTCTC 2242

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RESULT 12  
 AAA46327  
 ID AAA46327 standard; DNA; 1858 BP.  
 XX

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AC AAA46327;
XX
DT 04-SEP-2000 (first entry)
XX
DE Exon 1 and promoter of Interphotoreceptor matrix proteoglycan, IPM150.
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW chromosome 6q13-q15; ocular disease; retinal detachment;
KW choroidretinal degeneration; retinal degeneration; cone degeneration;
KW age related macular degeneration; photoreceptor degeneration;
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;
KW rod-cone dystrophy; cone-rod dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO200026367-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025440.
XX
PR 29-OCT-1998; 98US-00183972.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI, 2000-365616/31.
XX
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT preventing, diagnosing and treating ocular disorders such as retinal
PT detachment and choroidretinal degeneration.
XX
PS Claim 3; Fig 17; 183bp; English.
XX
XX
CC The present sequence represents exon 1 and the promoter of human DNA
CC encoding interphotoreceptor matrix (IPM) proteoglycan, designated IPM150.
CC The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150
CC and IPM200, exist. The human IPM150 gene is located on chromosome 6q13-
CC q15, between markers CHLC.GAT11P10 and D6S284. The IPM proteins may be
CC used to supplement a patient's own production of the protein or to rectify
CC alterations in their nucleic acids that result in expression of an
CC inactive protein. The IPM nucleic acids may be used in this way to treat
CC ocular diseases such as retinal detachment, choroidretinal degeneration,
CC retinal degeneration, age related macular degeneration, photoreceptor
CC degeneration, RPE (retinal pigment epithelium) degeneration, cone
CC degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod
CC dystrophy. The nucleic acids and proteins may also be used to assay for
CC other modulators of IPM proteoglycan expression and activity that may be
CC used to treat ocular diseases. The nucleic acids and proteins may also be
CC used as diagnostic reagents to detect the presence of IPM nucleic acids
CC and their products in samples from patients according to standard
CC methodologies
XX
SQ Sequence 1858 BP; 667 A; 293 C; 316 G; 581 T; 0 U; 1 Other;
XX
XX
Query Match 5.9%; Score 197; DB 3; Length 1858;
Best Local Similarity 100.0%; Pred. No. 3.7e-85;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAACCAAGAGGTTATCTCATCATCTGGATCAATATATATTTTTCACATTTTC 60
DB 1070 TAAACCAAGAGGTTATCTCATCATCTGGATCAATATATATTTTTCACATTTTC 1129
QY 61 TGTTAATTTTATGAGATTTGAGGTTCTCTGATTTGTTATTCAGAAATTCAGATGCAC 120
DB 1130 TGTTAATTTTATGAGATTTGAGGTTCTCTGATTTGTTATTCAGAAATTCAGATGCAC 1189
QY 121 AAAAGCCAGAAATGTTTGGAAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCA 180
DB 1190 AAAAGCCAGAAATGTTTGGAAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCA 1249
QY 181 AGTTCAGAGAACCAAG 197

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Db      1250 AGTTCAGGAACCAAG 1266
|||||
RESULT 13
ACC57949
ID ACC57949 standard; DNA; 1858 BP.
XX ACC57949;
XX ACC57949;
XX 11-AUG-2003 (first entry)
XX
DE Human interphotoreceptor matrix IPM 150 gene regulatory region.
XX
KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW receptor; ophthalmological; gene therapy; promoter; ss.
XX
OS Homo sapiens.
XX WO2003039346-A2.
XX
PD 15-MAY-2003.
PF 08-NOV-2002; 2002WO-US0360930.
PR 08-NOV-2001; 2001US-00077270.
PA (IOWA ) UNIV IOWA RES FOUND.
PI Hageman GS, Kuehn MH;
PI WPI; 2003-441440/41.
XX
PT New interphotoreceptor matrix proteins and polynucleotides, useful for
PT treating or preventing photoreceptor death or retinal detachment, or for
PT treating ocular disorders.
XX
XX Claim 12; Page 80-81; 105pp; English.
XX
CC The present sequence is that of the regulatory region of the human human
CC interphotoreceptor matrix 150 (IPM 150) gene on chromosome 6q13-q15. This
CC chromosomal region also contains loci for progressive bilateral
CC choriorretinal atrophy, autosomal dominant Starckard's-like macular
CC dystrophy, North Carolina macular dystrophy and Salla disease. IPM 150 is
CC a member of the newly identified interphotoreceptor matrix component
CC (IPMC) gene family. Members of the IPMC gene family have been identified
CC in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
CC subfamilies are designated IPM 150 (or IMPG1) and IPM 200 (or IMPG2). The
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
CC antibodies that specifically bind the polypeptides, and vectors
CC comprising the polynucleotides, including claimed vectors in comprising a
CC promoter obtained from the present sequence. A claimed method of treating
CC or preventing photoreceptor death or retinal detachment involves
CC administering an IPMC polynucleotide, polypeptide or antibody. Also
CC claimed is a method for identifying a compound capable of modulating IPMC
CC gene expression
XX
SQ Sequence 1858 BP; 667 A; 293 C; 316 G; 581 T; 0 U; 1 Other;

Query Match          5.9%; Score 197; DB 9; Length 1858;
Best Local Similarity 100.0%; Pred. No. 3,7e-85;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TAAACCAAGAAGGTATCTCATCATCGATCATCATATATATATTTTGCATTTTC 60
DB TAAACCAAGAAGGTATCTCATCATCGATCATCATATATATATTTTGCATTTTC 11290
OY TGTTACTTTTTTAATAGATTGGAGTGTTCTGTGATGTTATCAGATTACCAATGCAC 120
DB TGTTACTTTTTTAATAGATTGGAGTGTTCTGTGATGTTATCAGATTACCAATGCAC 11890
OY AAAAGCCGAATGATTTTGGAAACTGAGAAGACTATTTTGTGTTTGGATTTTTCGCA 180

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Dd	1190	AAAAGCCAGATGTATTGGAAACTAGAAGGCTATTTTTGTTCGATTTCCTCCA	1249
Oy	181	AGTTCAGGAACCAAG	197
Dd	1250	AGTTCAGGAACCAAG	1266
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XX	ADAL4846	standard; cDNA; 1858 BP.	
XX	AC		
XX	ADAL4846;		
DT	06-NOV-2003	(first entry)	
DE	Human interphotoreceptor matrix component, IPMC, 150 regulatory region.		
XX			
KW	human; IPMC 150; gene therapy; interphotoreceptor matrix component; IPMC;		
KW	ocular disorder; macular degeneration; photoreceptor death;		
KW	retinal detachment; ds.		
XX			
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FH	promoter	1..1069	
FT		/*tag= a	
FT		/note= "Upstream IPM 150 promoter sequence"	
FT	exon	1070..1266	
FT		/*tag= b	
FT		/number= 1	
PN	US2002160954-A1.		
PD	31-OCT-2002.		
XX			
PF	08-NOV-2001; 2001US-00007270.		
XX			
PR	29-OCT-1998; 98US-00183972.		
PR	29-OCT-1999; 99US-00430195.		
XX			
PA	(IOWA ) UNIV IOWA RES FOUND.		
P1	Hageman GS, Kuehn MH;		
DR	WPI; 2003-238235/23.		
XX			
PT	New isolated or recombinant interphotoreceptor matrix component		
PT	polynucleotide and polypeptide, useful for diagnosing, preventing,		
PT	treating or prognosticating ocular disorders, e.g. macular degeneration		
XX	or retinal detachment.		
PS	Claim 12; Page 38-39; 76pp; English.		
XX			
CC	The invention relates to an isolated or recombinant interphotoreceptor		
CC	matrix component (IPMC) polynucleotide. Also disclosed is a vector		
CC	comprising a promoter of an interphotoreceptor matrix component (IPMC)		
CC	gene operatively linked to the IPMC polynucleotide. The IPMC		
CC	polynucleotides, polypeptides and antibodies are useful for diagnosing,		
CC	preventing, treating or prognosticating ocular disorders, e.g. macular		
CC	degeneration, photoreceptor death or retinal detachment. They are also		
CC	useful for identifying a compound capable of modulating IPMC gene		
CC	expression in a cell. The present sequence represents cDNA encoding human		
CC	interphotoreceptor matrix component, IPMC, 150 regulatory region.		
SO	Sequence 1858 BP; 667 A; 293 C; 316 G; 581 T; 0 U; 1 Other;		
<hr/>			
Oy	Query Match	5.9%; Score 197; DB 10; Length 1858;	
	Best Local Similarity	100.0%; Pred. No. 3.7e-85;	
Dd	Matches 197; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
<hr/>			
Oy	1	TAAACCAAGAGTGTTATCCTCATCATCTGGTATCATATATTAATTTTTCACATTTTC	60
Dd	1070	TAAACCAAGAGTGTTATCCTCATCATCTGGTATCATATATTAATTTTTCACATTTTC	1129

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Qy 61 TGTACTTTTATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTACCAATGAC 120
Db 1130 TGTACTTTTATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTACCAATGAC 1189
Qy 121 AAAAGCCAGAAATGATTTTGGAAACTGAAAGACTATTTTGTGTTTGGATTTTCTCCA 180
Db 1190 AAAAGCCAGAAATGATTTTGGAAACTGAAAGACTATTTTGTGTTTGGATTTTCTCCA 1249
Qy 181 AGTTCAGGAGACCAAG 197
Db 1250 AGTTCAGGAGACCAAG 1266

RESULT 15
AAA46204
ID AAA46204 standard; cDNA, 555 BP.
XX
AC AAA46204;
XX
DT 04-SBP-2000 (first entry)
XX
DE cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW chromosome 6q13-q15; ocular disease; retinal detachment;
KW choriorretinal degeneration; retinal degeneration; cone degeneration;
KW age related macular degeneration; photoreceptor degeneration;
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;
KW rod-cone dystrophy; cone-rod dystrophy; ss.
XX
OS Macaca sp.
XX
PN MO200026367-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025440.
XX
PR 29-OCT-1998; 98US-00183972.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hagaman GS, Kuehn MH;
XX
DR MPI: 2000-365616/31.
XX
P-PSDB; AAY93335.
XX
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT preventing, diagnosing and treating ocular disorders such as retinal
PT detachment and choriorretinal degeneration.
XX
PS Claim 2, Fig 2, 183pp; English.
XX
XX
CC The present sequence encodes an interphotoreceptor matrix (IPM)
CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).
CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
CC is located on chromosome 6q13-q15, between markers CHC.GAT11P10 and
CC D6S284. The IPM proteins may be used to supplement a patient's own
CC production of the protein or to rectify alterations in their nucleic
CC acids that result in expression of an inactive protein. The IPM nucleic
CC acids may be used in this way to treat ocular diseases such as retinal
CC detachment, choriorretinal degeneration, retinal degeneration, age related
CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment
CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
CC also be used to assay for other modulators of IPM proteoglycan expression
CC and activity that may be used to treat ocular diseases. The nucleic acids
CC and proteins may also be used as diagnostic reagents to detect the
CC presence of IPM nucleic acids and their products in samples from patients
CC according to standard methodologies
XX
SQ Sequence 555 BP; 162 A; 131 C; 131 G; 131 T; 0 U; 0 Other;

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Query Match 3.4%; Score 112; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.3e-43;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 403 CAGTCTTCAAGCTTATTTATGATTGAGGTGTGTCAGAGACGATATGGAAAGCATATCG 462
Db 60 CAGTCTTCAAGCTTATTTATGATTGAGGTGTGTCAGAGACGATATGGAAAGCATATCG 119
Qy 463 GATCTTCTGATGATCGATCCCTGACACAGGGGAAATATCAGACTGGGTCAAG 514
Db 120 GATCTTCTGATGATCGATCCCTGACACAGGGGAAATATCAGACTGGGTCAAG 171

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Search completed: January 13, 2006, 15:35:12  
Job time : 1946 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using bw model

Run on: January 13, 2006, 11:50:05 ; Search time 16555 Seconds  
(without alignments)  
11433.929 Million cell updates/sec

Title: US-10-007-270-1  
Perfect score: 3330  
Sequence: 1 ttaaccacaagaagttacacct.....tactatatagcataatcaat 3330

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Listing first 1000 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
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5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_ses:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hfg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	2578	77.4	3268	8	AF047492	Homo sapi
2	1316	39.5	2009	6	CQ725539	Sequence
3	722	21.7	90766	8	AL392166	Human DNA
4	722	21.7	132145	14	AL359817	Human DNA
5	653	19.6	1235	8	HSIMPG17	
6	534	16.0	816	8	HSIMPG13	
7	534	16.0	160719	14	AL157379	
8	249	7.5	444	8	HSIMPG10	
9	236	7.1	537	8	HSIMPG02	
10	236	7.1	132145	14	AL359817	
11	236	7.1	186301	8	AL359817	
12	204	6.1	477	8	HSIMPG15	
13	197	5.9	310	8	HSIMPG01	
14	170	5.1	448	8	HSIMPG14	
15	169	5.1	422	8	HSIMPG03	
16	141	4.2	377	8	HSIMPG07	
17	112	3.4	555	8	AF047491	Macaca fa
18	107	3.2	311	8	HSIMPG06	

19	81	2.4	438	8	HSIMPG12	AF017771 Homo sapi
20	79	2.4	347	8	HSIMPG11	AF017770 Homo sapi
21	79	2.4	380	8	HSIMPG16	AF017775 Homo sapi
22	67	2.0	304	8	HSIMPG05	AF017764 Homo sapi
23	62	1.9	300	8	HSIMPG08	AF017767 Homo sapi
24	60	1.8	60	6	COS46764	COS46764 Sequence
25	42	1.3	3552	4	AB047844	AB047844 Bos tauru
26	39	1.2	259413	14	AC161554	AC161554 Bos tauru
27	33	1.0	300	8	HSIMPG04	AF017763 Homo sapi
28	32	1.0	2850	9	AB047843	AB047843 Rattus no
29	32	1.0	2924	9	BC022970	BC022970 Mus muscu
30	32	1.0	3668	8	AF266478	AF266478 Mus muscu
31	32	1.0	3675	9	AF229929	AF229929 Mus muscu
32	32	1.0	41220	9	AC148244	AC148244 Mus muscu
33	32	1.0	110000	14	AC110108_1	Continuation (2 of
34	32	1.0	159816	14	AC136044_1	Continuation (2 of
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39	24	0.7	162013	14	AC019347	AC019347 Homo sapi
40	24	0.7	166022	14	AC156794	AC156794 Mus muscu
41	24	0.7	184346	14	AC157902	AC157902 Mus muscu
42	24	0.7	216014	14	AC008823	AC008823 Homo sapi
43	23	0.7	294	8	HSIMPG09	AF017768 Homo sapi
44	23	0.7	148747	14	AC140852	AC140852 Rattus no
45	23	0.7	153053	8	AL137179	AL137179 Human DNA
46	23	0.7	191166	8	AC009686	AC009686 Homo sapi
47	23	0.7	196806	8	AC104212	AC104212 Homo sapi
48	23	0.7	203335	14	AC121703	AC121703 Rattus no
49	22	0.7	772	10	BV609826	BV609826 S215P6102
50	22	0.7	3760	6	CQ841836	CQ841836 Sequence
51	22	0.7	3760	8	AK124882	AK124882 Homo sapi
52	22	0.7	4695	8	HSM802204	CS125450 Sequence
53	22	0.7	28536	6	CS125450	Continuation (2 of
54	22	0.7	70680	14	AC101265	Continuation (7 of
55	22	0.7	102591	14	AC165023	Continuation (2 of
56	22	0.7	103700	5	BX510946	Continuation (2 of
57	22	0.7	110000	14	AC095248_1	Continuation (2 of
58	22	0.7	110000	14	AC164423_6	Continuation (2 of
59	22	0.7	110472	15	AC146709	Continuation (2 of
60	22	0.7	112601	8	AP005140	AP005140 Homo sapi
61	22	0.7	119956	14	AC015789	AC015789 Homo sapi
62	22	0.7	136646	8	AL138726	AL138726 Human DNA
63	22	0.7	144885	9	AL731766	AL731766 Mouse DNA
64	22	0.7	147224	14	AP003779	AP003779 Homo sapi
65	22	0.7	157352	14	AC009687	AC009687 Homo sapi
66	22	0.7	157792	8	AC069209	AC069209 Homo sapi
67	22	0.7	158256	8	AC009024	AC009024 Homo sapi
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69	22	0.7	166888	9	AC158126	AC158126 Mus muscu
70	22	0.7	167437	14	CR450713	CR450713 Danio rer
71	22	0.7	169361	5	CR762498	CR762498 Zebrafish
72	22	0.7	170221	9	AC127421	AC127421 Mus muscu
73	22	0.7	170407	14	AC011177	AC011177 Homo sapi
74	22	0.7	171132	8	AL161771	AL161771 Human DNA
75	22	0.7	171727	9	AC113590	AC113590 Mus muscu
76	22	0.7	173468	14	AC112087	AC112087 Rattus no
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88	22	0.7	233627	14	AC127968	AC127968 Rattus no
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93	22	0.7	253544	14	AC115652	AC115652 Rattus no	c 166	21	0.6	225837	14	AC107092	AC107092 Rattus no
94	22	0.7	253985	14	AC097242	AC097242 Rattus no	c 167	21	0.6	225849	14	AC107092	AC107092 Rattus no
95	22	0.7	259413	14	AC161554	AC161554 Bos tauru	c 168	21	0.6	226754	9	AL645625	AL645625 Mouse DNA
96	22	0.7	281138	14	AC159058	AC159058 Bos tauru	c 169	21	0.6	227872	14	AC156885	AC156885 Bos tauru
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99	21	0.6	623	10	BV344326	BV344326 S230P6339	c 172	21	0.6	231498	14	AC120660	AC120660 Rattus no
100	21	0.6	3836	15	KLA96546	KLA96546 Kluyverom	c 173	21	0.6	231864	14	AC097246	AC097246 Rattus no
101	21	0.6	39993	8	AC108160	AC108160 Homo sapi	c 174	21	0.6	232033	14	AC137035	AC137035 Rattus no
102	21	0.6	52569	5	BX897713	BX897713 Zebrafish	c 175	21	0.6	233505	14	AC120061	AC120061 Rattus no
103	21	0.6	56575	8	AL355142	AL355142 Human DNA	c 176	21	0.6	233976	14	AC098467	AC098467 Rattus no
104	21	0.6	66001	8	AC087322	AC087322 Homo sapi	c 177	21	0.6	235178	14	AC098921	AC098921 Rattus no
105	21	0.6	73169	14	AC100699	AC100699 Mus muscu	c 178	21	0.6	235527	14	AC164258	AC164258 Bos tauru
106	21	0.6	108527	4	AC151045	AC151045 Macropus	c 179	21	0.6	236527	14	AC110370	AC110370 Rattus no
107	21	0.6	110000	14	AC098773_1	Continuation (2 of	c 180	21	0.6	239628	14	AC111118	AC111118 Rattus no
108	21	0.6	110000	14	AC110677_6	Continuation (7 of	c 181	21	0.6	241909	14	AC127399	AC127399 Rattus no
109	21	0.6	110000	14	AC113629_0	AC113629 Rattus no	c 182	21	0.6	245967	14	AC112091	AC112091 Rattus no
110	21	0.6	110000	15	AP008216_131	Continuation (132	c 183	21	0.6	250578	14	AC094142	AC094142 Rattus no
111	21	0.6	110000	15	CR382125_19	Continuation (20 o	c 184	21	0.6	255020	14	AC097336	AC097336 Rattus no
112	21	0.6	129254	9	AL672204	Mouse DNA	c 185	21	0.6	265858	14	AC133671	AC133671 Rattus no
113	21	0.6	134203	14	AC149272	AC149272 Mus muscu	c 186	21	0.6	280963	14	AC123393	AC123393 Rattus no
114	21	0.6	137496	14	AC141951	AC141951 Rattus no	c 187	21	0.6	292663	14	AC098151	AC098151 Rattus no
115	21	0.6	140186	14	AC125599	AC125599 Rattus no	c 188	21	0.6	294560	14	AC125870	AC125870 Rattus no
116	21	0.6	141059	8	AC078806	AC078806 Homo sapi	c 189	21	0.6	296338	14	AC132951	AC132951 Mus muscu
117	21	0.6	145504	14	AC141023	AC141023 Rattus no	c 190	21	0.6	306446	14	AC163425	AC163425 Bos tauru
118	21	0.6	145652	14	CR848721	CR848721 Dario rer	c 191	21	0.6	313264	14	AC023053	AC023053 Homo sapi
119	21	0.6	153133	8	AC091980	AC091980 Homo sapi	c 192	21	0.6	324367	15	AE017091	AE017091 Oryza sat
120	21	0.6	157596	9	AC120388	AC120388 Mus muscu	c 193	21	0.6	331363	14	AC113829	AC113829 Rattus no
121	21	0.6	157770	14	AC166853	AC166853 Cercopithec	c 194	21	0.6	3303	8	AY441510	AY441510 Galago mo
122	21	0.6	159867	14	AC130411	AC130411 Homo sapi	c 195	20	0.6	320	6	CO396024	CO396024 Sequence
123	21	0.6	163640	8	AC093328	AC093328 Homo sapi	c 196	20	0.6	320	6	CO402350	CO402350 Sequence
124	21	0.6	165720	9	AC127244	AC127244 Mus muscu	c 197	20	0.6	459	10	BV006288	BV006288 ORS 885 S
125	21	0.6	166124	14	AC122680	AC122680 Rattus no	c 198	20	0.6	466	6	CO408734	CO408734 Sequence
126	21	0.6	166357	8	AC026307	AC026307 Homo sapi	c 199	20	0.6	486	6	CO420192	CO420192 Sequence
127	21	0.6	166399	14	AC012584	AC012584 Homo sapi	c 200	20	0.6	529	6	CO408706	CO408706 Sequence
128	21	0.6	167095	5	CR381540	CR381540 Zebrafish	c 201	20	0.6	544	10	BV414400	BV414400 S223P6516
129	21	0.6	167237	8	AC007938	AC007938 Homo sapi	c 202	20	0.6	550	6	CO420191	CO420191 Sequence
130	21	0.6	167383	14	AC127860	AC127860 Rattus no	c 203	20	0.6	560	6	CO395994	CO395994 Sequence
131	21	0.6	167794	14	AE215844	AE215844 Homo sapi	c 204	20	0.6	560	6	CO402322	CO402322 Sequence
132	21	0.6	168508	14	AC094154	AC094154 Rattus no	c 205	20	0.6	576	10	BV343270	BV343270 S230P6224
133	21	0.6	169184	8	AL356969	AL356969 Human DNA	c 206	20	0.6	595	6	PE2A90925	PE2A90925 P1aemodiu
134	21	0.6	169270	15	AC083943	AC083943 Genomic s	c 207	20	0.6	607	10	BV335396	BV335396 S230P6878
135	21	0.6	172387	14	AC073579	AC073579 Homo sapi	c 208	20	0.6	637	10	BV406310	BV406310 S232P6465
136	21	0.6	174330	14	AC119605	AC119605 Rattus no	c 209	20	0.6	645	10	BV072043	BV072043 S212P6101
137	21	0.6	174414	5	AL954772	AL954772 Zebrafish	c 210	20	0.6	648	10	BV013840	BV013840 S212P6543
138	21	0.6	178853	14	AC121733	AC121733 Rattus no	c 211	20	0.6	652	10	BV392979	BV392979 S243P6126
139	21	0.6	180051	9	AC102510	AC102510 Mus muscu	c 212	20	0.6	678	6	CO429068	CO429068 Sequence
140	21	0.6	182285	9	AC153795	AC153795 Mus muscu	c 213	20	0.6	679	10	BV234085	BV234085 S234P644R
141	21	0.6	182582	14	AC114597	AC114597 Mus muscu	c 214	20	0.6	694	2	AY355317	AY355317 P1aemodiu
142	21	0.6	182995	9	AC152958	AC152958 Mus muscu	c 215	20	0.6	703	10	BV594768	BV594768 S215P6358
143	21	0.6	183883	15	AY673996	AY673996 Gracilari	c 216	20	0.6	712	2	AY355313	AY355313 P1aemodiu
144	21	0.6	185043	14	AC018964	AC018964 Homo sapi	c 217	20	0.6	714	2	AY355314	AY355314 P1aemodiu
145	21	0.6	185281	14	AC011214	AC011214 Homo sapi	c 218	20	0.6	714	2	AY355315	AY355315 P1aemodiu
146	21	0.6	185485	14	AC165997	AC165997 Salmiiri b	c 219	20	0.6	735	10	BV409771	BV409771 S223P6211
147	21	0.6	186421	9	AC164558	AC164558 Mus muscu	c 220	20	0.6	759	6	CO429067	CO429067 Sequence
148	21	0.6	187351	5	CR788305	CR788305 Zebrafish	c 221	20	0.6	769	10	BV664786	BV664786 S215P6012
149	21	0.6	187488	14	AC010454	AC010454 Homo sapi	c 222	20	0.6	772	2	AY355312	AY355312 P1aemodiu
150	21	0.6	189535	14	AC166775	AC166775 Mus muscu	c 223	20	0.6	785	10	BV675755	BV675755 S217P6141
151	21	0.6	190209	9	AC101740	AC101740 Mus muscu	c 224	20	0.6	791	6	BV659031	BV659031 S215P6108
152	21	0.6	191452	14	AC118966	AC118966 Rattus no	c 225	20	0.6	796	9	MMU310308	MMU310308 Mus muscu
153	21	0.6	200098	5	AL935317	AL935317 Zebrafish	c 226	20	0.6	887	6	CO413611	CO413611 Sequence
154	21	0.6	202533	9	AC093605	AC093605 Mus muscu	c 227	20	0.6	909	9	MMU13611	MMU13611 Sequence
155	21	0.6	207781	14	AC129022	AC129022 Mus muscu	c 228	20	0.6	915	15	AK119100	AK119100 Mus muscu
156	21	0.6	208959	9	BX544880	BX544880 Mouse DNA	c 229	20	0.6	942	5	AY355318	AY355318 P1aemodiu
157	21	0.6	211514	14	AC162082	AC162082 Bos tauru	c 230	20	0.6	984	5	BX935083	BX935083 Gallus ga
158	21	0.6	212522	14	AC166058	AC166058 Mus muscu	c 231	20	0.6	1218	15	AY128331	AY128331 Arabidops
159	21	0.6	214955	14	AC164131	AC164131 Bos tauru	c 232	20	0.6	1399	6	AR149576	AR149576 Sequence
160	21	0.6	215107	14	AC161630	AC161630 Bos tauru	c 233	20	0.6	1399	6	AX427267	AX427267 Sequence
161	21	0.6	217643	9	AL589871	AL589871 Mouse DNA	c 234	20	0.6	1399	6	BC058854	BC058854 Mus muscu
162	21	0.6	221604	14	AC109935	AC109935 Rattus no	c 235	20	0.6	1675	5	CR391485	CR391485 Gallus ga
163	21	0.6	223809	14	AC105474	AC105474 Rattus no	c 236	20	0.6	1716	6	AX651650	AX651650 Sequence
164	21	0.6	225286	9	AC154373	AC154373 Mus muscu	c 237	20	0.6	1716	6	AX651650	AX651650 Sequence



C 238	20	0.6	1849	15	AB004822	AB004822 Arabidops	C 311	20	0.6	110000	14	AC097780_1	Continuation (2 of
C 239	20	0.6	1897	15	AF015544	AF015544 Arabidops	C 312	20	0.6	110000	14	AC108277_3	Continuation (4 of
C 240	20	0.6	2002	6	AX654894	AX654894 Sequence	C 313	20	0.6	110000	14	AC109966_2	Continuation (3 of
C 241	20	0.6	2002	15	D89994	D89994 Arabidopsis	C 314	20	0.6	110000	14	AC110929_6	Continuation (7 of
C 242	20	0.6	2247	8	AB048929	AB048929 Macaca fa	C 315	20	0.6	110000	14	AC123076_4	Continuation (5 of
C 243	20	0.6	2679	6	AR023939	AR023939 Sequence	C 316	20	0.6	110000	14	AC129041_2	Continuation (3 of
C 244	20	0.6	2679	6	I15440	I15440 Sequence 11	C 317	20	0.6	110000	14	CR974473_1	Continuation (2 of
C 245	20	0.6	2698	2	AP423800	AP423800 Mergence11	C 318	20	0.6	110000	14	CT005257_1	Continuation (2 of
C 246	20	0.6	2958	6	CQ841646	CQ841646 Sequence	C 319	20	0.6	110000	14	CT009728_3	Continuation (4 of
C 247	20	0.6	2958	8	AK123336	AK123336 Homo sapi	C 320	20	0.6	110000	14	CT009728_3	Continuation (3 of
C 248	20	0.6	2994	5	BC079784	BC079784 Xenopus 1	C 321	20	0.6	110000	14	TAN3_11	Continuation (12 of
C 249	20	0.6	3021	6	AR270555	AR270555 Sequence	C 322	20	0.6	110000	15	AP008216_115	Continuation (117
C 250	20	0.6	3021	8	HSMLU7	X94552 H sapiens m	C 323	20	0.6	110000	15	AP008216_115	Continuation (117
C 251	20	0.6	3640	15	AB019944	AB019944 Arabidops	C 324	20	0.6	110000	15	AP008217_258	Continuation (259
C 252	20	0.6	3604	6	A43639	A43639 Sequence 3	C 325	20	0.6	110000	15	CR380951_3	Continuation (4 of
C 253	20	0.6	3804	6	AR149575	AR149575 Sequence	C 326	20	0.6	110000	15	CR382122_03	Continuation (4 of
C 254	20	0.6	3804	6	AX427265	AX427265 Sequence	C 327	20	0.6	110000	15	CR382125_03	Continuation (4 of
C 255	20	0.6	4312	6	AX548896	AX548896 Sequence	C 328	20	0.6	110000	15	CR382125_04	Continuation (5 of
C 256	20	0.6	4312	8	HSU92458	U92458 Human metab	C 329	20	0.6	110000	15	CR382125_10	Continuation (11 of
C 257	20	0.6	4751	9	AY133241	AY133241 Mus muscu	C 330	20	0.6	110000	15	AB162343	Continuation (336
C 258	20	0.6	4843	9	BC055400	BC055400 Mus muscu	C 331	20	0.6	110760	8	AC137009	AB162343 Oncorhync
C 259	20	0.6	4953	5	AB070714	AB070714 Gallus ga	C 332	20	0.6	113254	8	AC138135	AC138135 Homo sapi
C 260	20	0.6	5077	5	BC093448	BC093448 Danio rer	C 333	20	0.6	113254	8	AC139354	AC139354 Medicago
C 261	20	0.6	6446	6	AX251081	AX251081 Sequence	C 334	20	0.6	116879	8	AC106854	AC106854 Homo sapi
C 262	20	0.6	9820	8	AP057709	AP057709 Homo sapi	C 335	20	0.6	116897	14	AC134479	AC134479 Rattus no
C 263	20	0.6	12085	8	AP146651	AP146651 Homo sapi	C 336	20	0.6	118705	15	AC126009	AC126009 Medicago
C 264	20	0.6	15714	6	AX346074	AX346074 Sequence	C 337	20	0.6	118705	15	ATF5K20	ATF5K20 Arabidops
C 265	20	0.6	15714	6	AX458541	AX458541 Sequence	C 338	20	0.6	120964	14	AC124966	AC124966 Medicago
C 266	20	0.6	18945	14	CT009728_4	Continuation (5 of	C 339	20	0.6	121689	8	AP000478	AP000478 Homo sapi
C 267	20	0.6	23668	8	AX357592	AX357592 Sequence	C 340	20	0.6	121717	8	AL445488	AL445488 Human DNA
C 268	20	0.6	29867	8	AY207372	AY207372 Homo sapi	C 341	20	0.6	122143	14	AC161507	AC161507 Mus muscu
C 269	20	0.6	30093	2	AF016665	AF016665 Caenorhab	C 342	20	0.6	122982	9	AF0851871	AF0851871 Mus muscu
C 270	20	0.6	34749	14	AF010094	AF010094 Mus muscu	C 343	20	0.6	123530	8	AL139110	AL139110 Human DNA
C 271	20	0.6	38000	8	AF025422	AF025422 Homo sapi	C 344	20	0.6	123530	8	AL1713980	AL1713980 Human DNA
C 272	20	0.6	41319	14	AC107932	AC107932 Homo sapi	C 345	20	0.6	124514	5	BX469904	BX469904 Zebrafish
C 273	20	0.6	48103	8	CR478234	CR478234 Mouse DNA	C 346	20	0.6	125478	8	BX548016	BX548016 Zebrafish
C 274	20	0.6	48767	14	AC011133	AC011133 Homo sapi	C 347	20	0.6	126761	14	AC084129	AC084129 Homo sapi
C 275	20	0.6	53190	14	AC092292	AC092292 Homo sapi	C 348	20	0.6	127026	14	AC157868	AC157868 Felis cat
C 276	20	0.6	53504	14	AC027650	AC027650 Mus muscu	C 349	20	0.6	129166	15	AC126057	AC126057 Oryza sat
C 277	20	0.6	55574	15	H0421H08	AL442117 Oryza sat	C 350	20	0.6	129740	8	AC091525	AC091525 Homo sapi
C 278	20	0.6	55980	5	CR735113	CR735113 Zebrafish	C 351	20	0.6	132949	8	AC104049	AC104049 Homo sapi
C 279	20	0.6	56508	14	AC099896	AC099896 Mus muscu	C 352	20	0.6	133321	14	AC080160	AC080160 Mus muscu
C 280	20	0.6	56508	14	AC137082	AC137082 Danio rer	C 353	20	0.6	133321	14	AC134521	AC134521 Medicago
C 281	20	0.6	59632	14	AC102939	AC102939 Homo sapi	C 354	20	0.6	134267	15	AC155242	AC155242 Mus muscu
C 282	20	0.6	65465	15	AB007650	AB007650 Arabidops	C 355	20	0.6	134267	15	AC107613	AC107613 Homo sapi
C 283	20	0.6	65465	15	AC000015	AC000015 Homo sapi	C 356	20	0.6	134210	8	AC005052	AC005052 Homo sapi
C 284	20	0.6	67000	8	AP005018	AP005018 Homo sapi	C 357	20	0.6	135060	8	AC084678	AC084678 Homo sapi
C 285	20	0.6	67166	14	AC012546	AC012546 Homo sapi	C 358	20	0.6	136415	15	AC146310	AC146310 Oryza sat
C 286	20	0.6	67356	8	AL161658	AL161658 Human DNA	C 359	20	0.6	138128	14	AC022275	AC022275 Homo sapi
C 287	20	0.6	70752	14	AC141103	AC141103 Rattus no	C 360	20	0.6	139086	8	AL356127	AL356127 Human DNA
C 288	20	0.6	74577	8	AL391415	AL391415 Human DNA	C 361	20	0.6	140073	8	CNS01D70	AL1332819 Human chr
C 289	20	0.6	80368	5	CQ870264	CQ870264 Sequence	C 362	20	0.6	140552	9	HSBU1208	AL096678 Human DNA
C 290	20	0.6	83178	14	AC117537	AC117537 Magnaport	C 363	20	0.6	140552	9	AC154803	AC154803 Mus muscu
C 291	20	0.6	83366	14	AC144978	AC144978 Xenopus t	C 364	20	0.6	140552	9	AC137822	AC137822 Medicago
C 292	20	0.6	84495	5	AR366536	AR366536 Sequence	C 365	20	0.6	141669	15	AL805927	AL805927 Mouse DNA
C 293	20	0.6	84495	5	BX323462	BX323462 Zebrafish	C 366	20	0.6	141924	8	AL138830	AL138830 Human DNA
C 294	20	0.6	87434	8	HS4297357	HS4297357 Homo sapi	C 367	20	0.6	142281	8	HS429880	HS429880 Homo sapi
C 295	20	0.6	87434	8	HS4297357	HS4297357 Homo sapi	C 368	20	0.6	142704	9	AC157558	AC157558 Mus muscu
C 296	20	0.6	90300	14	AC166956	AC166956 Bos tauru	C 369	20	0.6	143104	8	AL606503	AL606503 Human DNA
C 297	20	0.6	92135	14	AC108277_4	Continuation (5 of	C 370	20	0.6	143111	14	CR626923	CR626923 Danio rer
C 298	20	0.6	98135	8	AC113150	AC113150 Homo sapi	C 371	20	0.6	143111	14	AC025157	AC025157 Homo sapi
C 299	20	0.6	98856	15	ATAC018363	ATAC018363 Arabidops	C 372	20	0.6	143960	8	AC021613	AC021613 Homo sapi
C 300	20	0.6	101318	9	AC132125	AC132125 Mus muscu	C 373	20	0.6	144174	14	AC166312	AC166312 Loxodonta
C 301	20	0.6	101318	9	AC132125	AC132125 Mus muscu	C 374	20	0.6	144523	8	AP051934	AP051934 Homo sapi
C 302	20	0.6	103522	14	AC161708	AC161708 Carollia	C 375	20	0.6	145342	14	AC142124	AC142124 Rattus no
C 303	20	0.6	104368	8	AC068120	AC068120 Homo sapi	C 376	20	0.6	145342	14	AC022548	AC022548 Homo sapi
C 304	20	0.6	105066	14	AP008498_8	Continuation (9 of	C 377	20	0.6	146015	9	AL671877	AL671877 Mouse DNA
C 305	20	0.6	105596	15	AL139233	AL139233 Human DNA	C 378	20	0.6	146436	9	AL831763	AL831763 Mouse DNA
C 306	20	0.6	109071	8	AC0095170	AC0095170 Arabidops	C 379	20	0.6	146586	8	AC104771	AC104771 Homo sapi
C 307	20	0.6	109071	8	AC009482	AC009482 Homo sapi	C 380	20	0.6	146742	14	AC016275	AC016275 Homo sapi
C 308	20	0.6	110000	1	CP000076_34	Continuation (35 of	C 381	20	0.6	146742	14	AC016275	AC016275 Homo sapi
C 309	20	0.6	110000	5	AB183488_2	Continuation (3 of	C 382	20	0.6	146742	14	AC016275	AC016275 Homo sapi
C 310	20	0.6	110000	14	AC095205_1	Continuation (2 of	C 383	20	0.6	146742	14	AC016275	AC016275 Homo sapi

384	20	0.6	147201	14	AC053469	457	20	0.6	168279	14	AC069186	AC069186 Homo sapi
C 385	20	0.6	147260	14	AC016340	458	20	0.6	168814	8	AL357672	AL357672 Human DNA
C 386	20	0.6	147481	14	AC0151497	459	20	0.6	168853	9	AC140468	AC140468 Homo sapi
C 387	20	0.6	147665	8	AL138691	C 460	20	0.6	168898	14	AC026974	AC026974 Homo sapi
C 388	20	0.6	147928	14	CR318612	C 461	20	0.6	169136	9	AC115877	AC115877 Mus muscu
C 389	20	0.6	148336	8	AC0077110	C 462	20	0.6	169510	9	AC102461	AC102461 Mus muscu
C 390	20	0.6	148392	9	AC140466	C 463	20	0.6	169552	8	AC015976	AC015976 Homo sapi
C 391	20	0.6	148463	8	AC146157	C 464	20	0.6	169677	14	AC036215	AC036215 Homo sapi
C 392	20	0.6	148588	14	AC073827	C 465	20	0.6	171392	9	AC102168	AC102168 Mus muscu
C 393	20	0.6	148609	14	AC011606	C 466	20	0.6	172195	8	AC093862	AC093862 Homo sapi
C 394	20	0.6	149337	8	AC012069	C 467	20	0.6	172802	9	AC110225	AC110225 Mus muscu
C 395	20	0.6	149612	14	AC157555	C 468	20	0.6	172872	9	AC140456	AC140456 Homo sapi
C 396	20	0.6	150011	14	AC068832	C 469	20	0.6	173045	14	AC007675	AC007675 Mus muscu
C 397	20	0.6	150152	14	AL355502	C 470	20	0.6	173237	8	AC091198	AC091198 Homo sapi
C 398	20	0.6	150313	8	AC137672	C 471	20	0.6	173356	14	AC155745	AC155745 Homo sapi
C 399	20	0.6	150385	5	BX511147	C 472	20	0.6	173585	14	AC021113	AC021113 Mus muscu
C 400	20	0.6	150606	14	AC027376	C 473	20	0.6	173655	9	AL646095	AL646095 Mouse DNA
C 401	20	0.6	151186	14	AC068750	C 474	20	0.6	173719	14	AC129890	AC129890 Homo sapi
C 402	20	0.6	151294	14	AC069364	C 475	20	0.6	173728	14	AC147489	AC147489 Homo sapi
C 403	20	0.6	151321	14	AC012276	C 476	20	0.6	173868	14	AC124820	AC124820 Homo sapi
C 404	20	0.6	151744	9	AL772406	C 477	20	0.6	174327	14	AL672191	AL672191 Homo sapi
C 405	20	0.6	151980	8	AC084209	C 478	20	0.6	174435	9	AC162292	AC162292 Mus muscu
C 406	20	0.6	152264	15	OS0N00090	C 479	20	0.6	174540	9	AC119900	AC119900 Mus muscu
C 407	20	0.6	152366	8	AL138894	C 480	20	0.6	175859	8	AC161486	AC161486 Homo sapi
C 408	20	0.6	152408	8	HS191078	C 481	20	0.6	175952	8	AC069285	AC069285 Mus muscu
C 409	20	0.6	153000	14	AC010934	C 482	20	0.6	176459	8	AC055732	AC055732 Homo sapi
C 410	20	0.6	153152	8	AC021999	C 483	20	0.6	176638	14	AC102137	AC102137 Mus muscu
C 411	20	0.6	155065	9	AC151530	C 484	20	0.6	176741	8	AC098476	AC098476 Homo sapi
C 412	20	0.6	155182	14	AC023890	C 485	20	0.6	176918	8	AC138473	AC138473 Homo sapi
C 413	20	0.6	155263	14	BX927284	C 486	20	0.6	176928	8	AC084239	AC084239 Homo sapi
C 414	20	0.6	155582	14	AC115929	C 487	20	0.6	177988	14	AC022760	AC022760 Homo sapi
C 415	20	0.6	156107	8	AC099543	C 488	20	0.6	178068	14	AC142046	AC142046 Homo sapi
C 416	20	0.6	156313	14	AL359702	C 489	20	0.6	178428	8	AL162742	AL162742 Human DNA
C 417	20	0.6	156839	14	AC011233	C 490	20	0.6	178904	8	AC092709	AC092709 Homo sapi
C 418	20	0.6	157056	5	BX469896	C 491	20	0.6	178916	14	AP002874	AP002874 Homo sapi
C 419	20	0.6	157392	14	AC129984	C 492	20	0.6	179177	9	AC127331	AC127331 Mus muscu
C 420	20	0.6	157726	14	AC166817	C 493	20	0.6	179413	14	AC079051	AC079051 Homo sapi
C 421	20	0.6	157956	9	AL772203	C 494	20	0.6	180072	14	AC160107	AC160107 Mus muscu
C 422	20	0.6	158285	8	AL772203	C 495	20	0.6	180087	14	AC149567	AC149567 Homo sapi
C 423	20	0.6	158375	14	CR456642	C 496	20	0.6	180114	9	AC145070	AC145070 Mus muscu
C 424	20	0.6	159179	9	MHHC322F16	C 497	20	0.6	180248	14	AC007871	AC007871 Homo sapi
C 425	20	0.6	159997	14	CR352334	C 498	20	0.6	180736	14	AC023925	AC023925 Homo sapi
C 426	20	0.6	160042	5	BX294128	C 499	20	0.6	180983	8	AC040978	AC040978 Homo sapi
C 427	20	0.6	160376	14	AC036118	C 500	20	0.6	181353	9	AC132881	AC132881 Mus muscu
C 428	20	0.6	160416	14	AC158862	C 501	20	0.6	181805	9	AL670660	AL670660 Mouse DNA
C 429	20	0.6	160574	9	AC140192	C 502	20	0.6	181828	9	AC121846	AC121846 Mus muscu
C 430	20	0.6	160814	14	AC119545	C 503	20	0.6	182333	9	AC150285	AC150285 Mus muscu
C 431	20	0.6	161612	8	AC020754	C 504	20	0.6	182550	5	BX901962	BX901962 Zebrafish
C 432	20	0.6	161739	8	AC013302	C 505	20	0.6	182569	8	AC092500	AC092500 Homo sapi
C 433	20	0.6	162391	14	AC114906	C 506	20	0.6	182759	9	AC123549	AC123549 Mus muscu
C 434	20	0.6	162616	8	AC099539	C 507	20	0.6	183314	14	AC024197	AC024197 Homo sapi
C 435	20	0.6	162771	8	AC027121	C 508	20	0.6	183548	14	AC162192	AC162192 Homo sapi
C 436	20	0.6	162976	8	HS310013	C 509	20	0.6	183607	14	AC121176	AC121176 Homo sapi
C 437	20	0.6	163157	14	AC012567	C 510	20	0.6	183694	8	AC005412	AC005412 Homo sapi
C 438	20	0.6	163197	14	AC091392	C 511	20	0.6	183872	14	CR339050	CR339050 Homo sapi
C 439	20	0.6	163273	14	AC142486	C 512	20	0.6	184039	8	CNS0180X	AL109767 Human chr
C 440	20	0.6	163307	9	AC1158384	C 513	20	0.6	184057	14	AC160008	AC160008 Bos tauru
C 441	20	0.6	164201	9	AC112969	C 514	20	0.6	184123	14	AC163215	AC163215 Mus muscu
C 442	20	0.6	164456	9	AC131709	C 515	20	0.6	184197	14	AC105154	AC105154 Mus muscu
C 443	20	0.6	164530	9	AL596104	C 516	20	0.6	184396	8	AC105424	AC105424 Homo sapi
C 444	20	0.6	164652	14	AC026923	C 517	20	0.6	184444	14	AC025065	AC025065 Homo sapi
C 445	20	0.6	164906	8	AC096637	C 518	20	0.6	184751	9	AC153556	AC153556 Mus muscu
C 446	20	0.6	165021	14	AC107019	C 519	20	0.6	184799	9	AC037448	AC037448 Homo sapi
C 447	20	0.6	165509	14	AC009886	C 520	20	0.6	185211	14	AC018707	AC018707 Homo sapi
C 448	20	0.6	165635	14	AC154533	C 521	20	0.6	185214	9	AC158394	AC158394 Mus muscu
C 449	20	0.6	165705	5	AL2929074	C 522	20	0.6	185315	8	AC087368	AC087368 Homo sapi
C 450	20	0.6	166046	14	AC080174	C 523	20	0.6	185465	14	AC160026	AC160026 Pan trogl
C 451	20	0.6	166338	8	AC026165	C 524	20	0.6	186102	9	AC163438	AC163438 Mus muscu
C 452	20	0.6	166615	5	BX927102	C 525	20	0.6	186241	14	AC123386	AC123386 Rattus no
C 453	20	0.6	167009	5	BX072530	C 526	20	0.6	186848	14	AC145556	AC145556 Mus muscu
C 454	20	0.6	167392	5	AL954359	C 527	20	0.6	187386	14	AC148921	AC148921 Callithrix
C 455	20	0.6	167944	8	AC023192	C 528	20	0.6	187456	14	AC036130	AC036130 Homo sapi
C 456	20	0.6	168265	8	AC013716	C 529	20	0.6	187660	8	AC119673	AC119673 Homo sapi

C 530	20	0.6 187811	14	AC153300	AC153300 Ictalurus	603	20	0.6 215278	9	AC069562	AC069562 Mus muscu
C 531	20	0.6 188605	9	BX005163	BX005163 Mouse DNA	604	20	0.6 215385	8	AP216808	AP216808 Homo sapi
C 532	20	0.6 188709	8	AC092897	AC092897 Homo sapi	605	20	0.6 215911	14	AC135441	AC135441 Rattus no
C 533	20	0.6 188775	14	AC026537	AC026537 Homo sapi	606	20	0.6 216041	14	AC137585	AC137585 Mus muscu
C 534	20	0.6 188783	14	AC164212	AC164212 Bos tauru	607	20	0.6 216340	14	AC073754	AC073754 Mus muscu
C 535	20	0.6 189003	9	AC139319	AC139319 Mus muscu	608	20	0.6 216380	9	AC131113	AC131113 Mus muscu
C 536	20	0.6 189044	14	AC127841	AC127841 Rattus no	609	20	0.6 216583	14	AC162202	AC162202 Rattus no
C 537	20	0.6 189055	14	AC073716	AC073716 Mus muscu	610	20	0.6 217253	14	AC156538	AC156538 Bos tauru
C 538	20	0.6 189356	14	AC128153	AC128153 Rattus no	611	20	0.6 217404	9	AC135639	AC135639 Mus muscu
C 539	20	0.6 189610	14	AC164396	AC164396 Mus muscu	612	20	0.6 217571	14	AC137358	AC137358 Rattus no
C 540	20	0.6 189747	14	AC087791	AC087791 Homo sapi	613	20	0.6 218776	14	AC134291	AC134291 Rattus no
C 541	20	0.6 189999	8	AC092756	AC092756 Homo sapi	614	20	0.6 218815	9	AL807384	AL807384 Mouse DNA
C 542	20	0.6 190194	8	AC068025	AC068025 Homo sapi	615	20	0.6 219404	14	AC115170	AC115170 Rattus no
C 543	20	0.6 191165	5	BX511211	BX511211 Zebrafish	616	20	0.6 219695	9	AL596384	AL596384 Mouse DNA
C 544	20	0.6 191747	9	AC165244	AC165244 Mus muscu	617	20	0.6 219699	9	AC133933	AC133933 Mus muscu
C 545	20	0.6 192035	14	AC162481	AC162481 Bos tauru	618	20	0.6 220702	14	AC114181	AC114181 Rattus no
C 546	20	0.6 192101	14	AC119622	AC119622 Rattus no	619	20	0.6 221000	9	AC163344	AC163344 Mus muscu
C 547	20	0.6 192338	14	AC022221	AC022221 Homo sapi	620	20	0.6 221136	5	AL845422	AL845422 Zebrafish
C 548	20	0.6 192433	14	AC161272	AC161272 Homo sapi	621	20	0.6 221420	14	AC011822	AC011822 Homo sapi
C 549	20	0.6 193119	9	AC117729	AC117729 Mus muscu	622	20	0.6 221886	14	AC181823	AC181823 Rattus no
C 550	20	0.6 193227	9	AC165969	AC165969 Mus muscu	623	20	0.6 222986	14	AC114188	AC114188 Rattus no
C 551	20	0.6 193421	8	AC107294	AC107294 Homo sapi	624	20	0.6 223418	9	AC090123	AC090123 Mus muscu
C 552	20	0.6 193427	8	AC023403	AC023403 Homo sapi	625	20	0.6 223491	14	AC127910	AC127910 Rattus no
C 553	20	0.6 193461	8	AC087286	AC087286 Homo sapi	626	20	0.6 223631	14	AC159363	AC159363 Bos tauru
C 554	20	0.6 193549	8	BX950862	BX950862 Zebrafish	627	20	0.6 223668	14	AC098621	AC098621 Rattus no
C 555	20	0.6 193558	5	BX950862	BX950862 Zebrafish	628	20	0.6 224691	14	AC137364	AC137364 Rattus no
C 556	20	0.6 194377	14	AC021726	AC021726 Homo sapi	629	20	0.6 224778	9	AC116071	AC116071 Rattus no
C 557	20	0.6 195027	9	AC121824	AC121824 Mus muscu	630	20	0.6 225453	14	AC097957	AC097957 Rattus no
C 558	20	0.6 196110	14	AC154270	AC154270 Mus muscu	631	20	0.6 225482	14	AC120653	AC120653 Rattus no
C 559	20	0.6 196273	8	AC122216	AC122216 Mus muscu	632	20	0.6 225588	14	AC095774	AC095774 Rattus no
C 560	20	0.6 197019	8	AC104435	AC104435 Homo sapi	633	20	0.6 225978	14	AC110150	AC110150 Rattus no
C 561	20	0.6 197424	9	AC079042	AC079042 Mus muscu	634	20	0.6 226374	14	AC111868	AC111868 Rattus no
C 562	20	0.6 198486	14	CR388036	CR388036 Danio rer	635	20	0.6 226495	9	AC087216	AC087216 Mus muscu
C 563	20	0.6 198515	9	AF129005	AF129005 Mus muscu	636	20	0.6 226594	9	AC130711	AC130711 Mus muscu
C 564	20	0.6 198519	8	AC012170	AC012170 Homo sapi	637	20	0.6 227406	14	AC134372	AC134372 Rattus no
C 565	20	0.6 198613	14	AC162893	AC162893 Mus muscu	638	20	0.6 227978	14	AC159744	AC159744 Mus muscu
C 566	20	0.6 198652	14	CT025521	CT025521 Mus muscu	639	20	0.6 228071	9	AC115750	AC115750 Mus muscu
C 567	20	0.6 198829	9	AC120548	AC120548 Mus muscu	640	20	0.6 228458	14	AC097670	AC097670 Rattus no
C 568	20	0.6 199557	14	AC123691	AC123691 Mus muscu	641	20	0.6 228657	9	AC131120	AC131120 Mus muscu
C 569	20	0.6 199797	8	AC077690	AC077690 Homo sapi	642	20	0.6 228760	14	AC128139	AC128139 Rattus no
C 570	20	0.6 200131	8	AC105213	AC105213 Homo sapi	643	20	0.6 229651	14	BX957256	BX957256 Danio rer
C 571	20	0.6 200131	9	AC146977	AC146977 Mus muscu	644	20	0.6 230719	14	AC161600	AC161600 Mus muscu
C 572	20	0.6 200803	8	AC025580	AC025580 Homo sapi	645	20	0.6 230898	14	AC120455	AC120455 Rattus no
C 573	20	0.6 200942	14	CR383681	CR383681 Danio rer	646	20	0.6 231393	14	AC161084	AC161084 Bos tauru
C 574	20	0.6 201035	14	AC016744	AC016744 Homo sapi	647	20	0.6 232876	9	AC164020	AC164020 Bos tauru
C 575	20	0.6 201088	8	AL589733	AL589733 Human DNA	648	20	0.6 232931	14	AC140338	AC140338 Mus muscu
C 576	20	0.6 202922	9	AC119807	AC119807 Mus muscu	649	20	0.6 232962	14	AC094067	AC094067 Rattus no
C 577	20	0.6 203155	14	AC079473	AC079473 Mus muscu	650	20	0.6 232993	14	AC129694	AC129694 Rattus no
C 578	20	0.6 203293	14	AC152659	AC152659 Bos tauru	651	20	0.6 232993	14	AC166063	AC166063 Mus muscu
C 579	20	0.6 203773	8	AC097369	AC097369 Homo sapi	652	20	0.6 233163	14	AC113904	AC113904 Rattus no
C 580	20	0.6 204504	14	AC022487	AC022487 Homo sapi	653	20	0.6 233422	9	AC123675	AC123675 Mus muscu
C 581	20	0.6 204846	14	AC159046	AC159046 Bos tauru	654	20	0.6 233443	14	CT009684	CT009684 Mus muscu
C 582	20	0.6 204846	14	AC159046	AC159046 Bos tauru	655	20	0.6 233763	14	AC119297	AC119297 Rattus no
C 583	20	0.6 205870	5	BX088695	BX088695 Zebrafish	656	20	0.6 234420	14	AC161489	AC161489 Mus muscu
C 584	20	0.6 206252	14	AC123669	AC123669 Mus muscu	657	20	0.6 234652	14	AC122474	AC122474 Rattus no
C 585	20	0.6 206470	9	AC115723	AC115723 Mus muscu	658	20	0.6 235771	14	AC109538	AC109538 Rattus no
C 586	20	0.6 206834	14	AC135066	AC135066 Homo sapi	659	20	0.6 236446	14	AC142152	AC142152 Rattus no
C 587	20	0.6 208310	8	AC091043	AC091043 Homo sapi	660	20	0.6 237108	14	AC126202	AC126202 Rattus no
C 588	20	0.6 208881	8	AC024171	AC024171 Homo sapi	661	20	0.6 237176	14	CR392026	CR392026 Danio rer
C 589	20	0.6 208924	8	AC018735	AC018735 Homo sapi	662	20	0.6 237619	14	AC073765	AC073765 Mus muscu
C 590	20	0.6 208944	9	AC131065	AC131065 Mus muscu	663	20	0.6 237630	14	AC106665	AC106665 Rattus no
C 591	20	0.6 208966	14	AC133761	AC133761 Rattus no	664	20	0.6 238078	14	AC108364	AC108364 Rattus no
C 592	20	0.6 209168	8	AC090955	AC090955 Homo sapi	665	20	0.6 239190	14	AC098990	AC098990 Rattus no
C 593	20	0.6 209619	14	AC156981	AC156981 Mus muscu	666	20	0.6 239467	14	AC111384	AC111384 Rattus no
C 594	20	0.6 209725	14	AC117365	AC117365 Rattus no	667	20	0.6 240092	14	AC095930	AC095930 Mus muscu
C 595	20	0.6 210494	9	AC158786	AC158786 Mus muscu	668	20	0.6 240711	14	AC115561	AC115561 Rattus no
C 596	20	0.6 212164	9	AC157783	AC157783 Mus muscu	669	20	0.6 240884	14	CR376795	CR376795 Danio rer
C 597	20	0.6 212885	9	AC090122	AC090122 Mus muscu	670	20	0.6 241206	14	AC120484	AC120484 Rattus no
C 598	20	0.6 212885	9	AC161419	AC161419 Mus muscu	671	20	0.6 241529	14	AC103153	AC103153 Rattus no
C 599	20	0.6 213468	9	AC155163	AC155163 Mus muscu	672	20	0.6 241557	14	AC098000	AC098000 Rattus no
C 600	20	0.6 214606	14	AC161819	AC161819 Gallus ga	673	20	0.6 242258	14	AC115189	AC115189 Rattus no
C 601	20	0.6 215077	8	AC112504	AC112504 Homo sapi	674	20				
C 602	20					675	20				

c 676	20	0.6	242301	14	AC010172	AC010172 Homo sapi	749	19	0.6	360	15	CNS01DHz	Al116847 Botrytis
c 677	20	0.6	242803	14	AC108557	AC108557 Rattus no	c 750	19	0.6	365	6	C0468879	C0468879 Sequence
c 678	20	0.6	243014	14	AC164300	AC164300 Mus muscu	c 751	19	0.6	391	6	C0478047	C0478047 Sequence
c 679	20	0.6	243588	14	AC130853	AC130853 Rattus no	c 752	19	0.6	410	6	C0050359	C0050359 Sequence
c 680	20	0.6	243772	14	AY491413	AY491413 Mus muscu	c 753	19	0.6	410	6	C0065406	C0065406 Sequence
c 681	20	0.6	245468	14	AC126657	AC126657 Rattus no	c 754	19	0.6	410	6	C0092366	C0092366 Sequence
c 682	20	0.6	245754	14	AC111243	AC111243 Rattus no	c 755	19	0.6	410	6	C0131181	C0131181 Sequence
c 683	20	0.6	245989	14	AC095691	AC095691 Rattus no	c 756	19	0.6	410	6	C0169784	C0169784 Sequence
c 684	20	0.6	246036	14	AC106274	AC106274 Rattus no	c 757	19	0.6	410	6	C0198924	C0198924 Sequence
c 685	20	0.6	246525	14	AC139234	AC139234 Rattus no	c 758	19	0.6	410	6	C0214387	C0214387 Sequence
c 686	20	0.6	247458	14	AC164607	AC164607 Mus muscu	c 759	19	0.6	410	6	C0252979	C0252979 Sequence
c 687	20	0.6	248280	14	AC114034	AC114034 Rattus no	c 760	19	0.6	410	6	C0290124	C0290124 Sequence
c 688	20	0.6	248333	14	AC097969	AC097969 Rattus no	c 761	19	0.6	410	6	C0327082	C0327082 Sequence
c 689	20	0.6	248573	14	AC096467	AC096467 Rattus no	c 762	19	0.6	432	6	C0499248	C0499248 Sequence
c 690	20	0.6	250174	14	AC125639	AC125639 Rattus no	c 763	19	0.6	432	6	C0508217	C0508217 Sequence
c 691	20	0.6	251050	5	BX323060	BX323060 Zebrafish	c 764	19	0.6	435	9	MP698910	MP698910
c 692	20	0.6	253412	14	AC094716	AC094716 Rattus no	c 765	19	0.6	454	10	HS390037	HS390037
c 693	20	0.6	254252	14	AC153229	AC153229 Bos tauru	c 766	19	0.6	466	6	BD031787	BD031787
c 694	20	0.6	254733	2	AC117075	AC117075 Dicyoste	c 767	19	0.6	466	6	AX896254	AX896254
c 695	20	0.6	254762	14	AC154483	AC154483 Mus muscu	c 768	19	0.6	480	13	FCSH25R2	FCSH25R2
c 696	20	0.6	255219	14	AC094421	AC094421 Rattus no	c 769	19	0.6	495	9	GPVWGFA	GPVWGFA
c 697	20	0.6	255447	14	AC096032	AC096032 Rattus no	c 770	19	0.6	510	6	AX164210	AX164210
c 698	20	0.6	255574	14	AC109072	AC109072 Rattus no	c 771	19	0.6	543	5	AJ601498	AJ601498
c 699	20	0.6	258045	14	AC126195	AC126195 Rattus no	c 772	19	0.6	543	5	AJ601502	AJ601502
c 700	20	0.6	259423	14	BX957297	BX957297 Dantio rer	c 773	19	0.6	543	5	AJ601503	AJ601503
c 701	20	0.6	260033	14	AC099297	AC099297 Rattus no	c 774	19	0.6	543	5	AJ601505	AJ601505
c 702	20	0.6	261776	14	BX293561	BX293561 Dantio rer	c 775	19	0.6	543	5	AJ601506	AJ601506
c 703	20	0.6	261990	14	AC111513	AC111513 Rattus no	c 776	19	0.6	543	5	AJ601512	AJ601512
c 704	20	0.6	263797	14	AC025117	AC025117 Mus muscu	c 777	19	0.6	543	5	AJ601515	AJ601515
c 705	20	0.6	264929	14	AC110692	AC110692 Rattus no	c 778	19	0.6	547	5	AJ601499	AJ601499
c 706	20	0.6	265363	14	AC127661	AC127661 Rattus no	c 779	19	0.6	548	5	AJ601500	AJ601500
c 707	20	0.6	265393	14	AC164197	AC164197 Bos tauru	c 780	19	0.6	547	5	AJ601525	AJ601525
c 708	20	0.6	265869	14	AC114038	AC114038 Rattus no	c 781	19	0.6	550	5	AJ601517	AJ601517
c 709	20	0.6	266114	14	AC103150	AC103150 Rattus no	c 782	19	0.6	551	5	AJ601507	AJ601507
c 710	20	0.6	266129	14	AC164660	AC164660 Pan trogl	c 783	19	0.6	551	5	AJ601509	AJ601509
c 711	20	0.6	267936	14	AC111640	AC111640 Rattus no	c 784	19	0.6	551	5	AJ601510	AJ601510
c 712	20	0.6	268644	14	AC091323	AC091323 Mus muscu	c 785	19	0.6	551	5	AJ601511	AJ601511
c 713	20	0.6	269212	14	AC137521	AC137521 Medicago	c 786	19	0.6	551	5	AJ601513	AJ601513
c 714	20	0.6	269898	14	AC158120	AC158120 Mus muscu	c 787	19	0.6	551	5	AJ601514	AJ601514
c 715	20	0.6	270422	14	AC131559	AC131559 Rattus no	c 788	19	0.6	551	5	AJ601516	AJ601516
c 716	20	0.6	270850	14	AC095807	AC095807 Rattus no	c 789	19	0.6	551	5	AJ601518	AJ601518
c 717	20	0.6	275877	14	AC112118	AC112118 Rattus no	c 790	19	0.6	551	5	AJ601520	AJ601520
c 718	20	0.6	277307	14	AC105149	AC105149 Rattus no	c 791	19	0.6	551	5	AJ601521	AJ601521
c 719	20	0.6	277376	14	AC128972	AC128972 Rattus no	c 792	19	0.6	551	5	AJ601523	AJ601523
c 720	20	0.6	278172	9	AC115725	AC115725 Mus muscu	c 793	19	0.6	552	5	AJ601508	AJ601508
c 721	20	0.6	279922	14	AC151096	AC151096 Bos tauru	c 794	19	0.6	559	10	BV259157	BV259157
c 722	20	0.6	280299	14	AC115448	AC115448 Rattus no	c 795	19	0.6	578	10	BV056713	BV056713
c 723	20	0.6	287900	14	AC160424	AC160424 Bos tauru	c 796	19	0.6	586	6	C0521924	C0521924
c 724	20	0.6	288857	14	AC128817	AC128817 Rattus no	c 797	19	0.6	588	10	BV317832	BV317832
c 725	20	0.6	298427	14	AC125585	AC125585 Rattus no	c 798	19	0.6	611	15	AY077997	AY077997
c 726	20	0.6	305166	14	AC106141	AC106141 Rattus no	c 799	19	0.6	611	15	AY078003	AY078003
c 727	20	0.6	307898	14	AC099184	AC099184 Rattus no	c 800	19	0.6	612	10	BV224352	BV224352
c 728	20	0.6	310021	14	AC092883	AC092883 Homo sapi	c 801	19	0.6	615	10	BV374011	BV374011
c 729	20	0.6	321435	14	AC094119	AC094119 Rattus no	c 802	19	0.6	622	3	AY781362	AY781362
c 730	20	0.6	324999	14	AC098418	AC098418 Rattus no	c 803	19	0.6	623	10	G75936	G75936
c 731	20	0.6	329223	14	AC109504	AC109504 Mus muscu	c 804	19	0.6	651	6	C0744933	C0744933
c 732	20	0.6	332236	14	CT0009529	CT0009529 Homo sapi	c 805	19	0.6	694	10	BV548237	BV548237
c 733	20	0.6	333201	14	CR753836	CR753836 Homo sapi	c 806	19	0.6	696	15	CNS0180G	CNS0180G
c 734	20	0.6	343000	8	HS21C068	AL163268 Homo sapi	c 807	19	0.6	696	15	CNS018A82	CNS018A82
c 735	20	0.6	348050	8	HS229042	AJ229042 Homo sapi	c 808	19	0.6	700	6	AR645540	AR645540
c 736	20	0.6	349505	14	AC130443	AC130443 Rattus no	c 809	19	0.6	700	6	AX183479	AX183479
c 737	20	0.6	349980	6	AX644550	AX14550 Sequence	c 810	19	0.6	706	2	AY355316	AY355316
c 738	20	0.6	349999	6	AX647271	AX647271 Sequence	c 811	19	0.6	720	10	CNS01ATT	CNS01ATT
c 739	19	0.6	105	6	CS101169	CS101169 Sequence	c 812	19	0.6	737	15	BV615404	BV615404
c 740	19	0.6	105	6	CS112417	CS112417 Sequence	c 813	19	0.6	752	10	AF106667	AF106667
c 741	19	0.6	201	10	BV175979	BV175979 sqm85488	c 814	19	0.6	758	10	AV106667	AV106667
c 742	19	0.6	228	15	ATHS22773	AJ522773 Arabidops	c 815	19	0.6	788	6	C0429833	C0429833
c 743	19	0.6	233	6	BD026686	BD026686 Sequence	c 816	19	0.6	791	10	BV534838	BV534838
c 744	19	0.6	233	6	AX887076	AX887076 Sequence	c 817	19	0.6	802	10	BV068643	BV068643
c 745	19	0.6	289	8	AB091027	AB091027 Macaca fu	c 818	19	0.6	812	6	AX241740	AX241740
c 746	19	0.6	293	8	AB091018	AB091018 Macaca fu	c 819	19	0.6	818	6	BV664833	BV664833
c 747	19	0.6	293	8	AB091031	AB091031 Macaca fu	c 820	19	0.6	843	6	C0717543	C0717543
c 748	19	0.6	293	8	AB091034	AB091034 Macaca fu	c 821	19	0.6	881	8	AY091978	AY091978

C 822	19	0.6	921	10	BVS21108	895	19	0.6	5981	6	AX346665	AX346665 Sequence
C 823	19	0.6	930	8	AY092059	896	19	0.6	5997	6	AX251909	AX251909 Sequence
C 824	19	0.6	938	8	HSXJ3349	897	19	0.6	5997	6	AX344307	AX344307 Sequence
825	19	0.6	996	6	CO714979	898	19	0.6	5997	6	AX348718	AX348718 Sequence
826	19	0.6	1029	6	AB549892	899	19	0.6	6077	6	AX346148	AX346148 Sequence
827	19	0.6	1140	6	AX590007	900	19	0.6	6077	6	AX346756	AX346756 Sequence
828	19	0.6	1140	6	AX651633	901	19	0.6	6077	6	AX767473	AX767473 Sequence
829	19	0.6	1281	6	CS071573	902	19	0.6	6077	6	AX767549	AX767549 Sequence
830	19	0.6	1281	6	AR352268	903	19	0.6	6077	6	AX822331	AX822331 Sequence
C 831	19	0.6	1301	6	AR439784	904	19	0.6	6077	6	AX822459	AX822459 Sequence
C 832	19	0.6	1371	1	AP401662	905	19	0.6	6077	6	AX825971	AX825971 Sequence
C 833	19	0.6	1308	15	AY088151	906	19	0.6	6077	6	AX826099	AX826099 Sequence
C 834	19	0.6	1405	6	AX194524	907	19	0.6	6123	6	AX345938	AX345938 Sequence
C 835	19	0.6	1411	15	AK118017	908	19	0.6	6308	6	CS114295	CS114295 Sequence
C 836	19	0.6	1452	5	CR761628	909	19	0.6	6381	6	AX281408	AX281408 Sequence
C 837	19	0.6	1481	5	BC091622	910	19	0.6	6381	6	AX345869	AX345869 Sequence
C 838	19	0.6	1596	15	BN002277	911	19	0.6	6381	6	AX348676	AX348676 Sequence
C 839	19	0.6	1686	6	BD127532	912	19	0.6	6518	6	CS114313	CS114313 Sequence
C 840	19	0.6	1686	6	CQ783212	913	19	0.6	6923	6	AX251897	AX251897 Sequence
C 841	19	0.6	1686	8	AK075145	914	19	0.6	6923	6	AX344293	AX344293 Sequence
C 842	19	0.6	1760	8	HSXJ3350	915	19	0.6	6923	6	AX348708	AX348708 Sequence
C 843	19	0.6	1761	15	AY084884	916	19	0.6	7089	6	AX277904	AX277904 Sequence
C 844	19	0.6	1820	5	BC076906	917	19	0.6	7089	6	AX273583	AX273583 Sequence
C 845	19	0.6	1827	6	AX653173	918	19	0.6	7541	5	BC090383	BC090383 Xenopus t
C 846	19	0.6	1854	15	AY091170	919	19	0.6	7586	13	PVH1MLJ	AY01978 Vaccinia v1
C 847	19	0.6	1942	8	F32722AS05	920	19	0.6	7659	6	AX345091	AX345091 Sequence
C 848	19	0.6	1954	5	OMW427868	921	19	0.6	7659	6	AX251433	AX251433 Sequence
C 849	19	0.6	1967	8	AX093261	922	19	0.6	7969	6	AX458821	AX458821 Sequence
C 850	19	0.6	1989	6	AX488828	923	19	0.6	8049	6	AX346939	AX346939 Sequence
C 851	19	0.6	2028	1	AB034947	924	19	0.6	8140	9	AF003838	AF003838 Mus muscu
C 852	19	0.6	2202	5	BC078006	925	19	0.6	8143	6	AX346798	AX346798 Sequence
C 853	19	0.6	2278	6	CQ716913	926	19	0.6	8693	6	AX346413	AX346413 Sequence
C 854	19	0.6	2279	8	HSXJ3351	927	19	0.6	8693	6	AX347423	AX347423 Sequence
C 855	19	0.6	2283	5	CR926276	928	19	0.6	8693	6	AX349144	AX349144 Sequence
C 856	19	0.6	2292	8	F432182913	929	19	0.6	8693	6	AX657793	AX657793 Sequence
C 857	19	0.6	2301	9	BC059855	930	19	0.6	8693	6	AX659067	AX659067 Sequence
C 858	19	0.6	2318	8	BC005088	931	19	0.6	8717	8	HS1226F1	HS12267 Human DNA v
C 859	19	0.6	2387	15	CRO011840	932	19	0.6	8998	6	AX346608	AX346608 Sequence
860	19	0.6	2418	1	ASP316584	933	19	0.6	9798	13	AB093607	AB093607 Turnip mo
861	19	0.6	2500	6	CS039251	934	19	0.6	9798	13	AB093608	AB093608 Turnip mo
862	19	0.6	2500	6	CS039251	934	19	0.6	9798	13	AB093608	AB093608 Turnip mo
863	19	0.6	2501	6	CS039251	934	19	0.6	9798	13	AB093608	AB093608 Turnip mo
864	19	0.6	2501	6	CS039251	934	19	0.6	9798	13	AB093608	AB093608 Turnip mo
865	19	0.6	2559	9	AF314527	935	19	0.6	10857	13	AB114858	AB114858 Yokose v1
C 866	19	0.6	2559	9	AF314527	935	19	0.6	10857	13	AB114858	AB114858 Yokose v1
C 867	19	0.6	2673	8	HSX251881	936	19	0.6	11029	6	CO806853	CO806853 Sequence
C 868	19	0.6	2673	8	HSX251881	936	19	0.6	11029	6	CO806853	CO806853 Sequence
C 869	19	0.6	2684	9	BC027790	937	19	0.6	11029	6	CO807127	CO807127 Sequence
C 870	19	0.6	3025	9	AF314527	938	19	0.6	11029	6	CO807127	CO807127 Sequence
C 871	19	0.6	3077	6	CO806933	939	19	0.6	11029	6	CO807127	CO807127 Sequence
C 872	19	0.6	3077	6	CO807207	940	19	0.6	11029	6	CO807127	CO807127 Sequence
C 873	19	0.6	3077	6	CO807207	941	19	0.6	11029	6	CO807127	CO807127 Sequence
C 874	19	0.6	3103	13	ASF279830	942	19	0.6	11029	6	CO807127	CO807127 Sequence
C 875	19	0.6	3163	15	AK064865	943	19	0.6	11029	6	CO807127	CO807127 Sequence
C 876	19	0.6	3501	4	BC073100	944	19	0.6	11029	6	CO807127	CO807127 Sequence
C 877	19	0.6	3828	4	CATFMS	945	19	0.6	11029	6	CO807127	CO807127 Sequence
C 878	19	0.6	4001	6	CQ787287	946	19	0.6	11029	6	CO807127	CO807127 Sequence
C 879	19	0.6	4001	6	CQ787287	947	19	0.6	11029	6	CO807127	CO807127 Sequence
C 880	19	0.6	4023	6	AX684950	948	19	0.6	11029	6	CO807127	CO807127 Sequence
C 881	19	0.6	4272	15	AY566624	949	19	0.6	11029	6	CO807127	CO807127 Sequence
C 882	19	0.6	4475	9	AF509568	950	19	0.6	11029	6	CO807127	CO807127 Sequence
C 883	19	0.6	4475	9	AF509568	951	19	0.6	11029	6	CO807127	CO807127 Sequence
C 884	19	0.6	4607	6	CS124548	952	19	0.6	11029	6	CO807127	CO807127 Sequence
C 885	19	0.6	4607	6	CS124548	953	19	0.6	11029	6	CO807127	CO807127 Sequence
C 886	19	0.6	4607	6	CS124548	954	19	0.6	11029	6	CO807127	CO807127 Sequence
C 887	19	0.6	4897	9	AX173222	955	19	0.6	11029	6	CO807127	CO807127 Sequence
C 888	19	0.6	4897	9	AX173222	956	19	0.6	11029	6	CO807127	CO807127 Sequence
C 889	19	0.6	5010	13	VACCH2	957	19	0.6	11029	6	CO807127	CO807127 Sequence
C 890	19	0.6	5013	6	AX598997	958	19	0.6	11029	6	CO807127	CO807127 Sequence
C 891	19	0.6	5312	6	AX345098	959	19	0.6	11029	6	CO807127	CO807127 Sequence
C 892	19	0.6	5331	15	AX123148	960	19	0.6	11029	6	CO807127	CO807127 Sequence
C 893	19	0.6	5559	6	AX346325	961	19	0.6	11029	6	CO807127	CO807127 Sequence
C 894	19	0.6	5888	6	CS105991	962	19	0.6	11029	6	CO807127	CO807127 Sequence
895	19	0.6	5888	6	CS105991	963	19	0.6	11029	6	CO807127	CO807127 Sequence
896	19	0.6	5888	6	CS105991	964	19	0.6	11029	6	CO807127	CO807127 Sequence
897	19	0.6	5888	6	CS105991	965	19	0.6	11029	6	CO807127	CO807127 Sequence
898	19	0.6	5888	6	CS105991	966	19	0.6	11029	6	CO807127	CO807127 Sequence
899	19	0.6	5888	6	CS105991	967	19	0.6	11029	6	CO807127	CO807127 Sequence
900	19	0.6	5888	6	CS105991	968	19	0.6	11029	6	CO807127	CO807127 Sequence
901	19	0.6	5888	6	CS105991	969	19	0.6	11029	6	CO807127	CO807127 Sequence
902	19	0.6	5888	6	CS105991	970	19	0.6	11029	6	CO807127	CO807127 Sequence
903	19	0.6	5888	6	CS105991	971	19	0.6	11029	6	CO807127	CO807127 Sequence
904	19	0.6	5888	6	CS105991	972	19	0.6	11029	6	CO807127	CO807127 Sequence
905	19	0.6	5888	6	CS105991	973	19	0.6	11029	6	CO807127	CO807127 Sequence
906	19	0.6	5888	6	CS105991	974	19	0.6	11029	6	CO807127	CO807127 Sequence
907	19	0.6	5888	6	CS105991	975	19	0.6	11029	6	CO807127	CO807127 Sequence
908	19	0.6	5888	6	CS105991	976	19	0.6	11029	6	CO807127	CO807127 Sequence
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910	19	0.6	5888	6	CS105991	978	19	0.6	11029	6	CO807127	CO807127 Sequence
911	19	0.6	5888	6	CS105991	979	19	0.6	11029	6	CO807127	CO807127 Sequence
912	19	0.6	5888	6	CS105991	980	19	0.6	11029	6	CO807127	CO807127 Sequence
913	19	0.6	5888	6	CS105991	981	19	0.6	11029	6	CO807127	CO807127 Sequence
914	19	0.6	5888	6	CS105991	982	19	0.6	11029	6	CO807127	CO807127 Sequence
915	19	0.6	5888	6	CS105991	983	19	0.6	11029	6	CO807127	CO807127 Sequence
916	19	0.6	5888	6	CS105991	984	19	0.6	11029	6	CO807127	CO807127 Sequence
917	19	0.6	5888	6	CS105991	985	19	0.6	11029	6	CO807127	CO807127 Sequence
918	19	0.6	5888	6	CS105991	986	19	0.6	11029	6	CO807127	CO807127 Sequence
919	19	0.6	5888	6	CS105991	987	19	0.6	11029	6	CO807127	CO807127 Sequence
920	19	0.6	5888	6	CS105991	988	19	0.6	11029	6	CO807127	CO807127 Sequence
921	19	0.6	5888	6	CS105991	989	19	0.6	11029	6	CO807127	CO807127 Sequence
922	19	0.6	5888	6	CS105991	990	19	0.6	11029	6	CO807127	CO807127 Sequence
923	19	0.6	5888	6	CS105991	991	19	0.6	11029	6	CO807127	CO807127 Sequence
924	19	0.6	5888	6	CS105991	992	19	0.6	11029	6	CO807127	CO807127 Sequence
925	19	0.6	5888	6	CS105991	993	19	0.6	11029	6	CO807127	CO807127 Sequence
926	19	0.6	5888	6	CS105991	994</						

968	19	0.6	26253	8	AL672212	Human DNA
969	19	0.6	26997	8	AX251506	Sequence
C 970	19	0.6	28652	8	AC144903	Homo sapi
971	19	0.6	31001	2	CEW0704	Caenorhabdi
C 972	19	0.6	31041	8	AC104114	Homo sapi
973	19	0.6	31853	2	CEB44D12	Caenorhabdi
C 974	19	0.6	32158	2	CEW0403	Caenorhabdi
975	19	0.6	32919	14	CEH37L19	Caenorhabdi
C 976	19	0.6	33373	14	AC104975	Homo sapi
977	19	0.6	34769	6	AX251533	Homo sapi
978	19	0.6	35503	2	CEW0906	Sequence
C 979	19	0.6	36154	14	AC100446	Caenorhabdi
980	19	0.6	36846	15	AC149390	Mus muscu
C 981	19	0.6	38046	2	CERT16G12	Phakopox
982	19	0.6	38480	8	AC004090	Caenorhabdi
983	19	0.6	38480	8	AC004090	Homo sapi
C 984	19	0.6	39786	14	AC004256	Homo sapi
C 985	19	0.6	40214	15	AC11622.4	Continuation (5 of
C 986	19	0.6	40251	14	Y8CL8003	U17243 Saccharomyc
C 987	19	0.6	40333	9	AC160852	Homo sapi
988	19	0.6	42100	2	AP001916	Mus muscu
989	19	0.6	42563	14	CEG52A11	Z46792 Caenorhabdi
990	19	0.6	43619	8	AC165828	Bos tauru
991	19	0.6	45114	8	AC118137	Homo sapi
992	19	0.6	45714	15	AC004511	Homo sapi
C 993	19	0.6	46650	14	AC006224	Arabidops
994	19	0.6	47780	13	AC090548	Caenorhabdi
995	19	0.6	48718	15	X67119	Varicella vir
C 996	19	0.6	49386	14	AP006412	Lotus cor
997	19	0.6	50550	7	AF271693	Homo sapi
998	19	0.6	51277	7	AF271693	Mycobacte
999	19	0.6	51962	7	AY500152	Human DNA
C1000	19	0.6	53890	8	AL589990	Human DNA

## ALIGNMENTS

RESULT 1	AF047492	3268 bp	mRNA	linear	PRI 26-OCT-1999
LOCUS	Homo sapiens Interphotoreceptor matrix proteoglycan 150 (IMPG1)				
DEFINITION	mRNA, complete cds.				
ACCESSION	AF047492				
VERSION	AF047492.2 GI:6118565				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 3268)				
AUTHORS	Kuehn,M.H. and Hageman,G.S.				
TITLE	Expression and characterization of the IPM 150 gene (IMPG1) product, a novel human photoreceptor cell-associated chondroitin-sulfate proteoglycan				
JOURNAL	Matrix Biol. 18 (5), 509-518 (1999)				
PUBMED	10601738				
REFERENCE	2 (bases 1 to 3268)				
AUTHORS	Kuehn,M.H. and Hageman,G.S.				
TITLE	Direct Submision				
JOURNAL	Submitted (10-FEB-1998) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 1190E PFP, Iowa City, IA 52240, USA				
REFERENCE	3 (bases 1 to 3268)				
AUTHORS	Kuehn,M.H. and Hageman,G.S.				
TITLE	Direct Submision				
JOURNAL	Submitted (26-OCT-1999) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 1190E PFP, Iowa City, IA 52240, USA				
REMARK	Sequence update by submitter				
COMMENT	On Oct 26, 1999 this sequence version replaced gi:2906231.				
FEATURES	Location/Qualifiers				

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ORIGIN		
Query Match	77.4%;	Score 2578; DB 8; Length 3268;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches 2578;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
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QY	933	CAAGGCAAGGCTCGCTGACTCCCAAGTCCCATATTACACGAGAGCTGACGAGAAAGTCCCA
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DB	991	ATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCAACTTAGGAGCAT
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RESULT 2  
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LOCUS CQ725539 2009 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 11473 from Patent WO02068579.  
ACCESSION CQ725539  
VERSION CQ725539.1 GI:42286477  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;







http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chromosome6>  
RP11-758J17 is from the library RP11-11.3 constructed by the group of Pierre de Jong. For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pBACE3.6

----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)  
-----

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

## FEATURES

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## CDS

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## ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DEFINITION AL359817  
ACCESSION AL359817 GI:12225447  
VERSION HTG; HTGS PHASE1; HTGS\_CANCELLED.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
1 McIlroy, K. Direct Submission Sanger Centre, Hinxton, Cambridgeshire,  
TITLE Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
JOURNAL CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk

## COMMENT

On Jan 14, 2001 this sequence version replaced gi:12214326.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
----- Project Information  
Center project name: ba505B21  
----- Summary Statistics  
Assembly program: XGAP4, version 4.5  
Sequencing vector: plasmid, L08752, 100% of reads  
Chemistry: Dye-terminator Big Dye, 100% of reads  
Consensus quality: 11761 bases at least Q40  
Consensus quality: 12343 bases at least Q30  
Consensus quality: 126505 bases at least Q20  
Insert size: 129645; sum-of-contigs  
Insert size: 166195; 8.3% error; agarose-fp  
Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality  
coverage: 2.65x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 8912: contig of 8912 bp in length  
\* 8913 9012: gap of 100 bp  
\* 9013 12665: contig of 3653 bp in length  
\* 12666 12765: gap of 100 bp  
\* 12766 16825: contig of 4660 bp in length  
\* 16826 16925: gap of 100 bp  
\* 16926 22958: contig of 6033 bp in length  
\* 22959 23058: gap of 100 bp  
\* 23059 25080: contig of 2022 bp in length  
\* 25081 25180: gap of 100 bp  
\* 25181 27272: contig of 2092 bp in length  
\* 27273 27372: gap of 100 bp  
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\* 40755 40854: gap of 100 bp  
\* 40855 45147: contig of 4293 bp in length  
\* 45148 45247: gap of 100 bp  
\* 45248 48493: contig of 3246 bp in length  
\* 48494 48593: gap of 100 bp  
\* 48594 52881: contig of 4288 bp in length  
\* 52882 52981: gap of 100 bp  
\* 52982 57112: contig of 4131 bp in length  
\* 57113 57212: gap of 100 bp  
\* 57213 60637: contig of 3425 bp in length  
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\* 60738 62745: contig of 2008 bp in length  
\* 62746 62845: gap of 100 bp  
\* 62846 70684: contig of 7839 bp in length  
\* 70685 70784: gap of 100 bp  
\* 70785 74560: contig of 3776 bp in length  
\* 74561 74660: gap of 100 bp  
\* 74661 77242: contig of 2582 bp in length  
\* 77243 77342: gap of 100 bp  
\* 77343 81104: contig of 3762 bp in length  
\* 81105 81204: gap of 100 bp  
\* 81205 83750: contig of 2546 bp in length  
\* 83751 83850: gap of 100 bp  
\* 83851 92862: contig of 9112 bp in length  
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\* 93063 106092: contig of 13030 bp in length  
\* 106093 106192: gap of 100 bp  
\* 106193 110995: contig of 4803 bp in length  
\* 110996 111095: gap of 100 bp  
\* 111096 114862: contig of 3767 bp in length  
\* 114863 114962: gap of 100 bp  
\* 114963 118827: contig of 3865 bp in length

\* 118828 118927: gap of 100 bp  
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\* 124085 124184: gap of 100 bp  
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LOCUS Homo sapiens Interphotoreceptor matrix gene (IPM150), exon 17 and
complete cds.
ACCESSION AF017776
VERSION AF017776.1 GI:3800731
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhina;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1235)
AUTHORS Felbor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
GENOMIC ORGANIZATION AND CHROMOSOMAL LOCALIZATION OF THE
INTERPHOTORECEPTOR MATRIX PROTEOGLYCAN-1 (IMPGL) GENE: A CANDIDATE
FOR 6q-Linked RETINOPATHIES
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
9691169
JOURNAL 2 (bases 1 to 1235)
PUBLISHED Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Husels,I.E.
AUTHORS and Weber,B.H.F.
TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bilateral choriorretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDB1)
Unpublished
JOURNAL 3 (bases 1 to 1235)
REFERENCE Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
AUTHORS Direct Submision
JOURNAL Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
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QY 2567 AAGATTGGAGAGAAATTAAGAAATGTAACAATTAATCACTTAAGCTATCTCAAGA 2626
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QY 2627 GAGATGATTCGCTTCTCAAGAAATGAGACAGGCAATTCATGGGTCAATCAAAATCC 2686
DB 531 GAGATGATTCGCTTCTCAAGAAATGAGACAGGCAATTCATGGGTCAATCAAAATCC 590
QY 2687 AGACATACAGTCAACACATGAGATGACACACACCATATTTCAAAATATAGAAAGTCAATG 2746
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QY 2866 GATTGCTTCACACCTCCCTGAAATTTTACTACAGATCAATTCGACAAAGATAGCTT 2925
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QY 2926 ACTATTGTTTAAAGGACGTGAACAATTTTATTTGGAGAGCAAACTTTATATGTAGAAAGT 2985
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 VERSION AF017772.1  
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 ORGANISM Homo sapiens  
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 Homnidae; Homo.  
 1 (bases 1 to 816)  
 REFERENCE  
 AUTHORS Felbor, U., Gehrig, A., Sauer, C.G., Marguardt, A., Kohler, M.,  
 Schmidt, M. and Weber, B.H.  
 TITLE Genomic organization and chromosomal localization of the  
 JOURNAL interphotoreceptor matrix proteoglycan-1 (IPM1) gene: a candidate  
 PUBMED for 6q-linked retinopathies  
 CYTOGENET. Cell Genet. 81 (1), 12-17 (1998)  
 9691169  
 2 (bases 1 to 816)  
 REFERENCE  
 AUTHORS Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussell, I.E.  
 and Weber, B.H.F.  
 TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150)  
 JOURNAL localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
 macular dystrophy, progressive bilateral choriorretinal atrophy  
 (PBCRA), and North Carolina macular dystrophy (MCDN1)  
 UNPUBLISHED  
 3 (bases 1 to 816)  
 REFERENCE  
 AUTHORS Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am  
 Hubland, Wuerzburg D-97074, Germany  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
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 REFERENCE  
 AUTHORS Wall, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonequest@sanger.ac.uk  
 On Sep 12, 2001 this sequence version replaced gi:11991356.  
 COMMENT  
 ----- Genome Center  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: d062L18  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Sequencing vector: plasmid; 108752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 160382 bases at least Q40  
 Consensus quality: 160493 bases at least Q20  
 Consensus quality: 160578 bases at least Q20  
 Insert size: 158939; 9.3% error; agarose-fp  
 Quality coverage: 8.32x in Q20 bases; sum-of-contigs Quality  
 coverage: 8.41x in Q20 bases; agarose-fp  
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 \* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
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QY 1543 TTTATGGCATCAAGCATCTTCTCTGATGATCAAGGACCAAGATTCATGGCCACT 1602  
DB 7702 TTTATGGCATCAAGCATCTTCTCTGATGATCAAGGACCAAGATTCATGGCCACT 7643  
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QY 1783 TCTGAGATACAGAGCTCAGCAATATGTTTCTGTCCAGATCATTTCTTGAAGGATACC 1842  
DB 7462 TCTGAGATACAGAGCTCAGCAATATGTTTCTGTCCAGATCATTTCTTGAAGGATACC 7403  
QY 1843 ACTCTGTCTCAGCTTTACAGTATACCACTAGTCTTATGACCAATGCCCCAAGGAC 1902  
DB 7402 ACTCTGTCTCAGCTTTACAGTATACCACTAGTCTTATGACCAATGCCCCAAGGAC 7343  
QY 1903 CGAGAGCTGTAGTGTCTTCAAGTCTGCGTGTGTTGTAACATGCGCTTCTCCACAGACTG 1962  
DB 7342 CGAGAGCTGTAGTGTCTTCAAGTCTGCGTGTGTTGTAACATGCGCTTCTCCACAGACTG 7283  
QY 1963 TTCACACAGAGCTCTCTGAGTACCGAGCTCTGAGCAACATTCACACAGCTG 2016  
DB 7282 TTCACACAGAGCTCTCTGAGTACCGAGCTCTGAGCAACATTCACACAGCTG 7229

RESULT 8  
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LOCUS Homo sapiens interphotoreceptor matrix gene (IPM150), exon 10.  
DEFINITION AF017769.1 GI:3800724  
ACCESSION AF017769.1 GI:3800724  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
Homo sapiens (human)  
10 of 17  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homniidae; Homo.  
1 (bases 1 to 444)  
Fehlor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,  
Schmid,M. and Weber,B.H.  
Genomic organization and chromosomal localization of the  
interphotoreceptor matrix proteoglycan-1 (IPM1) gene: a candidate  
for 6q-linked retinopathies  
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
JOURNAL  
PUBMED 9691169  
AUTHORS  
REFERENCE  
2 (bases 1 to 444)  
Gehrig,A., Fehlor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.  
and Weber,B.H.F.  
Assessment of a novel interphotoreceptor matrix gene (IPM150)  
TITLE

localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
macular dystrophy, progressive bilateral chorioretinal atrophy  
(PBCRA), and North Carolina macular dystrophy (MCDRI)

JOURNAL  
AUTHORS  
REFERENCE  
3 (bases 1 to 444)  
Fehlor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.  
Direct Submission  
Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am  
Hubland, Wuerzburg D-97074, Germany  
Location/Qualifiers

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Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 91 GCTCAAGCTCCACAGATGACCTTACGGCCATCTTTAAGACACAGTCAGAAAGCA 150  
QY 1139 AAAGCCTGCAAGTACCTCTGCTTTTGAATTCACAAATGAAAGTGAAGTCT 1198  
DB 151 AAAGCCTGCAAGTACCTCTGCTTTTGAATTCACAAATGAAAGTGAAGTCT 210  
QY 1199 ATCATGGAACATGAGAGAGGACAAACCAAAATTAATCTCACAGTACAGACTCA 1258  
DB 211 ATCATGGAACATGAGAGAGGACAAACCAAAATTAATCTCACAGTACAGACTCA 270  
QY 1259 AAAGCTGATGACAAAGACATAGAGAAACAATCTTGGATGTGGGACAATTCACT 1318  
DB 271 AAAGCTGATGACAAAGACATAGAGAAACAATCTTGGATGTGGGACAATTCACT 330  
QY 1319 TCACGTATG 1327  
DB 331 TCACGTATG 339

RESULT 9  
HSIMP02 537 bp DNA linear PRI 28-OCT-1998  
LOCUS Homo sapiens interphotoreceptor matrix gene (IPM150), exon 2.  
DEFINITION AF017761.1 GI:3800716  
ACCESSION AF017761.1 GI:3800716  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
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2 of 17  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homniidae; Homo.  
1 (bases 1 to 537)  
Fehlor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,  
Schmid,M. and Weber,B.H.  
Genomic organization and chromosomal localization of the  
interphotoreceptor matrix proteoglycan-1 (IPM1) gene: a candidate  
for 6q-linked retinopathies  
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
JOURNAL  
PUBMED 9691169  
AUTHORS  
REFERENCE  
2 (bases 1 to 537)  
Gehrig,A., Fehlor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.  
and Weber,B.H.F.  
Assessment of a novel interphotoreceptor matrix gene (IPM150)  
localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
macular dystrophy, progressive bilateral chorioretinal atrophy  
(PBCRA), and North Carolina macular dystrophy (MCDRI)  
TITLE

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Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality
coverage: 2.65x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 8912: contig of 8912 bp in length
* 8913 9012: gap of 100 bp
* 9013 12665: contig of 3653 bp in length
* 12666 12765: gap of 100 bp
* 12766 16885: contig of 4060 bp in length
* 16826 16925: gap of 100 bp
* 16926 22958: contig of 6033 bp in length
* 22959 23058: gap of 100 bp
* 23059 25080: contig of 2022 bp in length
* 25081 25180: gap of 100 bp
* 25181 27272: contig of 2092 bp in length
* 27273 27372: gap of 100 bp
* 27373 40754: contig of 1382 bp in length
* 40755 40854: gap of 100 bp
* 40855 45147: contig of 4293 bp in length
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* 45248 48493: contig of 326 bp in length
* 48494 48593: gap of 100 bp
* 48594 52881: contig of 4288 bp in length
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* 52982 57112: contig of 4131 bp in length
* 57113 57212: gap of 100 bp
* 57213 60637: contig of 3425 bp in length
* 60638 60737: gap of 100 bp
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* 62746 62845: gap of 100 bp
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* 74561 74660: gap of 100 bp
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* 77243 77342: gap of 100 bp
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* 92963 93062: gap of 100 bp
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* 106093 106192: gap of 100 bp
* 106193 110995: contig of 4803 bp in length
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* 114963 118827: contig of 3865 bp in length
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Db 130597 AGATATCTCCATTACATATACCATTTGTAAGACATAGACATCCCGCAAGAAA 130538
QY 256 TGAACCAACCTGAAGTACGAAAAATGACAAAATGCACTATGACACGAATTTCGA 315
Db 130537 TGAACCAACCTGAAGTACGAAAAATGACAAAATGCACTATGACACGAATTTCGA 130478
QY 316 TTTCGCAAGCATCGAACAACAAAGATCCGCAATTTTCCCAACGCGGCTTAAAGTGTCC 375
Db 130477 TTTCGCAAGCATCGAACAACAAAGATCCGCAATTTTCCCAACGCGGCTTAAAGTGTCC 130418
QY 376 ACAGGAATCCATGGAACAGATTTTACAGAGTCTTCAAGCTTATATAGATTGAGAG 431
Db 130417 ACAGGAATCCATGGAACAGATTTTACAGAGTCTTCAAGCTTATATAGATTGAGAG 130362

RESULT 11
AL356962/186301 bp DNA linear PRI 18-MAY-2005
LOCUS Human DNA sequence from clone Rpl1-453C2 on chromosome 6 Contains
DEFINITION the 5' end of the IMPG1 gene for Interphotoreceptor matrix
proteoglycan 1, complete sequence.
ACCESSION AL356962
VERSION AL356962.8 GI:11024485
KEYWORDS HTG; IMPG1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
  1 (bases 1 to 186301)
REFERENCE Pearce,A.
  Direct Submision
  Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
  Clone requests: clonerequests@sanger.ac.uk
  On Oct 26, 2000 this sequence version replaced gi:10944194.
  The following abbreviations are used to associate primary accession
  numbers given in the feature table with their source databases:
  Bm., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMBEP; Information
  on the WORMBEP database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormbep This sequence
  was generated from part of bacterial clone contigs of human
  chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
  Group. Further information can be found at
  http://www.sanger.ac.uk/HGP/Chr6
  Rpl1-453C2 is from the library RPl1-11.2 constructed by the group
  of Pletzer de Jong. For further details see
  http://www.chori.org/bacpac/home.htm
  VECTOR: pBACe3.6
  ----- Genome Center
  Center: Wellcome Trust Sanger Institute
  Genet. code: SC
  Web site: http://www.sanger.ac.uk
  Contact: vegas@sanger.ac.uk
  -----
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one subclone; and the assembly was confirmed by restriction digest,
  except on the rare occasion of the clone being a YAC.

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complement(25288..25454),complement(24982..25010),
complement(15861..15925),complement(12783..12866),
complement(9385..9525),complement(1833..1891),
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complement(AL392166.19:4967..5039),
complement(AL392166.19:2448..3499))
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DB 32795 AGATATCTCCATTAAACATATACATTCGAACTAAGACATAGCAATCCCCAAGAAA 32736
QY 256 TGAACAACATGAAAGTACTGAAAAAATGTACAAAATGTCACTATGAGACGAATTTGCA 315
DB 32735 TGAACAACATGAAAGTACTGAAAAAATGTACAAAATGTCACTATGAGACGAATTTGCA 32676
QY 316 TTGGCAAGCATGCAACAAAAGATCCGACATTTTCCACACGGGGTTAAAGTCGCC 375
DB 32675 TTGGCAAGCATGCAACAAAAGATCCGACATTTTCCACACGGGGTTAAAGTCGCC 32616
QY 376 ACAGAAATCCATGAAACAGATTTTGAAGAGTCCTCAAGCTTATTTAGATTGAGAG 431
DB 32615 ACAGAAATCCATGAAACAGATTTTGAAGAGTCCTCAAGCTTATTTAGATTGAGAG 32560
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LOCUS Homo sapiens interphotoreceptor matrix gene (IMP150), exon 15.
DEFINITION AF017774
ACCESSION AF017774.1 GI:3800729
VERSION 1
KEYWORDS 15 of 17
SEGMENT
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 477)
REFERENCE Felbor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,
AUTHORS Genomic organization and chromosomal localization of the
TITLE interphotoreceptor matrix proteoglycan-1 (IMPg1) gene: a candidate
for 6q-linked retinopathies
JOURNAL Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
PUBMED 9691169
JOURNAL 2 (bases 1 to 477)
REFERENCE Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Huissels,I.E.,
AUTHORS and Weber,B.H.F.
TITLE Assessment of a novel interphotoreceptor matrix gene (IMP150)
mapped to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bilateral chorioretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDRI)
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 477)
AUTHORS Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am
Hudland, Wuerzburg D-97074, Germany
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VERSION AF017760.1 GI:3800715  
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SEGMENT  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo  
1 (bases 1 to 310)  
Felbor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,  
Schmid,M. and Weber,B.H.  
Genomic organization and chromosomal localization of the  
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate  
for 6q-linked retinopathies  
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
9691169  
JOURNAL  
PUBMED  
2 (bases 1 to 310)  
Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.  
and Weber,B.H.F.  
Assessment of a novel interphotoreceptor matrix gene (IPM150)  
localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
macular dystrophy, progressive bilateral choroidretinal atrophy  
(PBCRA), and North Carolina macular dystrophy (MCDRI)  
Unpublished  
3 (bases 1 to 310)  
Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.  
Direct Submission  
Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am  
Hubland, Wuerzburg D-97074, Germany  
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DB 27 TAAACCAAGAGTTATCTCATCATCTGTATCATATATATTTTCACTTC 86  
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LOCUS HSIMPG14 448 bp DNA linear PRI 28-OCT-1998  
DEFINITION Homo sapiens interphotoreceptor matrix gene (IPM150), exon 14.  
ACCESSION AF017773  
VERSION AF017773.1 GI:3800728  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo  
1 (bases 1 to 448)  
Felbor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,  
Schmid,M. and Weber,B.H.  
Genomic organization and chromosomal localization of the  
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate  
for 6q-linked retinopathies  
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
9691169  
JOURNAL  
PUBMED  
2 (bases 1 to 448)  
Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.  
and Weber,B.H.F.  
Assessment of a novel interphotoreceptor matrix gene (IPM150)  
localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
macular dystrophy, progressive bilateral choroidretinal atrophy  
(PBCRA), and North Carolina macular dystrophy (MCDRI)  
Unpublished  
3 (bases 1 to 448)  
Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.  
Direct Submission  
Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am  
Hubland, Wuerzburg D-97074, Germany  
Location/Qualifiers  
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DB 290 CCATCTGGAATATAGACAGCTACTCTCTCAACATTTGAACAG 330  
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RESULT 15
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DEFINITION       Homo sapiens interphotoreceptor matrix gene (IPM150), exon 3.
ACCESSION        AF017762
VERSION          AF017762.1  GI:3800717
KEYWORDS
SEGMENT
SOURCE
ORGANISM         Homo sapiens (human)
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                 Homidae; Homo.
REFERENCE        1 (bases 1 to 422)
AUTHORS          Gehrig, A., Gehrig, A., Sauer, C.G., Marguardt, A., Kohler, M.,
                 Schmidt, M. and Weber, B.H.
TITLE            Genomic organization and chromosomal localization of the
                 interphotoreceptor matrix proteoglycan-1 (IMPGL) gene: a candidate
                 for 6q-linked retinopathies
JOURNAL          Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
PUBMED           9691169
REFERENCE        2 (bases 1 to 422)
AUTHORS          Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E.
                 and Weber, B.H.F.
TITLE            Assessment of a novel interphotoreceptor matrix gene (IPM150)
                 localized to 6q14.2-q15 in autosomal dominant Stargardt-like
                 macular dystrophy, progressive bifocal choriorretinal atrophy
                 (PBCRA), and North Carolina macular dystrophy (MCDRI)
                 Unpublished
REFERENCE        3 (bases 1 to 422)
AUTHORS          Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
TITLE            Direct Submission
JOURNAL          Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
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Best Local Similarity 100.0%; Pred. No. 5.6e-83;
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Db 110 AGTGTCTCAGAAGCAGTATGGAGACATATCGATCTTCTGATCCGATCCCTGACAC 169
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2006, 07:32:00 ; Search time 12643 Seconds  
(without alignments) 12323.102 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_esc4:\*  
5: gb\_esc5:\*  
6: gb\_esc6:\*  
7: gb\_esc7:\*  
8: gb\_esc8:\*  
9: gb\_esc9:\*  
10: gb\_esc10:\*  
11: gb\_esc11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2635.6	79.1	5829	4	CR749572 Homo sapi
2	1642.4	49.3	1665	10	AY415971 Homo sapi
3	943.6	28.3	1647	10	AY415973 Mus muscu
4	739.2	22.2	1587	10	AY415972 Pan trogl
5	716.2	22.5	801	2	BG196799 RST16026
6	640.2	13.2	836	5	BI752112 603022362
7	634	13.0	690	5	BX510244 DKFZp686P
8	628.8	13.9	633	3	BM659587 UI-E-CKI-
9	626	18.8	626	5	BQ639265 hd31d04.Y
10	617.2	18.5	622	5	BQ638902 hd29d06.Y
11	615.6	18.5	653	3	BM685921 UI-E-CKI-
12	589.4	17.7	675	3	BM690735 UI-E-CKI-
13	577.6	17.3	598	3	BM690735 UI-E-CKI-
14	498.4	15.0	508	6	CA393958 hd11h02.Y
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23	385.6	11.6	851	3	BI733865 603353151
24	380.2	11.4	393	5	BQ636351 hd07h06.Y
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27	354.4	10.6	405	8	H38604 yp48e04.r1
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#### ALIGNMENTS

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DEFINITION Homo sapiens mRNA; cDNA DKFZp686K0887 (from clone DKFZp686K0887).  
ACCESSION CR749572  
VERSION CR749572.1 GI:51476810  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 5829)  
Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fodor, G., Han, M. and  
Wiemann, S.  
The German cDNA Consortium  
Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuberberg, GERMANY  
COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
Sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFZp686K0887) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneid=DKFZp686K0887  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

FEATURES  
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Db	3041	CACCTCTCTCAATGAAATTTCTGATATACCTCAACGACCAAGATGCTTACACAGA	3100				
Qy	861	AGAGCAAAATTCAGATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTCACTCTGATGA	920				
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Db	4781	CGTAGAATATGAGAAATTTAAACATCAAGATTTGGAGAGAAATTTAAATCTGAAATGTA	4840
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Qy 3321 CATATTCAT 3330
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LOCUS Homo sapiens IMPG1 gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION AY415971
ACCESSION AY415971.1 GI:39771931
VERSION 1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Molecular Systematic: Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1665)
Clack,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Interferring nonneutral evolution from human-chimp-mouse orthologous
gene tios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 1665)
AUTHORS Clack,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Qy 1342 CTGCCAGCTTTGATCTGACACACCAATCAGAGTCCACACATCTTTGCTGTTAACA 1401
Db 421 CTGCCAGCTTTGATCTGACACACCAATCAGAGTCCACACATCTTTGCTGTTAACA 480
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 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
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 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
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 2 (bases 1 to 1647)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,  
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 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
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ACCESSION
AY415972
VERSION
AY415972.1 GI:39771932
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE
1 (bases 1 to 1587)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1587)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submision
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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source
1..1587
/organism="Pan troglodytes"
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Best Local Similarity 46.7%; Pred.No. 2.2e-180;
Matches 741; Conservative 0; Mismatches 846; Indels 0; Gaps 0;
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REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
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Creation of genome-wide protein expression libraries using random
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Nat. Biotechnol. 19 (5), 440-445 (2001)
11329013
JOURNAL
PUBMED
COMMENT
Athersys, Inc.
Contact: Scott J. Cain
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scotina@atersys.com
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Matches 757; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

Qy      2449 TCTGAAATTCAGACATCAAAATAGTGTAAAGTTCCAAATCAACAAATTAACAG 2508
Db      23 TCTGAAATTCAGACATCAAAATAGTGTAAAGTT-CAAAATCAACAAATTAACAG 81
Qy      2509 GTAATCACTAATAAGAAATTCGAAATTAAGACCGTGAATATGAAGAAATTTAACATCA 2568
Db      82 GTAATCACTAATAAGAAATTCGAAATTAAGACCGTGAATATGAAGAAATTTAACATCA 141
Qy      2569 GATTGGGAAGAAATTTAAATCTGAAATATGTAATTTTCACTTAGGCTATCTCAAGAGA 2628
Db      142 GATTGGGAAGAAATTTAAATCTGAAATATGTAATTTTCACTTAGGCTATCTCAAGAGA 201
Qy      2629 GATGATTTGCTTCAAGAAATGAGACAGGATATTCATGGATCAAAATTCAG 2688

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Db	202	GATGATTTGCCCTTCTCAAGAAAATATGAGACAGGCAATTTATCGGTCATCAAAATCCAG	261
QY	2699	ACATTCAGTCAACACTGGAATCAGCAACACCATATTTCAAATATAGAAAGTCATGTA	2748
Db	262	ACATTCAGTCAACACTGGAATCAGCAACACCATATTTCAAATATAGAAAGTCATGTA	321
QY	2749	CTTGCGCAACAGTAATCTCTGAAAAAAGAACACTTACTTATTTAAACCCCAATGC	2808
Db	322	CTTGCGCAACAGTAATCTCTGAAAAAAGAACACTTACTTATTTAAACCCCAATGC	381
QY	2809	AATCAGCGAAACATATTTTACTATTTCTTGATGTAGTCAAAATGATCATPAGCCAGT	2868
Db	382	AATCAGCGAAACATATTTTACTATTTCTTGATGTAGTCAAAATGATCATPAGCCAGT	441
QY	2869	TTGCTTCCACCTTCCCTGAAAAATTTTACTCACATCATTTTGCAACAAAGATAGCTTACT	2928
Db	442	TTGCTTCCACCTTCCCTGAAAAATTTTACTCACATCATTTTGCAACAAAGATAGCTTACT	501
QY	2929	TATGTTTAGGGAACCTGAACAAATTTATTTGGGAACAACTCTTTATATGCTTGAAGAATCA	2988
Db	502	TATGTTTAGGGAACCTGAACAAATTTATTTGGGAACAACTCTTTATATGCTTGAAGAATCA	561
QY	2989	TTTAAAAATGACTACTTACGACGAGGAGATGCAAGTCTCTGTAACGCAATGATATGT	3048
Db	562	TTTAAAAATGACTACTTACGACGAGGAGATGCAAGTCTCTGTAACGCAATGATATGT	621
QY	3049	AGTGTGTAAGGCACTGTAGTGAATGATATATATGCTTCACACTACGCTGTATTAACACAAC	3108
Db	622	AGTGTGTAAGGCACTGTAGTGAATGATATATATGCTTCACACTACGCTGTATTAACACAAC	681
QY	3109	CTCAGTATTCAGTATTTTGGGCACTAGTTTATTCGCACTACTGCTTACATAGTATGAC	3168
Db	682	CTCAGTATTCAGTATTTTGGGCACTAGTTTATTCGCACTACTGCTTACATAGTATGAC	741
QY	3169	TGTTTGTGTCGAATATCTTTGAATGTTCTTTAAAGAAACAGAGTTGAGAT	3223
Db	742	TGTTTGTGTCGAATATCTTTGAATGTTCTTTAAAGAAACAGAGTTGAGAT	794
RESULT 6			
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LOCUS	60302236221	NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192991 5',	
DEFINITION		mRNA sequence.	
ACCESSION	B1752112		
VERSION	B1752112.1	GI:15743690	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE	1 (bases 1 to 836)		
AUTHORS	NIH-MGC http://mgs.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: L14M11482 row: 1 column: 16 High quality sequence stop: 822. Location/Qualifiers 1. 836 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5192991"		
FEATURES			
source			

Query Match	19.2%	Score 640.2	DB 3	Length 836
Best Local Similarity	96.8%	Pred. No. 1e-154		
Matches 693	Conservative 0	Mismatches 18	Indels 5	Gaps 4

  

ORIGIN	Query Match	19.2%	Score 640.2	DB 3	Length 836
Best Local Similarity	96.8%	Pred. No. 1e-154			
Matches 693	Conservative 0	Mismatches 18	Indels 5	Gaps 4	

  

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/lab host="NDH10B"
/clone.lib="NIH_MGC_114"
/name="Organ: brain; Vector: pCMV-SPORT6; site_1: NotI;
site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(introgen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

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KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 630)  
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,  
Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
Wiemann,S.  
TITLE EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,  
Wellenreuther,R., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp686P2496) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
LOCATION/Qualifiers  
1..630  
/organism="Homo sapiens"  
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/lab\_host="DH10B"  
/clone\_lib="686 (synonym: h1c3)"  
/note="Vector: pTriblox2; Site\_1: SfilA; Site\_2: SfilB;  
cDNA-collection"

ORIGIN  
Query Match 19.0%; Score 634; DB 5; Length 630;  
Best Local Similarity 100.0%; Pred. No. 3.9e-153;  
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCAAGAGGATCTCAATCATCTGATCAATATATATATATTTTTCACATTC 60  
DB 57 TAAACCAAGAGGATCTCAATCATCTGATCAATATATATATATTTTTCACATTC 116  
QY 61 TGTACTTTTATAGATTGAGGTTGTTCTGTGATTTGTTATCAGAAATTCAGATGAC 120  
DB 117 TGTACTTTTATAGATTGAGGTTGTTCTGTGATTTGTTATCAGAAATTCAGATGAC 176  
QY 121 AAAAGCCAGAAATGTATTTGGAAAGTAAAGACCTATTTTGTGTTTGGATTTTCTCA 180  
DB 177 AAAAGCCAGAAATGTATTTGGAAAGTAAAGACCTATTTTGTGTTTGGATTTTCTCA 236  
QY 181 AGTTCAAGAAACCAAGATATCTCCATTACATATACATTTCTGAACCTAAAGACATGA 240  
DB 237 AGTTCAAGAAACCAAGATATCTCCATTACATATACATTTCTGAACCTAAAGACATGA 296  
QY 241 CAATCCCCCAGAAATGAAACACTGAAAGTAAAGTAAAGTAAAGTCAATAT 300  
DB 297 CAATCCCCCAGAAATGAAACACTGAAAGTAAAGTAAAGTCAATAT 356  
QY 301 GAGAGGAATATTCGATTTGGCAAGCATCGAAACAAAGATCCGATTTTCCCAACGGG 360  
DB 357 GAGAGGAATATTCGATTTGGCAAGCATCGAAACAAAGATCCGATTTTCCCAACGGG 416  
QY 361 GGTAAAGTGTCCACAGAAATCCATGAAACAGATTTTGAAGTCTTCAAGCTTATTA 420  
DB 417 GGTAAAGTGTCCACAGAAATCCATGAAACAGATTTTGAAGTCTTCAAGCTTATTA 476  
QY 421 TAGATTGAGAGTGTCTCAGAAAGCATGTATGGAAACATATCGATCTTTCTGGATCGAT 480

DB 477 TAGATTGAGAGTGTCTCAGAAAGCATGTATGGAAACATATCGATCTTTCTGGATCGAT 536  
QY 481 CCTGACACAGAGGAATATTCGAGACTGGGTAGACTTCGCACAGACGAGACCTTGTGCT 540  
DB 537 CCTGACACAGAGGAATATTCGAGACTGGGTAGACTTCGCACAGACGAGACCTTGTGCT 596  
QY 541 CTTTGACATTTGAAAAAACTTCAGCAATTCACAGAGCAGCTGTGATCTTCTTCACAGAG 600  
DB 597 CTTTGACATTTGAAAAAACTTCAGCAATTCACAGAGCAGCTGTGATCTTCTTCACAGAG 656  
QY 601 AATAAACAGAGAAAGTTTCCCTGACAGAAAGAT 634  
DB 657 AATAAACAGAGAAAGTTTCCCTGACAGAAAGAT 690

RESULT 8  
BM695987  
LOCUS  
DEFINITION  
UI-E-CL1-afa-m-11-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone  
BM695987  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 633)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
8889548  
COMMENT  
JOURNAL PUBMED  
AUTHORS  
TITLE  
FEATURES  
SOURCE  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-CL1-afa-m-11-0-UI"  
/tissue\_type="human retina"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CL1"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-E-CL1 is a normalized cDNA library containing the  
following tissue(s): retina. The library was constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pT73-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CCGCG. This library was  
created for the program, Gene Discovery in the Visual  
System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 18.8%; Score 628.8; DB 3; Length 633;  
 Best Local Similarity 99.5%; Pred. No. 8.5e-152;  
 Matches 630; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2529 TGAATTAATGACCGTGAATGAGAAATTTAAACATCAAGATTTGGGAAAGAAATTTAAA 2588  
 1 TGAATTAATGACCGTGAATGAGAAATTTAAACATCAAGATTTGGGAAAGAAATTTAAA 60

2589 ACTGAAATGTAACAATTAATCACTTAGGCTATCTCAAGAGATGATTTGCTTCTCAAG 2648  
 61 ACTGAAATGTAACAATTAATCACTTAGGCTATCTCAAGAGATGATTTGCTTCTCAAG 120

2649 AAAATGAGACAGGCTATTTGATGAGTCAAAATCCAGACATTAAGTCAACATGAGA 2708  
 121 AAAATGAGACAGGCTATTTGATGAGTCAAAATCCAGACATTAAGTCAACATGAGA 180

2709 ATCAGACACACCATATTTCAAAATATAGAAAGTCAATGTAATTTGGACACAGTAATTC 2768  
 181 ATCAGACACACCATATTTCAAAATATAGAAAGTCAATGTAATTTGGACACAGTAATTC 240

2769 GAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTT 2828  
 241 GAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTT 300

2829 ACTATTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2888  
 301 ACTATTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

2889 AATTTTACTCAGACATTTTGGCAACACATAGCTTACTTATTTGTTTGGGACGTGA 2948  
 361 AATTTTACTCAGACATTTTGGCAACACATAGCTTACTTATTTGTTTGGGACGTGA 420

2949 ATTATTTGGGAACAACCTCTTATATGCTAGAAATGATATTTAAAGATGACTACTTAC 3008  
 421 ATTATTTGGGAACAACCTCTTATATGCTAGAAATGATATTTAAAGATGACTACTTAC 480

3009 GCAAGGAGATGCAAGTCTCTTAAACGATGAAATGTAATGATGATGATGATGATGAT 3068  
 481 GCAAGGAGATGCAAGTCTCTTAAACGATGAAATGTAATGATGATGATGATGATGAT 540

3069 AGTGTATATATGCTCCACACTGCTGCTGATTAACAAACCTCAGATTCAGTTATTA 3128  
 541 AGTGTATATATGCTCCACACTGCTGCTGATTAACAAACCTCAGATTCAGTTATTA 600

3129 CACACTAGTTTATAGCAACTACTGCTTACAT 3161  
 601 CACACTAGTTTATAGCAACTACTGCTTACAT 633

Db

RESULT 9  
 LOCUS B0639265 626 bp mRNA linear EST 15-JUL-2002  
 DEFINITION hd33d04.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
 VERSION B0639265  
 KEYWORDS B0639265.1 GI:21763724  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 626)  
 Wistow G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.,  
 Expressed sequence tag analysis of human retina for the NEIBank  
 Project: Rebinding, an abundant, novel retinal cDNA and alternative  
 splicing of other retina-preferred gene transcripts  
 Mol. Vis. 8 (4), 196-204 (2002)  
 JOURNAL PUBMED 12107411  
 COMMENT Contact: Wistow G

Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: gtaeme@helix.nih.gov  
 Plate: 33 row: d column: 04  
 Seq primer: M13RP1 reverse primer (AB1).  
 Location/Qualifiers

## FEATURES

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 unamplified): hd/he"  
 /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
 was dissected from two 80 year old donors with no observed  
 eye disease. 100ug of total RNA was used for library  
 construction. A directionally cloned cDNA library in the  
 pSPORT1 vector (Life Technologies) was constructed at  
 Bioserve Biotechnology (laurel MD) essentially following  
 the protocols of the SuperScript Plasmid System full  
 details of which are contained in the manufacturer's  
 instruction manual (http://www.lifetech.com/). First  
 strand synthesis was carried out using a Not I  
 primer-adaptor  
 [5'-pGACTTACTTGAATCGGACGGCCGCTT5'-3']. EST analysis  
 was performed on the unamplified library at the NIH  
 Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 18.8%; Score 626; DB 5; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-151;  
 Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

968 ACCAGAGCTAGCAGAAAGTCCCACTCAGATGCAAAAGATTTAAGAACTTCCAG 1027  
 1 ACCAGAGCTAGCAGAAAGTCCCACTCAGATGCAAAAGATTTAAGAACTTCCAG 60

1028 GATTCAAAAAATCCATGTTGTTAGATTTAGACCAAGAAAGAAAGATGCTCAAGCT 1087  
 61 GATTCAAAAAATCCATGTTGTTAGATTTAGACCAAGAAAGAAAGATGCTCAAGCT 120

1088 CCACAGAGATGCAACTTACGGCCATCTTTAAGACACAGTCCAGAGCAAAAGCCCG 1147  
 121 CCACAGAGATGCAACTTACGGCCATCTTTAAGACACAGTCCAGAGCAAAAGCCCG 180

1148 CAAGTGAAGCTCTGCTCTTTTGAATCCAAATAATTTGAAGAGAGATCTATCATGAA 1207  
 181 CAAGTGAAGCTCTGCTCTTTTGAATCCAAATAATTTGAAGAGATCTATCATGAA 240

1208 CCATGAGAGGAGCAAGCAACCAAAATCTATCTCAAGCTACAGACTCAAAAAGGCTGA 1267  
 241 CCATGAGAGGAGCAAGCAACCAAAATCTATCTCAAGCTACAGACTCAAAAAGGCTGA 300

1268 TCAGAGAAAGCACTAAGAGAAACAATCTTTGAGATGAGGAGCAATTCAGTCACTGAG 1327  
 301 TCAGAGAAAGCACTAAGAGAAACAATCTTTGAGATGAGGAGCAATTCAGTCACTGAG 360

1328 AAATGCTGATCACTGACAGCTTTGCTGTCGACACCAATCAGAGCTGCCACATCTT 1387  
 361 AAATGCTGATCACTGACAGCTTTGCTGTCGACACCAATCAGAGCTGCCACATCTT 420

1388 TTGCTGTTTAAACAGAGATGCTACTTTGATGTCGAAGTCTCTCTGTTGAACCCACG 1447  
 421 TTGCTGTTTAAACAGAGATGCTACTTTGATGTCGAAGTCTCTCTGTTGAACCCACG 480

1448 TTGAGACAGTGAAGGAGAGAGAGATGCTACTGACACTTCTTGCTGACCTGCTA 1507

Db

Db 481 TTGACAGATGACGAGACGAGATGCTTCTACCTTCTTCTCCACCTGTCTA 540  
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Db 601 TGACGATCAAGGACCAAGCATATAGA 626

RESULT 10  
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LOCUS hd29a06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
DEFINITION Homo sapiens cDNA clone hd29a06 5', mRNA sequence.  
ACCESSION BQ638902.1 GI:21763361  
VERSION BQ638902.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 622)  
Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A.,  
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
Expressed sequence tag analysis of human retina for the NEIBank  
Project: Retbindin, an abundant, novel retinal cDNA and alternative  
splicing of other retina-preferred gene transcripts  
Mol. Vis. 8 (4), 196-204 (2002)  
12107411  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: gwaem@helix.nih.gov  
Plate: 29 row: a column: 06  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
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/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_1fb="Human Retina cDNA (Un-normalized,  
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/note="Organ: Eye; Vector: pSPORT1, Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
the protocols of the Superscript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTGATGTTTGAATCGGACGCGCCCT(T)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

ORIGIN  
Query Match 18.5%; Score 617.2; DB 5; Length 622;  
Best Local Similarity 99.5%; Pred. No. 8.8e-149;  
Matches 619; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2480 AAAAGTCCAAATCAACAAATTAACAGATATCAGTAAAGAAATCTGAAATTAAGTA 2539

Db 1 AAAAGTCCAAATCAACAAATTAACAGATATCAGTAAAGAAATCTGAAATTAAGTA 60  
Qy 2540 CCGTGAATATGAAGAAATTTAAACATCAAGATTTGGAGAGAAATTTAAATCTGAAATATGT 2599  
Db 61 CCGTGAATATGAAGAAATTTAAACATCAAGATTTGGAGAGAAATTTAAATCTGAAATATGT 120  
Qy 2600 ACAATATCACTTAGGCTATCTCAAGAGATGATTTTCTCTCAAGAGAAATTTGAAGAC 2659  
Db 121 ACAATATCACTTAGGCTATCTCAAGAGATGATTTTCTCTCAAGAGAAATTTGAAGAC 180  
Qy 2660 AGGCATATTCATGGGTCAATCAAAATCCAGACATACATGCAACCTGAGAAATCAGACACA 2719  
Db 181 AGGCATATTCATGGGTCAATCAAAATCCAGACATACATGCAACCTGAGAAATCAGACACA 240  
Qy 2720 CCATTTTCAATATGAAGAGTCACTGACTTTGGCAACCATTAATTTCTGAAAAAATGA 2779  
Db 241 CCATTTTCAATATGAAGAGTCACTGACTTTGGCAACCATTAATTTCTGAAAAAATGA 300  
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Db 301 CACTTACTTATTTAAACCCCAATGCAAGCAATCAATATTTTACTATTTCTTGG 360  
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Qy 2960 AGCAAACTCTTATATGCTAGTAAAGTACATTTAAAGATGACTACTTACGACGAGAGATG 3019  
Db 481 AGCAAACTCTTATATGCTAGTAAAGTACATTTAAAGATGACTACTTACGACGAGAGATG 540  
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Db 541 CAGGTCTCTTAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
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Db 601 GCTCGACACTAGCTGTGATTA 622

RESULT 11  
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LOCUS UI-E-CR0-sas-h-07-0-UI.r1 UI-E-CR0 Homo sapiens cDNA clone  
DEFINITION UI-E-CR0-sas-h-07-0-UI 5', mRNA sequence.  
ACCESSION BQ685921  
VERSION BQ685921.1 GI:18995817  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 653)  
Bonald, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL  
PUBMED  
COMMENT  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MBBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse.

## FEATURES

SOURCE

Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="UI-E-CKO-aav-h-07-0-UI"  
 /tissue\_type="Retina Foveal and Macular"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-CKO"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Ecor I; Site 2: Not I;  
 UI-E-CKO is a cDNA library containing the following  
 tissue(s): Retina Foveal and Macular. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an Ecor I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is GTCC.  
 This library was created for the program, Gene Discovery  
 in the Visual System, supported by National Eye Institute  
 (NEI)."

## ORIGIN

Query Match 18.5%; Score 615.6; DB 3; Length 653;  
 Best Local Similarity 99.4%; Pred. No. 2.3e-148;

Matches 618; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2709 ATCAGCAGCACCATTATTTCAATATAGAGGTGATGACTTGGACCGATAATCT 2768  
 10 AACGACACACCAATATTTCAATATAGAGGTGATGACTTGGACCGATAATCT 69  
 2769 GAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCAATATTTT 2828  
 70 GAAAGAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCAATATTTT 129  
 2829 ACTATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2888  
 130 ACTATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189  
 2889 AATTTTCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2948  
 190 AATTTTCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249  
 2949 AATTTTGGGAAGCAACTCTTATATGCTAGAAAGTACATTTAAAGATGACTTAC 3008  
 250 AATTTTGGGAAGCAACTCTTATATGCTAGAAAGTACATTTAAAGATGACTTAC 309  
 3009 GCAGGGAATGAGGCTCTCTTAAACGATGATGATGATGATGATGATGATGATG 3068  
 310 GCAGGGAATGAGGCTCTCTTAAACGATGATGATGATGATGATGATGATGATG 369  
 3069 AGTATATATGCTCTCAGATGATGATGATGATGATGATGATGATGATGATGATG 3128  
 370 AGTATATATGCTCTCAGATGATGATGATGATGATGATGATGATGATGATGATG 429  
 3129 CACACTAGTTTATAGCAACTGCTTACATAGTAGAGTGTGTTGGCAATATCT 3188  
 430 CACACTAGTTTATAGCAACTGCTTACATAGTAGAGTGTGTTGGCAATATCT 489  
 3189 TTGAATTTGTTCTTTAAAGAACTGAGTTCAATATGATGATGATGATGATGATG 3248  
 490 TTGAATTTGTTCTTTAAAGAACTGAGTTCAATATGATGATGATGATGATGATG 549  
 3249 TTCTTTGTTTACACAAAGCATTTTAAAGAAAGTGTGATGTTGGGAAGGGCAAGT 3308

Db 550 TTCTCTGTTACTACCAAGCATTTTAAAGAAAGTGTGATGATGATGATGATGATG 609  
 Qy 3309 TGTACTATATGACATATATCAAT 3330  
 Db 610 TGTACTATATGACATATATCAAT 631

## RESULT 12

BM690735

LOCUS 675 bp mRNA linear EST 28-PEB-2002  
 DEFINITION UI-E-CKO-aav-c-12-0-UI .x1 UI-E-CKO Homo sapiens cDNA clone  
 UI-E-CKO-aav-c-12-0-UI 5', mRNA sequence.

ACCESSION

BM690735

VERSION

BM690735.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 675)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1. .675

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-CKO-aav-c-12-0-UI"

/tissue\_type="Retina Foveal and Macular"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-CKO"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site 1: Ecor I; Site 2: Not I;

UI-E-CKO is a cDNA library containing the following

tissue(s): Retina Foveal and Macular. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an Ecor I

adaptor, digested with Not I, and cloned directionally

into pT73-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is GTCC.

This library was created for the program, Gene Discovery

in the Visual System, supported by National Eye Institute

(NEI)."

## ORIGIN

Query Match 17.7%; Score 589.4; DB 3; Length 675;  
 Best Local Similarity 99.7%; Pred. No. 1.6e-141;  
 Matches 601; Conservative 0; Mismatches 1; Indels 1; Gaps 1;



QY	2728	CAAAATATGGAAGACATGTA	CTTGGCAACAGTAATTCGAAAAAAGACGCTTACT	2787
Db	8	CAAAATATGGAAGA-TCATGTA	CTTGGCAACAGTAATTCGAAAAAAGACGCTTACT	66
QY	2788	TATATATTTAAAAACCCCAAT	TGCATCAGGAAACAATATTTTACATTTCTTGGATGATAGT	2847
Db	67	TATATATTTAAAAACCCCAAT	TGCATCAGGAAACAATATTTTACATTTCTTGGATGATAGT	126
QY	2848	CAAAATGATCATTAAGCCAG	TTTGCTTCCAGTAAATTTTATCTCACAGATCAT	2907
Db	127	CAAAATGATCATTAAGCCAG	TTTGCTTCCAGTAAATTTTATCTCACAGATCAT	186
QY	2908	TTGCAACAGAGATGAGTCTTA	TTTGTTTAGGGACTGAAACAATTTATTTGGGAACCAACT	2967
Db	187	TTGCAACAGAGATGAGTCTTA	TTTGTTTAGGGACTGAAACAATTTATTTGGGAACCAACT	246
QY	2968	CTTTATATGCTAGAAAAAGTA	CACTTTAAAAAGATGACTTACTTACGACGGAGATGACAGTCTC	3027
Db	247	CTTTATATGCTAGAAAAAGTA	CACTTTAAAAAGATGACTTACTTACGACGGAGATGACAGTCTC	306
QY	3028	TCTTAAACGCATGAAATGTA	TGTAGTGTAGGCACTGTAGTAGTATATATATGCTCCACA	3087
Db	307	TCTTAAACGCATGAAATGTA	TGTAGTGTAGGCACTGTAGTAGTATATATATGCTCCACA	366
QY	3088	CTAGCGTCTGATTAACACAA	CAACCTCAGTATTCAGTTATTTAGGACACACTAGTTTATAGCA	3147
Db	367	CTAGCGTCTGATTAACACAA	CAACCTCAGTATTCAGTTATTTAGGACACACTAGTTTATAGCA	426
QY	3148	ACTACTGCTTACATAGTAGTA	CTGTTTGTGSCAAATATCTTTGATATGTTCTTTTAAAG	3207
Db	427	ACTACTGCTTACATAGTAGTA	CTGTTTGTGSCAAATATCTTTGATATGTTCTTTTAAAG	486
QY	3208	AAACTGAGGTTCAGATACACA	TACATCCATGGAATAATCTTACTTTCTTGTGTACTACACAA	3267
Db	487	AAACTGAGGTTCAGATACACA	TACATCCATGGAATAATCTTACTTTCTTGTGTACTACACAA	546
QY	3268	GCTATTTTAAAGAGATGCTA	TGTTGGAGAAAGGCGAAGTTGTACTATAGACATATATC	3327
Db	547	GCTATTTTAAAGAGATGCTA	TGTTGGAGAAAGGCGAAGTTGTACTATAGACATATATC	606
QY	3328	AAT 3330		
Db	607	AAT 609		
RESULT 13				
LOCUS	B0636596	598 bp	mRNA	linear
DEFINITION	hd11h02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he			
ACCESSION	B0636596			
VERSION	B0636596.1	GI:21761055		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
TITLE	Homnidae; Homo.			
JOURNAL	1 (bases 1 to 598)			
PUBMED	Wietow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,			
COMMENT	Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.			
	Expressed sequence tag analysis of human retina for the NEIRank			
	Project: Retbindin, an abundant, novel retinal cDNA and alternative			
	splicing of other retina-preferred gene transcripts			
	MOL. VIS. 8 (4), 196-204 (2002)			
	12107411			
	Contact: Wietow G			
	Section on Molecular Structure and Function			
	National Eye Institute			
	6/331, NIH, Bethesda, MD 20892-2740, USA			
	Tel: 301 402 3452			
	Fax: 301 496 0078			
	Email: gzieme@helix.nih.gov			

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Plate: 11 row: h column: 02
Seq primer: M13R1 reverse primer (ABI)
Location/Qualifiers
1. .598
FEATURES
source
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/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="hd1h02"  
 /tissue\_type="Retina"  
 /dev\_stage="adult"  
 /lab\_host="BMD10B"  
 /clone\_id="human Retina cDNA (un-normalized,  
 unamplified)": hd/he"  
 /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
 was dissected from two 80 year old donors with no observed  
 eye disease. 100ug of total RNA was used for library  
 construction. A directionally cloned cDNA library in the  
 pSPORT1 vector (Life Technologies) was constructed at  
 Bioserve Biotechnology (Laurel MD) essentially following  
 the protocols of the Superscript Plasmid System full  
 details of which are contained in the manufacturer's  
 instruction manual (<http://www.lifetech.com/>). First  
 strand synthesis was carried out using a Not I  
 primer-adaptor  
 [5'-pGACGTGTTTACAGTCGCGAGCGCCGCC(715-3')]. EST analysis  
 was performed on the unamplified library at the NIH  
 Intramural Sequencing Center (NISC)."

**ORIGIN**

Query Match	17.3%	Score 577.6;	DB 5;	Length 598;
Best Local Similarity	99.3%	Pred. No. 1.8e-138;		
Matches 580; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

OY	1490	CTTGAGTCCACCTGATAGGACCTTACCTCCCTGTCAGAAAGCTCCA	CTTCTCTTATATG	1545
Db	15	CTTGAGTCCACCTGCTATAGGACCTTACCTCCCTGTCAGAAAGCTCCA	CTTCTCTTATATG	74
OY	1550	CATCAAGCATCTTCTCTGACTGATCAAGGACACACAGATACAATGGCA	CTGACACAGA	1605
Db	75	CATCAAGCATCTTCTCTGACTGATCAAGGACACACAGATACAATGGCA	CTGACACAGA	134
OY	1610	CAATGCTAGTACAGAGGCTCCATCCCAACAGTATTATTCGCAATCAGCCAA	CTGG	1665
Db	135	CAATGCTAGTACAGAGGCGGACCAATCCCAACAGTATTATTCGCAATCAGCCAA	CTGG	194
OY	1670	CTCTGGGAATTTCAATCCACCTGCACTTTCAAGTACAGCCGATCAAGTGA	GGTGGCG	1722
Db	195	CTCTGGGAATTTCAATCCACCTGCACTTTCAAGTACAGCCGATCAAGTGA	GGTGGCG	254
OY	1730	AAAGTATGCTAGACACCTTAGATGAAATGATCTGTGACATCTCGGCCCAT	TTGAGG	1785
Db	255	AAAGTATGCTAGACACCTTAGATGAAATGATCTGTGACATCTCGGCCCAT	TTGAGG	314
OY	1790	TACAGAGCTCAGGGAATATGTTTCTGTCCAGATCATTTCTGGAGGATACACT	CTCTG	1844
Db	315	TACAGAGCTCAGGGAATATGTTTCTGTCCAGATCATTTCTGGAGGATACACT	CTCTG	374
OY	1850	TCTCAGCTTACAGTATATCAACACTAGTCTATGACCATTTGCCCCCAAGGCG	CCGAGAGC	1904
Db	375	TCTCAGCTTACAGTATATCAACACTAGTCTATGACCATTTGCCCCCAAGGCG	CCGAGAGC	434
OY	1910	TGGTAGTGTCTCAAGTCTGGCGTGTGCTAACATGACCCTTCTCCACGAC	CTGTTCACA	1965
Db	435	TGGTAGTGTCTCAAGTCTGGCGTGTGCTAACATGACCCTTCTCCACGAC	CTGTTCACA	494
OY	1970	AGAGCTCTGAGAGTACCGAGCTCTGGAGCAACAATTCAACACAGTCTG	TGTTCCATATC	2023
Db	495	AGAGCTCTGAGAGTACCGAGCTCTGGAGCAACAATTCAACACAGTCTG	TGTTCCATATC	554
OY	2030	TACGATCCAACTTTACAGAGATTTTAAGCACTTGAATCTTAAC	2073	
Db	555	TACGATCCAACTTTACAGAGATTTTAAGCACTTGAATCTTAAC	598	



RESULT	14
LOCUS	CA393958
DEFINITION	CA393958 508 bp mRNA linear EST 06-NOV-2002
ACCESSION	cs44g04.y1 Human Retinal pigment epithelium/choroid CDNA
KEYWORDS	(Un-normalized, unamplified) : cs Homo sapiens CDNA clone cs44g04 5'', mRNA sequence.
SOURCE	CA393958
ORGANISM	CA393958.1 GI:24728064
AUTHORS	EST. Homo sapiens (human)
TITLE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 508) Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K. Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants Mol. Vis. 8 (4), 205-220 (2002) 12107410
JOURNAL	Contact: Wistow G
PUBMED	Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: grame@helix.nih.gov plate: 44 row: 9 column: 04 Seq primer: M13RP1 reverse primer (ABI).
COMMENT	

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FEATURES
source
location/Qualifiers
1..508
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/mol_type="mRNA"
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/clone="cs44904"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the Superscript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>". The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/Mlu sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."
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ORIGIN	Query Match	15.0%	Score 498.4	DB 6	Length 508
	Best Local Similarity	98.8%	Prod. No. 6.8e-118		
	Matches 502	Conservative	0	Mismatches 6	Indels 0
				Gaps 0	
QY	1442	CCGACGCTGAGACAGTGGACGAGGAGGAGCGATGGCTCTACCTGACACTCTTGGTCCAC	1501		
Db	1	CCGACGTTGAGACCACTGGACCGAGGACGACATGGCTCTACCTGACACTCTTGGTCCAC	60		
QY	1502	CTGCTATGGGCTCTACCTCCCTGTGCAAGCTCCACTTTCTTATATGGCATCAAGCACT	1561		
Db	61	CTGCTATGGGCTCTACCTCCCTGTGCAAGCTCCACTTTCTTATATGGCATCAAGCACT	120		
QY	1552	TCTCTCTATCTGATATTAAGGCACACACATTAACAATGGCCACTGACCGACCAATGCTATGAC	1621		
Db	121	TCTCTCTGACCTGATCAAGGCACACACATTAACAATGGCCACTGACCGACCAATGCTATGAC	180		

Qy	1622	CAGGGCTCACATCCCAACGAGTATTATCTGAAATCAGACCACTGGCTCTGGGAATTT	1681
Db	181	CAGGGCTCACATCCCAACGAGTATTATCTGAAATCAGACCACTGGCTCTGGGAATTT	240
Qy	1682	CACATCCACCCGCATCTTCAGATGACGACCGATCAAGTGCAGGAGGGGAAGATTAGTCA	1741
Db	241	CACATCCACCCGCATCTTCAGATGACGACCGATCAAGTGCAGGAGGGGAAGATTAGTCA	300
Qy	1742	GACACCTAGATGAATGATCTGTCTGACACTCTCGGCCCATCTGAAGTACCAAGCTCA	1801
Db	301	GACACCTAGATGAATGATCTGTCTGACACTCTCGGCCCATCTGAAGTACCAAGCTCA	360
Qy	1802	GCGAATATGTTCTCTGTCGCCAGATCATTTCTTGGAGATACCACTCTGTCTCAGCTTTAC	1861
Db	361	TCGAATATGTTCTCTGTCGCCAGATCATTTCTTGGAGATACCACTCTGTCTCAGCTTTAC	420
Qy	1862	AGTATATCACACATAGTTCTATAGCCATTGCCCCCAAGGGCCGAGAGCTGTAGTGTCT	1921
Db	421	AGTATATCACACATAGTTCTATAGCCATTGCCCCCAAGGGCCGAGAGCTGTAGTGTCT	480
Qy	1922	TCAGTCTGCGGTGTGCTAACATGGCCCTT	1949
Db	481	TCAGTCTGCGGTGTGCTAACATGGCCCTT	508

RESULT 15	LOCUS	DEFINITION	ACCSSION	VERSION
EX097138	472 bp	mRNA	linear	EST 04-FEB-2003
EX097138	Soares retina NDb4Hr Homo sapiens cDNA clone			
IMAGP998N11359 ; IMAGE:1190666	mRNA sequence.			
EX097138				
EX097138.1	GI:27843098			

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 472)
AUTHORS	Ebert, J., Heil, O., Hennig, S., Neubert, P., Partsch, B., Peters, M., Redelfs, U., Schneider, D. and Korn, B.
TITLE	Human Unigeneset - RZPD3
JOURNAL	Unpublished (2003)
COMMENT	Contact: Ina Rolfs

**FEATURES**

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998N11359.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
<http://www.rzpd.de/Clonecard/cgsl-bln/Blowlib.pl.cgi?response#libNo=972> Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)  
This clone is available royalty-free from RZPD;  
contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
M3tr, primer sequence: TTTCACACAGAAACAGCTATATAC.  
Location/Qualifiers

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source
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998N11359 ; IMAGE:190666"
/sex="male"
/issue_type="retina"
/dev_stage="55 Year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_id="Soares retina N2bSHR"
/note="Organ: eye; Vector: pVTJ3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

```

strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCCATCTGAGTGGAGCGCGCGGCTTTTCTTTTCTTTT 3']. double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)<sup>+</sup> RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Facima Bernaldo. "

## ORIGIN

```
Query Match      14.2%; Score 472; DB 5; Length 472;
Best Local Similarity 100.0%; Pred. No. 4.9e-111;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1307 GAGCAATTCAGTTCACTGATGAAATGCTGATCACTGCCAGCCTTTGGTCTTCAACCC 1366
    |||
DB 1 GAGCAATTCAGTTCACTGATGAAATGCTGATCACTGCCAGCCTTTGGTCTTCAACCC 60
    |||

QY 1367 AATCAGAGTGGCCCATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCCAGAAC 1426
    |||
DB 61 AATCAGAGTGGCCCATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCCAGAAC 120
    |||

QY 1427 TTCTCTGTTGAACCCCACTTTGAGACAGTGAAGAGAGAGATGCTTACTGACA 1486
    |||
DB 121 TTCTCTGTTGAACCCCACTTTGAGACAGTGAAGAGAGATGCTTACTGACA 180
    |||

QY 1487 CTTCTTGATCTGCACCTGTATGAGCTTACTCTCTGTGAGAACTCCACCTTTCTTTA 1546
    |||
DB 181 CTTCTTGATCTGCACCTGTATGAGCTTACTCTCTGTGAGAACTCCACCTTTCTTTA 240
    |||

QY 1547 TGGCATCAAGCATCTTCTCTGATGATCAAGGCAACCAAGATCAATGGCCACTGACC 1606
    |||
DB 241 TGGCATCAAGCATCTTCTCTGATGATCAAGGCAACCAAGATCAATGGCCACTGACC 300
    |||

QY 1607 AGACAATGCTAGTACCAAGGCTCACCATGCCCAAGATGATTATCTGCAATCAGCCAAC 1666
    |||
DB 301 AGACAATGCTAGTACCAAGGCTCACCATGCCCAAGATGATTATCTGCAATCAGCCAAC 360
    |||

QY 1667 TGGCTCTGGGAATTTTCATCCACTGCACTTTCAGATGACAGCCGATCAAGTGCAGGTG 1726
    |||
DB 361 TGGCTCTGGGAATTTTCATCCACTGCACTTTCAGATGACAGCCGATCAAGTGCAGGTG 420
    |||

QY 1727 GCGAAGATATGTCAGACACCTAAGTGAATGATCTGTGACACTCTCTGC 1778
    |||
DB 421 GCGAAGATATGTCAGACACCTAAGTGAATGATCTGTGACACTCTCTGC 472
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Search completed: January 14, 2006, 16:49:06  
Job time : 12650 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 21:55:36 ; Search time 7693 Seconds  
(without alignments)  
4847.173 Million cell updates/sec

Title: US-10-007-270-2  
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Sequence: 1 MYLERRRAIFVFWIFLQVQG.....NSELLTVEXEERHNDWEGN 797

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-OUTFMT=Pct -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10007270@cgn2.1.5655@runac.11012006.110803.10633 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb\_esc2: +  
3: gb\_esc3: +  
4: gb\_hic: +  
5: gb\_esc4: +  
6: gb\_esc5: +  
7: gb\_esc6: +  
8: gb\_esc7: +  
9: gb\_gsa1: +  
10: gb\_gsa2: +  
11: gb\_gsa3: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3222.5	78.3	5829	4 CR749572	CR749572 Homo sapi
2	2801	68.0	1665	10 AY115971	AY115971 Homo sapi
3	1683	40.9	1647	10 AY115973	AY115973 Mus muscu
4	1054	25.6	626	5 B0639265	B0639265 hnd33d04.Y
5	971	23.6	1587	10 AY415972	AY415972 Pan trogl
6	955	23.2	598	5 B0636596	B0636596 hnd1h02.Y
7	902	21.9	3713	10 AY118611	AY118611 Homo sapi

8	893	21.7	690	5 BX510244	BX510244 DKFZp686P
9	829	20.1	963	5 BUS06195	BUS06195 AGENCOURT
10	819.5	19.9	3734	10 AY118613	AY118613 Mus muscu
11	817.5	19.9	3713	10 AY118612	AY118612 Pan trogl
12	815	19.8	508	6 CA393958	CA393958 cs44g04.Y
13	799	18.4	472	5 BX097138	BX097138 BX097138
14	759	18.4	510	1 AL713329	AL713329 DKFZp686P
15	751	18.2	618	6 CA391789	CA391789 cs18h07.Y
16	738	17.9	561	8 W26960	W26960 16h10 Human
17	737	17.9	754	8 CS568203	CS568203 UI-M-IBO-
18	730.5	17.7	914	5 BX743511	BX743511 BX743511
19	714.5	17.4	824	3 BI738733	BI738733 603358767
20	708	17.2	797	4 AK020862	AK020862 Mus muscu
21	707	17.2	624	7 CK619878	CK619878
22	688.5	16.7	722	8 DN897153	DN897153
23	686	16.7	422	8 BM726533	BM726533 UI-B-EJO-
24	685	16.6	886	6 CF549501	CF549501 AGENCOURT
25	674	16.4	753	3 BI735383	BI735383 603356869
26	649	15.8	448	3 BM681190	BM681190 UI-E-EJO-
27	642.5	15.6	1447	4 CNG0FUDV	CNG0FUDV
28	637	15.5	393	5 B0636351	B0636351
29	636	15.4	851	3 BI733865	BI733865
30	634	15.4	836	3 BI752112	BI752112 603022362
31	631	15.3	813	5 BX743512	BX743512 BX743512
32	624	15.2	802	3 CNG0G50F	BI735091
33	612.5	14.9	1146	4 CNG0G50F	CR702515 Tetradon
34	612	14.9	405	8 H38604	H38604 yp48e04.r1
35	584	14.2	878	6 CF549297	CF549297 AGENCOURT
36	561.5	13.6	963	5 BU287197	BU287197 603604306
37	528	12.8	666	5 BY742200	BY742200 BY742200
38	508.5	12.4	642	7 CK617565	CK617565 mk06h08.Y
39	507	12.3	322	1 AA326863	AA326863 EST30113
40	493	12.0	309	8 H38594	AA326863 EST30113
41	487	11.8	701	10 AG128736	AG128736 Pan trogl
42	466	11.3	611	7 CK621236	CK621236 ml22a05.Y
43	458.5	11.1	1167	9 DN682360	DN682360 G02X2P-F08
44	437.5	10.6	567	8 AZ974344	AZ974344 CM0248P20
45	435.5	10.6	481	1 A1510373	A1510373 mp95e12.Y

## ALIGNMENTS

RESULT 1	CR749572	5829 bp	mRNA	linear	HTC 19-AVG-2004
LOCUS	CR749572				
DEFINITION	Homo sapiens mRNA; cDNA DKFZp686K0887 (from clone DKFZp686K0887).				
ACCESSION	CR749572				
VERSION	CR749572.1	GI:51476810			
KEYWORDS	HTC				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 5829)				
AUTHORS	Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Well,B., Amlid,C., Ossanger,A., Fobo,G., Han,M. and Wiemann,S.				
CONSRMT	The German cDNA Consortium				
TITLE	Direct Submission				
JOURNAL	Submitted (17-AUG-2004) MTPS, Ingolstaedter Landstr.1, D-85764				
COMMENT	Neuberberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; Sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686K0887) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686K0887 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/ Location/Qualifiers				
FEATURES					

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ALIGNMENT SCORES:
Pred. No.:      3.7e-312      Length:      5829
Score:          3222.50      Matches:      719
Percent Similarity: 44.30%      Conservative: 0
Best Local Similarity: 44.30%      Mismatches: 0
Query Match:    78.27%      Indels:      904
DB:             4           Gaps:      2

US-10-007-270-2 (1-797) x CR749572 (1-5829)

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QY      21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
DB      251 ACCAAA----- 256
QY      41 AcGAsnGluThrThrgLuserThrgLusMetTyrLysMetSerThrMetArgArgIle 60
DB      256 ----- 256
QY      61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrgLysValLysVal 80
DB      256 ----- 256
QY      81 CysProGlnGlnSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
DB      256 ----- 256
QY      101 ValCysGlnGluAlaValAlaTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
DB      257 GGTGTCTGAGGAAGAGCTATGGAAGCATTCGATCTTTCTGATCGCATCTCTGACACA 316
QY      121 GlyIuTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
DB      317 GGGGAATATCAGAGACTGGGTGAGCATCTGCCAGCAGAGAACCTTGTGCTTTTGAACATT 376
QY      141 GlyLysAspPheSerLysSerGlnGlnIleGluAspLeuLeuGlnGlnArgIleLysGln 160
DB      377 GGAATAAACTTCAGCAATTCACAGAGACCTGGATCTTCTCCAGAGAGAAATAAAACG 436
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DB      437 AGAAGTTTCCCTGACAGAAAGATGAATATCTGCAAGAGAAACATTTGGGAAGCCTGAT 496
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DB      917 GCCAAATTTTTCAGAAATTTTGTGTTACAAATTTAATATCCACTGGCAGAAAGACA 976
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RESULT 2
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LOCUS AY415971 1665 bp DNA linear GSS 17-DEC-2003

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genomic survey sequence.
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VERSION AY415971.1 GI:39771931
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1665)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trles
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1665)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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them based on alignment.
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ORIGIN
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Best Local Similarity: 98.56% Mismatches: 8
Query Match: 68.03% Indels: 0
DB: 10 Gaps: 0
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QY 284 HlValLeuGlyPheArgProLysGlyLysAspGlySerSerSerThrGluMetGln 303
Db 121 CATGTGTAGGATTTTAGNNNNNNNNNNNNNNNNNNNNNNNNCTCAAGCTCCACAGAGATGCA 180
QY 304 LeuThrAlaIlePheLysArgHlSerAlaGluAlaLysSerProAlaSerAspLeuLeu 323
Db 181 CTACGGCCATCTTTAAGAGACACAGTCCAGAACGCAAAAGCCCTGCAAGTGACTCTCG 240
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Db 241 TCTTTTGAATTCACAAATTTGAAGTGAAGTCTATCATGAAACCATGGAAGAGGAC 300
QY 344 LysGlnProGluLlLTrLeuThrAlaThrAspLeuLysArgLeuLlSerLysAlaLeu 363
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Qy 424 GIYAlaGluHISglYleuProAspThrSerTrpSerProProAlaMetAlaSerThrSer 443
Db 541 GAGAGCAGACATGCTTACTTCACTTCTGTGCTCCACCTGCTACTATGGCTCTTACTTC 600
Qy 444 LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerleuThrAspGlnGly 463
Db 601 CTGTCAAGAGCTCCACCTTCTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGC 660
Qy 464 ThrThrAspThrMetAlaThrAspGlnThrMetleuValProGlyleuThrIleProThr 483
Db 661 ACCACAGATACATAGCCACTGACAGACAAATGCTAGTACAGGGCTCACCAATCCCAACC 720
Qy 484 SerAspTySerAlaIleSerGlnleuAlaLeuGlyIleSerHisProProAlaSerSer 503
Db 721 AGTGATTAATTCGCAATACAGCACTGGCTCTGGGAATTCACATCCACTGATCTTCA 780
Qy 504 AspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisleuAspGluMetAsp 523
Db 781 GATGACAGCGCATCAAGTCAAGTGGCGAAGATATGCTGACAGCACTTAATGAATGAT 840
Qy 524 LeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyValSerValPro 543
Db 841 CTGTCTGACACTCTGCCCCATCTGAGTACAGAGCTCAGCAAGCAATATTTCTGTCCCA 900
Qy 544 AspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyThrIleThrSerSer 563
Db 901 GATCATTTTGTGAGATACCACTCTGCTCAAGCTTACAGATATACCACTGATCTTCT 960
Qy 564 MetThrIleAlaProIlysglyArgGluLeuValPhePheSerleuArgValAlaAsn 583
Db 961 ATGACCATTTGCCCCCAAGGCGGAGAGCTGTGATGTTCTTCAAGTGTGCTGTGATAC 1020
Qy 584 MetAlaPheSerAsnAspLeuPheAsnIlySerSerleuGluTyArgAlaLeuGluGln 603
Db 1021 ATGGCCCTCTCCAAACCACTGTTCACAAAGAGCTCTGAGATACCAAGCTCTGGAGCAA 1080
Qy 604 GlnPheThrGlnleuLeuValProTyTrleuArgSerAsnleuThyGlyPheIlysglnleu 623
Db 1081 CAATTCACACAGCTGTGTTGCTCATATTCATCAATTCATCAAGATTTTAAGCAACTT 1140
Qy 624 GlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerIleMetIlyspheAlaIlyS 643
Db 1141 GAAATTACTTAATCTTCAGAAACGGAAGTGTGATTTGCAATAGCAAAATGAAGTTTCTAAG 1200
Qy 644 SerValProTyAsnleuThrIlyValAlaHisglYValleuGluAspPheArgSerAla 663
Db 1201 TCAGTGCCGTATTAACCTTCACCAAGGCTGTGACAGGGGTCTTGAAGATTTTCTGTCTGT 1260
Qy 664 AlaAlaGlnGlnleuHISleuGluIleAspSerTyTrSerleuAsnIleGluProAlaAsp 683
Db 1261 GAGAGCCCAACCACTCATCTGAAATAGACAGCTACTCTCTCAACATTAACCAAGCTGTAT 1320
Qy 684 GlnAlaAspProCylyspheleuAlaCySGlyGluPheAlaGlnCyValIlysaAsnGlu 703
Db 1321 CAAGCAGATCCCTGCAAGTTCTCTGGCTCGGCGAATTTGCCAATGTTTAAGAAAGCA 1380
Qy 704 ArgThrGlnGluAlaGluCyArgCylyspProGlyTyTrAspSerGlnIlySerleuAsp 723
Db 1381 CGGACTGAGAAAGCGAGGTGTGCTGCAAAACAGATATAGACAGCCAGGGAGCTGTGAC 1440
Qy 724 GlyLeuGluProGlyLeuCySGlyProGlyTyThrIlysgluCySGluValleuGlnIlyS 743

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Db 1441 GGTCTGGAACCAAGGCTCTGTGCCCCCTGGCCAAAGAAATGCGAGTCTCCAGGAAAG 1500
Qy 744 GIYAlaProCyArgLeuProAspHisSerGluAsnGlnAlaTyTrIlyThrSerValIlyS 763
Db 1501 GGAGCTCCATGACAGGTGGCAGATCATCTGTGAAAATCAAGCATACAAAATCTAGTGTAA 1560
Qy 764 IlyspheGlnAsnGlnIleAsnAsnIlyValIleSerIlyArgAsnSerGluLeuLeuThr 783
Db 1561 AGTTCCAAATCAACAAATTAACAAGGTAACTAGTAAAGAAATTTGAAATTAATGACCC 1620
Qy 784 ValGluTyGluGluPheAsnHisGlnAspTyTrGluGluGlyAsn 797
Db 1621 GTAGAAATGAAGATTTTAACCATCAAGATTTGGAGAAAGAAAT 1662.

RESULT 3
AY415973      1647 bp   DNA      linear   GSS 17-DEC-2003
LOCUS       Mus musculus IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION  genomic survey sequence.
ACCESSION   AY415973
VERSION     AY415973.1 GI:39771933
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 1647)
  Clark A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
  Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B.,
  Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.D.,
  Adams, M.D. and Cargill, M.
  Direct Submission
  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
  Rockville, MD 20850, USA
  This sequence was made by sequencing genomic exons and ordering
  them based on alignment.
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                     /mol_type="genomic DNA"
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Score:              1683.00        Matches:      354
Percent Similarity: 73.47%         Conservative: 53
Best Local Similarity: 63.90%      Mismatches:  141
Query Match:        40.88%         Indels:       6
DB:                  10            Gaps:         5
US-10-007-270-2 (1-797) x AY415973 (1-1647)
Qy 244 AbngInIlyPheIlyValIGluLeuAlaAspSerGlnSerProTyTyTrGlnGluLeuAla 263
Db 1 AACCAAGATTCAGAGCAGAGCTCACCAACTCTGGTCACTACTACAGAGAACTGGTG 60
Qy 264 GlyIlySerGlnleuGlnMetGlnIlyIlePheIlyValleuProGlyPheIlyValIle 283

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QY 390 AAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409
DB 361 GACACCCCAATCAGAGCTGCCACATCTTTGCTGTTATACAGAAATGCTACTTTGAGT 420
QY 410 ProGluLeuProProValGluProGluLeuGlnThrValAspGlyValAGluIleGlyLeu 429
DB 421 CCAGAACTTCTCTTGTGAAACCCAGCTTGAGACAGTGAGCAGAGCATGGTCTA 480
QY 430 ProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449
DB 461 CCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 540
QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
DB 541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600
QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle 489
DB 601 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 660
QY 490 SerGlnLeuAlaLeuGlyIleSerIleProProAlaSerSerAspAspSerArgSerSer 509
DB 661 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720
QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
DB 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
QY 530 ProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAsp 549
DB 781 CCATCTGAGAGTACAGAGCTCAGCGAAATGTTTCTGCTCCAGATCTTCTTGAGAGAT 840
QY 550 ThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProIlys 569
DB 841 ACCACTCCCTGCTCTGCTTACAGATATACACACTAGTCTATGACCATTCGCCCCAG 900
QY 570 GlyArgGluLeuValPhePheSerLeuArgValAlaAspMetAlaPheSerAspAsp 589
DB 901 GGCACGAGAGCTGATGCTGTTCTTCACTGCTGCGTGTCTTCAACATGACCTTCCACAGAC 960
QY 590 LeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609
DB 961 CTGTTCAACAAGAGCTCTCGAGTACGAGCTCGAGCAANNNNNNNNNNNNNNNNNNCTG 1020
QY 610 ValProTyrLeuArgSerAsnLeuThrGlyPheIleGlnLeuGluIleLeuAsnPheArg 629
DB 1021 GTTCATATCTACGATCCATCTNNCAGGATTTAAGCAACTTGAATACTTAACCTTCAGA 1080
QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649
DB 1081 AACGGAGAGTGAATGTCGATGCAATGCAAAATGAAGTTTNCATCACTGCTCCGATNNNNNC 1140
QY 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaLeuGlnLeuHis 669
DB 1141 ACCAAGAGCTGTCAAGGGGCTTTGAGAGATTTGCTTGCNNCAGCCCAACACTCCAT 1200
QY 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
DB 1201 CTGGAAATAGANANCACTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1260
QY 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709
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QY 710 CysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729
DB 1321 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1380
QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyValAlaProCysArgLeu 749
DB 1381 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1440

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QY 750 ProAspHisSerGluAsnGluAlaTyrLysThrSerValLysLysPheGlnAsnGln 769
DB 1441 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1500
QY 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGluGluPhe 789
DB 1501 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1560
QY 790 AsnHisGlnAspTyrProGluGlyAsn 797
DB 1561 AACCATCAAGATGGAGAGAAAT 1584

RESULT 6
LOCUS B0636596
DEFINITION hdl1h02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
ACCESSION B0636596
VERSION B0636596.1 GI:21761055
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 598)
Wistow,G., Bernstejn,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIRank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferrd gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
12107411
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gissem@helix.nih.gov
Plate: 11 row: h column: 02
Seq primer: M13RP1 reverse primer (ABI).
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="EMH10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ng of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTAGTCTAGATCGGAGCGGCCGC(TT)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
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Alignment Scores:  
Pred. No.: 2.5e-85  
Score: 955.00  
Percent Similarity: 98.47%

Length: 598  
Matches: 190  
Conservative: 3

Best Local Similarity: 96.94% Mismatches: 3  
 Query Match: 23.20% Indels: 0  
 DB: 5 Gaps: 0

US-10-007-270-2 (1-797) x BQ636596 (1-598)

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 DB 11 TCGCTGGGTCTTCACCTGCTATGGCTCTTACCTCTCCGACAGAGCTCCACCTTCTT 70

QY 452 MetAlaSerSerLeuPheSerLeuThrAspGlnGlyThrThraPheMetAlaThrAsp 471  
 : : : : :  
 DB 71 ATGGCATCAAGCATCTTCTCTGATGATCAAGGACCAAGATCAATGGCCACTGAC 130

QY 472 GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491  
 : : : : :  
 DB 131 CAGACATCTACTATACAGGCGACACATCCACCAAGATTAATCTGCAATCAGCCAA 190

QY 492 LeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerAspSerSerAlaGly 511  
 : : : : :  
 DB 191 CTGGCTCTGGGATTTCAATCCACTGCTTCATGATGACGCGATCAAGTCAAGTCA 250

QY 512 GlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSer 531  
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 DB 251 GGGAGATATATGGTCAAGACCTAGATGAATGATCTGTGACACTCTCCGCCATCT 310

QY 532 GluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThr 551  
 : : : : :  
 DB 311 GAGGTACCAAGACTCAGCGAATATGTTTGTCTCCAGATCATTTCTTGGAGATACACT 370

QY 552 ProValSerAlaLeuGlnTyrIleThrTrpSerSerMetThrIleAlaProGlySerGly 571  
 : : : : :  
 DB 371 CCGTCTCAGCTTACAGTATACACACACTGATTCATGACCAATGCCCCCAAGGGCCCA 430

QY 572 GluLeuValValPhePheSerLeuArgValAlaAspMetAlaPheSerAspLeuPhe 591  
 : : : : :  
 DB 431 GAGCTGGTATGTTCTTCAATCGCGTGTTCCTAATAGCCCTTCCAAAGACCTGTT 490

QY 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuValPro 611  
 : : : : :  
 DB 491 AACAGAGCTCTCTGAGTACCGAGCTGAGCAACAATTCACAGCGTGGGTCCA 550

QY 612 TyrLeuArgSerAspLeuThrGlyPheLeuGlnLeuGlnIleLeuAsn 627  
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 DB 551 TATCTACGATCCATCTTACGAGATTTAAGCAACTTAATCTTAAC 598

RESULT 7  
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 LOCUS  
 DEFINITION Homo sapiens IMPG2 gene, VIRUTUAL TRANSCRIPT, partial sequence.  
 ACCESSION AY418611  
 VERSION AY418611.1 GI:39774571  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 3713)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3713)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,  
 Adams,M.D. and Cargill,M.

TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT These sequences were made by sequencing genomic exons and ordering  
 them based on alignment.  
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ORIGIN  
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 Pred. No.: 9,98e-79 Length: 3713  
 Score: 902.00 Matches: 290  
 Percent Similarity: 39.08% Conservative: 145  
 Best Local Similarity: 26.06% Mismatches: 274  
 Query Match: 21.91% Indels: 405  
 DB: 10 Gaps: 34

US-10-007-270-2 (1-797) x AY418611 (1-3713)

QY 2 TyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThr 21  
 : : : : :  
 DB 11 TTCCTCTTTTGGGAAGATTTCTCGGTATTTTG-ATATTTGCTCCTGATTAAGAGAC 69

QY 22 ---LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro--- 39  
 : : : : :  
 DB 70 TTTCATCATTAACAGCAACAACTACTATCT--ATAGAGAGATCCAGAACCCAG 126

QY 40 -----ProArgAsnGluThr-----ThrgIuser 47  
 : : : : :  
 DB 127 AGTGCAGTTCTTCTTCTCCTGCTGAAGATCAAGACACTTCTTACTACCAAAAG 186

QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67  
 : : : : :  
 DB 187 AACAGCCCTCTGACCGCAGAGAACTGAAAGACAGTGGTTA-----ATCAGA 234

QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnIuserMetLys 87  
 : : : : :  
 DB 235 AGCGGAGATCTATTTCTGTTCTTAATGAGGAAATCTGCCAGATGAAGTGTGCA 294

QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGlnAlaValTyr 107  
 : : : : :  
 DB 295 GAGGCTGGGCAAAATCAGTGAAGTATTTTAAGTCCGAGTGTGTGAGAACTGTCTGG 354

QY 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTyrVal 127  
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 DB 355 GAGGCTTCAGACATTTTGGATGACACTTCTGGGCGGTGAGAAATATCATTAATCTGAGT 414

QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
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 DB 415 AATTTGTGAGAGATGAGACTCAAGATATATTGAATGGGCAAAATTTTGTGATCT 474

QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
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 DB 475 GTGGAACATGAAAGCTTAATCATGAAGAACTGACTAT-----GCMAAG 519

QY 166 AspGluIleSerAlaGluLysThrLeuGlyLysPro-----GlyGluThrIleVal 184  
 : : : : :  
 DB 520 GAAAGCTGAAGCAGCTGGA---CTGTCTTCCAGTTCCTGTGGTGTATCTTCAACA 576

QY 185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200  
 : : : : :  
 DB 577 TTGGAGACACTACTCTCAGTGT-----CCACATCCAGAGGTGAGCCCTATGAA 627

QY 201 -----ProAspAspThrLeuLeuAsnGluIleLeuAsp 211  
 : : : : :  
 DB 628 GGTGCTCAGAGAGAGAGCTTGAAGGCGCAGAGAGATTAAGCAATGAATTT---GAG 684



Db 2779 CTGAGCAAGATTTCTTAGAATGTGTCGTCCTATCTCCAGTCAATCTCAGGGGTTTC 2838

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 Db 2839 CAGAACTTGAATTCCTCAACTTCAGAAATGACGATGCTGTGAACAGTCCAAATGAAG 2898

Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValIleGluAspPhe 660  
 Db 2899 TTTCGCAATTCCTCTCCCTTCCTTACACATATGCGGCTGATGATTTTCGAAAGACTTT 2958

Qy 661 ArgSerAlaAlaIleGlnIleuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680  
 Db 2959 TGTACACCTGCGTCAACATACCAATGAGACTTGGCTATTGATTAATCTCTTATGTGGA 3018

Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
 Db 3019 TCAGGTGATGAGACCAACCTTGCAAGTTTCAGGCGCTGATATGATTTTCAGAGTCTG 3078

Qy 701 LysAsnGluArgThrGluGluIleGluCysArgCysLysProGlyTyrTrpSerGln--- 719  
 Db 3079 GTCAACCTCGAGTGAAG 3138

Qy 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735  
 Db 3139 GAACGGCCCTGTCAGAGTCTCTGTGACCTACAGCCTGACTTCTGTAATGATGAGAAAG 3198

Qy 736 GluCysGluValLeuGlnGlyLysGlyAlaProCysArg 748  
 Db 3199 ---TGTGACATTATGCTGCGGACGCGGCGCATTTGAGG 3234

RESULT 8  
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 DEFINITION DKFP686P2496.r1 686 (synonym: hicc3) Homo sapiens cDNA clone  
 ACCESSION BXS10244  
 VERSION BXS10244.1 GI:32050551  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo  
 1 (bases 1 to 690)  
 Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,  
 Mewes,H.W., Weill,B., Amld,C., Oesinger,A., Fobo,G., Han,M. and  
 Wiemann,S.  
 EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,  
 Wellenreuther,R., et al.)  
 Unpublished (2003)  
 JOURNAL COMMENT  
 TITLE MIPs  
 CONTACT: MIPs  
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
 This is the 5' sequence of the clone insert.  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
 Heidelberg/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No al sequence available.  
 This clone (DKFP686P2496) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
 Location/Qualifiers  
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 /lab\_host="DH10B"  
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 /note="Vector: pTriplEx2; Site\_1: SfiI; Site\_2: SfiIB;

ORIGIN cDNA-collection"

Alignment Scores:  
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 Score: 893.00 Matches: 168  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 21.69% Indels: 0  
 DB: 5 Gaps: 0

US-10-007-270-2 (1-797) x BXS10244 (1-690)

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 Db 187 ATGTATTTGGAAACTAGAAAGACTATTTGTTGTTTGGATTTTCTCCAAAGTTCAAGGA 246

Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 Db 247 ACCAAAGATATCTCAATTAACTATACCAATTCGTAAACATAAGACATAGACAAATCCCCCA 306

Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrmcArgArgIle 60  
 Db 307 AGAAATGAAACAACAGAAAGTCTGAAAAAATGTCAAAATCTCAATATGAGACGAATA 366

Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 367 TTGCATTTGGCAAGATCGAAGCAAAAGATCGCATTTTCCCAACGGGGGTTAAAGTC 426

Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 427 TGTCCACAGGAATCCATGAAACAGATTTTAAACAGTCTTCAAGCTTATATGATTTGACA 486

Qy 101 ValCysGlnGluAlaValIleProGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 487 GTGTCTCAGGAAGACGATGGAACATATCGAATCTTCTGATCGCATCCCTGACACA 546

Qy 121 GlyIuTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 547 GGGGAATATCAGAGATCGGTGATGATCTGCACGACAGAGACCTTGCTGCTTTGACATT 606

Qy 141 GlyLysAsnPheSerAsnSerGlnIleHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
 Db 607 GGAATAAACTTCAGAAATTCACAGAGACCTGATCTTCTCCACAGAGATTAATAACAG 666

Qy 161 ArgSerPheProAspArgLysAsp 168  
 Db 667 AGAAGTTTCCTGACAGAAAGAT 690

RESULT 9  
 BUS06195  
 LOCUS BUS06195 963 bp mRNA linear EST 12-SEP-2002  
 DEFINITION AGENCOURT\_10015502 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:649245  
 ACCESSION BUS06195  
 VERSION BUS06195.1 GI:22812428  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 963)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL COMMENT  
 TITLE Contact: Robert Strausberg, Ph.D.  
 AUTHORS Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be

Found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LNL14050 row: c column: 14  
 High quality sequence stop: 637.  
 Location/Qualifiers

## FEATURES

source

1..963

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:6494245"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 3.3 kb. Library enriched for

full-length clones and constructed by ligo technologies.

Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	2,636-72	Length:	963
Score:	829.00	Matches:	182
Percent Similarity:	74.13%	Conservative:	30
Best Local Similarity:	63.64%	Mismatches:	65
Query Match:	20.14%	Indels:	11
DB:	5	Gaps:	2

US-10-007-270-2 (1-797) x BU506195 (1-963)

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QY      1 MetTyrLeuGluThrArgRgaAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
DB      118 ATGAATTGGCAATTAACAATGCTATCTTTGGGATTTTCTCCAGATTCAGAGA 177
QY      21 ThrTyrAspIleSerIleAsnIleTyrHisSerGluThrTyrAspIleAspAsnProPro 40
DB      178 ATCAAGATACCTCTATTAATAATATCTGAAATTAATAACATAGACAAACCCCA 237
QY      41 ArgAsnGluThrThrGluSerThrGluTyrMetTyrLeuMetSerThrMetArgArgIle 60
DB      238 AGAATTCGAACAATTGAAAGTACTTCACACAGTCGCAAAAGTGCACCAATGAAAGCAATA 297
QY      61 PheAspLeuAlaIleHisIleArgThrTyrAspSerAlaPhePheProThrGlyValIleVal 80
DB      298 TTCGATTGGCCAAAGCTTGAACCAAAAGATCAGACCTTTCCCA--GCTGCTAACATC 354
QY      81 CysProGlnGluSerMetTyrGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
DB      355 TGTCCACAGGAATCCTTGAGACAGATTTCAGACAGCTTCAAGATATTATAGACTGAGA 414
QY      101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
DB      415 GATATGCAAGAGTCTGTGGGAGAGCATATCGATCTTTCGACCGAATTCCTAGACACA 474
QY      121 GlyIuTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
DB      475 GAGGATATCAAGACAGCTGGGTCAAGCTCTGCCAGAAAGAAACCTTCGCTCTTTGACATT 534
QY      141 GlyTyrAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLeuGln 160
DB      535 GGGAAATCACTCAGCAACTCCAGAGACACTAGATCTTCTCAGACAGAAATTAAGACG 594
QY      161 ArgSerPheProAspArgTyrAspArgIleSerAlaGluTyrThrLeuGlnGluProGly 180
DB      595 AAGAGCTTCCCTGGGAGGAAAGATGAGACAGCTTCATGAGACACATGGAACACACTACT 654
QY      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
DB      655 GAAAGCCCTGTGTATCCACAGATGTTTCCAGAGATTCCTGGGGCCCTTCCACATTCCT 714
QY      201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrIleAsnPro 220
DB      715 TCGATGACACAGACCTCAAGAGATTCAGTGTCACCCCTCAGACATTCGAAAGACCA 774

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QY 221 ThrThrGluArgGluThrGluPheAlaValLeuGlnGlu-----GlnArgVal 236

DB 775 CA-ACAGAAATTAACCGGACCTAATCAT-CTGTCTGAAATCTCATCAAGAGAGAAAGG 832

QY 237 GluLeuSerValSerLeuValAsnGlnIlePheIleValAla-GluLeuAlaAspSer-Glns 256

DB 833 GAATTCAGCATCTCTGTGCCACACACAGTTTCAGGCGCAGAGCTCACCAACTCTGGGCT 892

QY 256 ERPOTYRTYRGLNGLUENLA--GLYLSERSGLNGLNGLNGLNGLNGLNGLNGLNGLNGLN 275

DB 893 CCCCTACTTAACAGAGAACTGTGTGGGACAGTCCCACTGACAGTTGCCAAAGAAATTTAA 952

QY 275 slyLeuPro 278

DB 953 GAAACTCCA 962

RESULT 10

AY418613

LOCUS

DEFINITION

AY418613

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

<1..>3734

/gene="IMPG2"

/locus\_tag="HMC6615"

Alignment Scores:

Pred. No.: 2,066-70 Length: 3734

Score: 819.50 Matches: 275

Percent Similarity: 36.60% Conservative: 128

Best Local Similarity: 24.98% Mismatches: 273

Query Match: 19.91% Indels: 425

DB: 10 Gaps: 33

US-10-007-270-2 (1-797) x AY418613 (1-3734)

QY 27 AsnIleTyrHisSerGluThrTyrAspIleAspAsnProProAspArgAsnGluThrGlu 46

DB 91 AGCATCTTTCGCAAGAGAGAGA-----CAAGAACCAATGACATGCGCTCTGTCTCTC 144



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Db      2185 AAACCACTCTTACCGGTAACTATAGCAATCCGCTTCCACTAAGAAAAGATGAG 2244
Qy      491 GlnLeuAlaLeuGlyIleSerHisProPheAlaSerSerAsp-----AspSerArg 507
Db      2245 GTACTCAAGAAAGATATGTTATACATACATCATCCAGTCAACAAAGAACTTACAGATGAG 2304
Qy      508 SerSerAlaGlyIleGlyIleAspMet----- 515
Db      2305 GTTCCAGTGTCAAGGCCAGATATGCAAGCTGTGTGAGCAATGTGTCAGAAATCAATAC 2364
Qy      516 -----ValArgHisLeuAspGluMetAspLeuSerAspThrPro 528
Db      2365 GTTTGACACAAAGAACTTCTCTTACGGAATATGTCCAGAGACACACAGTCCACTGAATGCTTCA 2424
Qy      529 -----AlaProSerGluValPro--- 534
Db      2425 GAGAGCACTGACAGACTGTGTTGAAAGCTTCCATGACACACAGTCCACTGAATGCTTCA 2484
Qy      535 -----GluLeuSerGluIleValSerVal----- 542
Db      2485 ACCACCACTCCACCCAGCTTACAGAGAGAAATATATATATGCGCGTCCAGATATTCATTA 2544
Qy      542 ----- 542
Db      2545 GAATAGATCAGATGAGCAGACAGATTTATATCATGCTCCAGCTAACTGAAGAACATGAGC 2604
Qy      543 ---ProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnIleThrThr 561
Db      2605 AAGCTGACGACTATGTGAAATGCTTACCAAGTGT-----CACTACACAGAGATG 2655
Qy      562 SerSerMetThrIleAlaProIleGly-----ArgGlu 572
Db      2656 CCTATTGTGCTCTGCCCAAAAGAGAGTGTCTTGAAGTACACACCAGCTGCAGAGAGA 2715
Qy      573 LeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsn 592
Db      2716 TTGGTGGTGTCTTCTGAGCTCCGCGTGAACAAATGTTTTCAGAAAGACTTGTATTAC 2775
Qy      593 LysSerSerLeuGluIleThrArgAlaLeuGluGlnIlePheThrGlnLeuValProIle 612
Db      2776 AAAAAGCTCTTGGAAATATAAGCCCTGGAAACAAAGTTTGAAGTGTGTTCCCTAT 2835
Qy      613 LeuArgSerAsnLeuThrGlyPheLeuGlnLeuGluIleLeuAsnPheArgAsnGlySer 632
Db      2836 CTCGAGTCAAAATCTGTCAAGGTTCCAGAACTTGAATCTGAGTTCCAGAAACGGCAGC 2895
Qy      633 ValIleValAsnSerIleMetIlePheAlaLysSerValProIleThrAsnLeuThrIle 652
Db      2896 ATTGTGTGTAACAGCCGAGTGTGAGGTTGCGCCGAGTGTGCCCCCTTAATGTCAACAGGCC 2955
Qy      653 ValHisGlyValLeuGluAspPheArgSerAlaAlaAlaGlnIleAsnIleLeuGluIle 672
Db      2956 AGTATAGAGATTCTGGAAGACTTTTGTACCACTGCTACCAACCACTGGAATGATATAC 3015
Qy      673 AspSerIleSerLeuAsnIleGluProAlaAspGlnAlaAspProCysIlePheLeuAla 692
Db      3016 GATTAATATCTCCTCGACGCGAATGAGATGAGAGCCACTTGTCAAGTTTCAAGGCC 3075
Qy      693 CysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlnAlaGlnCysArgCys 712
Db      3076 TGTAAAGAAATTTCTCAGTGTGTGTAATATCCATGAGTGAAGCAAGTGAAGTCAATATC 3135
Qy      713 LysProGlyIleThrAspSerGlnGly-----SerLeuAspGlyLeuGluPro 727
Db      3136 TACCCCTGGGTACTGTGATGATGATGAATGCTTGTCAAAAGTCTGTGATCTACAGCCT 3195
Qy      728 GlyLeuGlyGlyProGlyIleThrIleGlnCysGluValLeuGlnIleLysGlyAlaProCys 747
Db      3196 GACTTGTGCTTGAACATGAGAAAG---TGTGACATTAATGCTGTGGCATGAGACCTTTGT 3252
Qy      748 Arg 748
Db      3253 AGA 3255

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RESULT 11
AY148612 3713 bp DNA linear GSS 17-DEC-2003
LOCUS AY148612
DEFINITION Pan troglodytes IMPG2 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY148612
VERSION GI:39774572
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
REFERENCE 1 (bases 1 to 3713)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Infering nonneutral evolution from human-chimp-mouse orthologous
gene clones
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 3713)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 west Gude Drive,
Rockville, MD 20850, USA
COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>3713
/gene="IMPG2"
/locus_tag="HCM6615"
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Alignment Scores:
Pred. No.: 3,24e-70 length: 3713
Score: 817.50 Matches: 260
Percent Similarity: 36.87% Conservative: 119
Best Local Similarity: 25.29% Mismatches: 272
Query Match: 19.86% Indels: 377
De: 10 Gaps: 26
US-10-007-270-2 (1-797) x AY148612 (1-3713)
Qy 69 LysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLysGln 88
Db 228 CGGAGATCTATTCGTTCTTCTTAATGAGTGAATAATCTCCGCGGAGTGTGAGTGTGAG 297
Qy 89 IleLeuAspSerLeuGlnAlaIleThrArgLeuArgValCysGlnGluAlaValIlePro 108
Db 238 GCTGTGGCAATCATGATGAAAGTATTTAAAGTCCAGTGTGCAAGAGTGTCTGGGAA 357
Qy 109 AlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluIleThrGlnAspThrValSer 128
Db 358 GCTTCAGAGACTTTTGGATGACTTCTGCGCGCTGAGAAATATCATTAATCTGAGATG 417
Qy 129 IleCysGlnGlnGluThrPheCysLeuPheAspIleGlyIleAsnPheSerAsnSerGln 148
Db 418 TTGTGTGAGAGATGAGTCAACAAGTATATTTGAATGGCACAAATTTTATAGTGAATGTG 477
Qy 149 GluHisLeuAspLeuLeuGlnGlnIleLysGlnArgSerPheProAspArgIleValSer 168
Db 478 GAACATAGAAAGCTTAATCATGAAAGNNCTGACTTAT-----GCAAGAGAA 522

```





Db 2614 GTTCACTCCACAGAGTGTAGTGTGCTGCTGCCACAGAAAGAGATGATGCTTGAGT 2673

Qy 573 -----leuvalValPhePheSerLeuArgValAlaSerMetAla 585

Db 2674 TATACCAGACTTCAGAGCTTGAGTGTGCTTCTTCAGCTTCGAGTACTACATGATG 2733

Qy 586 PheSerAspLeuPheAsnIleSerSerLeuGluTyrArgAlaLeuGluGlnIlePhe 605

Db 2734 TTTTCAGGAAGATCTGTTTAATAAAACTCTTGAGATTAAGCCCTGAGCAAGATTC 2793

Qy 606 ThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheIleGlnLeuGlu 625

Db 2794 TTGAATTCCTGCTGCTTCCCTATCTCCAGTCAAACTCCACGCGGTTCAGAACTTAATC 2853

Qy 626 LeuAsnPheArgAsnGlySerValIleValAsnSerIleMetIlePheAlaIleSerVal 645

Db 2854 CTCACCTTGAAGAAATGGCAGCAATGTGGTGAACAGCCGAAATGAAGTTGCCAATTCGTGC 2913

Qy 646 ProTyrAsnLeuThrIleValIleValIleValIleValIleValIleValIleValIleVal 665

Db 2914 CCTCTCAAGTCAACAATGCGGTGTACATGATTTCTGGAAGACTTTTGTACCACTGCTTAC 2973

Qy 666 GlnGlnLeuLeuLeuGlnIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAla 685

Db 2974 AATACCATGAACTTGCTGCTATGATAAATCTCTTGAATGGAATCAAGTGAATGAGCC 3033

Qy 686 AspProCysIlePheLeuAlaCysGlyGluPheAlaGlnCysValIleAsnGlnIleArgThr 705

Db 3034 AACCCCTTGCAAGTTTCAGGCTGTATGAATTTTCAGAGTGTGTGTAACCCCTGAGAT 3093

Qy 706 GlnGlnAlaGluCysArgCysIleProGlyTyrAspSerGln-----Gly 720

Db 3094 GGAAGAAAGCAATGCGATGCTTCCCTGTTACCTGATCTGGAAGAAAGCCCTGTCTGAC 3153

Qy 721 SerLeuAspGlyLeuGlnProGlyLeuCysGlyProGlyThrIleGlnCysGlnValLeu 740

Db 3154 AGTCTCTGTGACCTACAGCCTGACTCTGCTGAATGATGAAG---TGTGACATTTATG 3210

Qy 741 GlnGlyIleGlyAlaIleProCysArg 748

Db 3211 CCTGGCAGCGGCGCCATTGTAGG 3234

RESULT 12

CA393958 508 bp mRNA linear EST 06-NOV-2002

LOCUS CA393958

DEFINITION cs44g04.y1 Human Retinal pigment epithelium/choroid cDNA

5', mRNA sequence.

ACCESSION CA393958

VERSION CA393958.1 GI:24728064

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

BuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 508)

AUTHORS Mistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A., Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.

TITLE Expressed sequence tag analysis of human RPS/choroid for the

NIH RIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants

JOURNAL Mol Vis. 8 (4), 205-220 (2002)

PUBMED 12107410

COMMENT Contact: Mistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: gream@helix.nih.gov

Plate: 44 row: 5 column: 04

Seq primer: M13RPI reverse primer (ABI).

FEATURES

source

Location/Qualifiers

1..508

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="cs44g04"

/tissue\_type="RPS/choroid"

/dev\_stage="Adult"

/lab\_host="BMDH10B"

/clone\_lib="Human Retinal pigment epithelium/choroid cDNA (un-normalized, unamplified): cs"

/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPS/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD), now part of Invitrogen Corp), essentially following the protocols of the Superscript plasmid system (Invitrogen Corp).

<http://www.invitrogen.com/> The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:

Pred. No.: 2,44e-71 Length: 508

Score: 815.00 Matches: 163

Percent Similarity: 97.02% Conservative: 0

Best Local Similarity: 97.02% Mismatches: 5

Query Match: 19.80% Indels: 0

DB: 6 Gaps: 0

US-10-007-270-2 (1-797) x CA393958 (1-508)

Qy 418 GlnLeuGlnThrValAspGlyAlaGlnIleGlyLeuProAspThrSerTyrSerProPro 437

Db 3 CAGCTTGAGACAGTGGACGAGCAGACAGATGCTTCACTGACATCTTGTGCTCCACT 62

Qy 438 AlaMetAlaSerThrSerLeuSerGlnAlaProPhePheMetAlaSerSerIlePhe 457

Db 63 GCTATGGCCTTACTCTCTGTCAGAGACTCACTTCTTATGATCAAGATCTTTC 122

Qy 458 SerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValPro 477

Db 123 TCTTGACTGATCAAGCAGCAGACATCAATGGCCACTGACCAACAATGCTTACTACA 182

Qy 478 GlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyTyrIleSer 497

Db 183 GGGCTCACCATCCCAACAGATGATTTATCTGCAATACCACTGGCTTGGGAATTTTCA 242

Qy 498 HisProProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArg 517

Db 243 CATCACTGATCTTTCAGATGACAGCCGATCAAGTGCAGAGTGGGAATGATGTCTACA 302

Qy 518 HisLeuAspGlnMetAspLeuSerAspThrProAlaProSerGlnValProGlnLeuSer 537

Db 303 CACCTAGATGAAGATGATCTGTGACACTCTCTGCCATCTGAGTACCGAGAGCTCATC 362

Qy 538 GluTyrValSerValProAspHisPheLeuGlnAspThrThrProValSerAlaLeuGln 557

Db 363 GAAATGTTCTGTCCAGATCAATTTCTTGAAGATACACTCTCTGCTACAGCTTATCAG 422

Qy 558 TyrIleThrThrSerSerMetThrIleAlaProIleGlyArgGlnLeuValPhePhe 577

Db 423 TATATCACACATAGTTCATATGACATTCGCCACAAAGGCCGATAGCTGTAAAGTTCTTC 482

Qy 578 SerLeuArgValAlaSerMetAla 585

Db 483 AGTCTGCGTGAATGTAACATGGCC 506

RESULT 13

BX097138  
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 DEFINITION BX097138 Soares retina N2b4RH Homo sapiens cDNA clone  
 IMAG9998N11359 ; IMAGE:190666, mRNA sequence.  
 ACCESSION BX097138  
 VERSION BX097138.1 GI:27843098  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 472)  
 Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
 Radloff,U., Schneider,D. and Korn,B.  
 Human UniGeneSet - RZPD3  
 Unpublished (2003)  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD: IMAG998N11359.  
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
 Human UniGeneSet - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response=libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r. Primer sequence: TTTCACACGGAACGCTATGAC.  
 Location/Qualifiers  
 1..472  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAG998N11359 ; IMAGE:190666"  
 /sex="male"  
 /tissue\_type="retina"  
 /dev\_stage="55 Year old"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares retina N2b4RH"  
 /note="Organ: eye; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dt) primer (5'  
 TGTTCACATCTGAGTGGAGCGCGCTTTTCTTTTCTTTT 3'),  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). The retinas were obtained from a 55 year old  
 Caucasian and total cellular poly(A)+ RNA was extracted 6  
 hrs after their removal. The retina RNA was kindly  
 provided by Roderick R. McInnes M.D. Ph.D. from the  
 University of Toronto. Library constructed by Bento  
 Soares and M.Facima Bonaldo."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 8, 89e-70 Length: 472  
 Score: 799.00 Matches: 156  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 19.41% Indels: 0  
 DB: 5 Gaps: 0

US-10-007-270-2 (1-797) x BX097138 (1-472)

QY 373 ThTtIeGlnPherThraSpGluIleAglYSerLeuProAlaBheGlyProAspThrGln 392  
 DB 3 ACAATTCAATTCATGATGAATTCGTCGATCACTCCAGCCCTTGTGCTGACCA 62

QY 393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412  
 DB 63 TCAGAGCTCCCAACATCTTGTGTTATPAACAGAGATGCTACTTGGATCCAGAACTT 122  
 QY 413 ProProValGluProGluLeuGluThrValAaSpGlyAlaGluHleGlyLeuProAspThr 432  
 DB 123 CCTCGTGTGAACCCAGCTTGAGACAGTGAAGGAGGAGCATGTGTACTGACACT 182  
 QY 433 SerTTPSerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPheMet 452  
 DB 183 TCTTGCTCCACCTGCTATGAGCTTACTCTCCCTGTGAGAGCTCCACCTTCTTATG 242  
 QY 453 AlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGln 472  
 DB 243 GCATCAAGCATCTTCTCTGACTGATCAAGGACCAAGATACATGAGCCACTGACCA 302  
 QY 473 ThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeu 492  
 DB 303 ACAATGCTAGTACAGAGGCTCAACATCCCAACAGATTAATTCTGCATCAGCCAACTG 362  
 QY 493 AlaLeuGlyIleSerThrIleProProAlaSerSerAspAspSerArgSerAlaGlyGly 512  
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 QY 513 GluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrPro 528  
 DB 423 GAAGATATGATGACACCTAGATGAATGATGTGTGACACATCTCT 470

RESULT 14  
 AL713229 510 bp mRNA 1 linear EST 04-SRP-2003  
 LOCUS AL713229  
 DEFINITION DKFZp666P1295\_r1 686 (synonym: hlc3) Homo sapiens cDNA clone  
 DKFZp686P1295\_5', mRNA sequence.

ACCESSION AL713229  
 VERSION AL713229  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

REFERENCE 1 (bases 1 to 510)  
 Bloecker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and  
 Wiemann,S.  
 EST (Bioecker,H., Boecker,M., Brandt,P., Mewes,H.W., Weill,B. and  
 Wiemann,S.)  
 Unpublished (1999)

TITLE  
 JOURNAL  
 COMMENT  
 CONTACT: MIPS

MIPS  
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by GFP (National Research Centre for Biotechnology Ltd.,  
 Braunschweig/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No si sequence available.  
 This clone (DKFZp686P1295) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
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 cDNA-collection"

ORIGIN

## Alignment Scores:

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US-10-007-270-2 (1-797) x AL713229 (1-510)

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QY 41 ArgAsnGluThrThrgLuserThrgLulysMetTYrLYsMetSerThrMetArgArgIle 60
DB 102 ----- 102
QY 61 PheAPLeuAlaLYsHISArgThrLYsArgSerAlaPhePheProThrgLYValLYsVal 80
DB 102 ----- 102
QY 81 CysProGlnGluSerMetLYsGlnIleLeuAspSerLeuGlnAlaTYrTYrArgLeuArg 100
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QY 101 ValCYsGlnGlnAlaValTrpGlnAlaTYrArgIlePheLeuAspArgIleProAspThr 120
DB 103 GGTGTGACGAGAGAGCTATGAGAGCATTCGATCTTCGATCGATCCCTGACACA 162
QY 121 GlyLYsTYrGlnAspTrpLYsIleSerIleCYsGlnGlnGluThrPheCYsLeuPheAspIle 140
DB 163 GGGGATATACAGAGACTGGCTGACATCTGCCAGCAGAGAACCTTCGCTTTCACATT 222
QY 141 GlyLYsAsnPheSerAsnSerGlnGlnIleAspLeuLeuGlnGlnArgIleLYsGln 160
DB 223 GGAATAAACTTCACGATTCCTCCAGAGACCTGGATCTTCTCCAGAGAAATAAAAACG 282
QY 161 ArgSerPheProAspArgLYsAspGlnIleSerAlaGlnLYsThrLeuGlnLYsProGly 180
DB 283 ABAAGTTTCCTGACAGAAAGATGAATATCTGCAGAGAAACATTTGGAGAGAGCTGCT 342
QY 181 -GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuTh 200
DB 343 TGAACACCATGTCATTTCACAGATGTGCCAACGCTTCACCTTGAGGCTTCCCTCAC 402
QY 200 rProAspAPLeThrLeuAsnGlnIleLeuAspAsnThrIleAsnAspThrLYsMetPr 220
DB 403 TCCCTATGACACCCCTCTCAATGAATTCGATTAATACCTCAACAGAACCAAGATGCC 462
QY 220 oThrThrgLusArgGluThrgLupheAlaValIleuGlnGlnArg 235
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## RESULT 15

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 LOCUS cs18h07.y1 Human Retinal pigment epithelium/choroid cDNA  
 DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs18h07  
 5', mRNA sequence.

ACCESSION CA391789  
 VERSION CA391789.1 GI:24723977  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 618)  
 Mammalia; Eutheria; Eumarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

## AUTHORS

Wistow, G., Bernstein, S. L., Wyatt, M. K., Farris, R. N., Behal, A.,  
 Touchman, J. W., Bouffard, G., Smith, D. and Peterson, K.

Expressed sequence tag analysis of human RPE/choroid for the  
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 Mol. Vis. 8 (4), 205-220 (2002)

## JOURNAL

PUBMED

12107410

## COMMENT

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: gtwistow@helix.nih.gov

Plate: 18 row: h column: 07

Seq primer: M13RPL reverse primer (ABI).

Location/Qualifiers

## FEATURES

source

1..618

/organism="Homo sapiens"

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/tissue\_type="RPE/choroid"

/dev\_stage="Adult"

/lab\_host="EMDH108"

/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs"/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
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 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD, now part of Invitrogen Corp),  
 essentially following the protocols of the Superscript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>). The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/Mui sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

## ORIGIN

## Alignment Scores:

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Score:	751.00	Matches:	152
Percent Similarity:	66.09%	Conservative:	0
Best Local Similarity:	66.09%	Mismatches:	0
Query Match:	18.24%	Indels:	78
DB:	6	Gaps:	1

US-10-007-270-2 (1-797) x CA391789 (1-618)

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QY 1 MetTYrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
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QY 21 ThrLYsAPLeSerIleAsnIleTyRHisSerGluThrLYsAPLeAspAsnProPro 40
DB 221 ACCAAA----- 226
QY 41 ArgAsnGluThrThrgLuserThrgLulysMetTYrLYsMetSerThrMetArgArgIle 60
DB 226 ----- 226
QY 61 PheAPLeuAlaLYsHISArgThrLYsArgSerAlaPhePheProThrgLYValLYsVal 80
DB 226 ----- 226
QY 81 CysProGlnGluSerMetLYsGlnIleLeuAspSerLeuGlnAlaTYrTYrArgLeuArg 100
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Qy      121 GlyIuTYrGluAspTrpValSerIleCysGInGInGluThrPheCysLeuPheAspIle 140
Db      287 GGGGAATATCAGGACTGGGTCAAGCATCTGCCAGCAGAGAGACCTTGCTTGACATT 346
Qy      141 GlyValAsnPheserAsnSerGInGluIleLeuAspLeuLeuGInGlnArgIleLysGln 160
Db      347 GGAATAAACTTCAGCAATCCCAAGAGCACTGGATCTTCCAGCAGAAATAAAACAG 406
Qy      161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
Db      407 AGAAGTTTCCTGACGAAAGATGAAATATCTGCAGAGAGACATTGGAGAGGCTGGT 466
Qy      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db      467 GAACCATTTGTCACTTCAACAGATGTTGCCAAGTCTCACTTGGGCTTTCCTCTCACT 526
Qy      201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
Db      527 CCTGATGACACCCCTCTCAATGAAATCTCGATTAATACACTCAACGACACCAAGATGCCT 586
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Job time : 7775 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2006, 02:03:01 ; Search time 1526 Seconds

(without alignments)  
4318.935 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLSTRRAIFVWIFLQVQ.....NSELTVEYERHODMEGN 797

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4073	98.9	3330	US-10-007-270-1	Sequence 1, Appl
2	4024.5	97.8	3361	US-10-007-270-27	Sequence 27, Appl
3	3619	87.9	2887	US-10-007-270-3	Sequence 3, Appl
4	3323	80.7	2244	US-10-007-270-5	Sequence 5, Appl
5	2548.5	61.9	3668	US-10-007-270-8	Sequence 8, Appl
6	1342.5	32.6	1726	US-10-007-270-10	Sequence 10, Appl
7	929.5	22.6	1321	US-10-007-270-12	Sequence 12, Appl
8	927	22.5	4165	US-10-783-528-9	Sequence 9, Appl

9	927	22.5	4166	5	US-10-007-270-16	Sequence 16, Appl
10	885	21.5	555	5 <td>US-10-007-270-14</td> <td>Sequence 14, Appl</td>	US-10-007-270-14	Sequence 14, Appl
11	846.5	20.6	2964	5 <td>US-10-007-270-18</td> <td>Sequence 18, Appl</td>	US-10-007-270-18	Sequence 18, Appl
12	841	20.4	4204	5 <td>US-10-007-270-23</td> <td>Sequence 23, Appl</td>	US-10-007-270-23	Sequence 23, Appl
13	248.5	6.0	592	9 <td>US-10-972-079-61156</td> <td>Sequence 61156, A</td>	US-10-972-079-61156	Sequence 61156, A
14	248.5	6.0	599	9 <td>US-10-972-079-61152</td> <td>Sequence 61152, A</td>	US-10-972-079-61152	Sequence 61152, A
15	248.5	6.0	600	9 <td>US-10-972-079-61153</td> <td>Sequence 61153, A</td>	US-10-972-079-61153	Sequence 61153, A
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17	248.5	6.0	600	9 <td>US-10-972-079-61155</td> <td>Sequence 61155, A</td>	US-10-972-079-61155	Sequence 61155, A
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20	189.5	4.6	4139	3 <td>US-09-964-824A-578</td> <td>Sequence 578, App</td>	US-09-964-824A-578	Sequence 578, App
21	189.5	4.6	4139	3 <td>US-09-864-864-334</td> <td>Sequence 334, App</td>	US-09-864-864-334	Sequence 334, App
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23	189.5	4.6	4139	3 <td>US-09-968-007A-751</td> <td>Sequence 751, App</td>	US-09-968-007A-751	Sequence 751, App
24	189.5	4.6	4139	3 <td>US-10-171-311-157</td> <td>Sequence 157, App</td>	US-10-171-311-157	Sequence 157, App
25	189.5	4.6	4139	6 <td>US-10-177-293-310</td> <td>Sequence 310, App</td>	US-10-177-293-310	Sequence 310, App
26	189.5	4.6	4139	7 <td>US-10-440-464-155</td> <td>Sequence 155, App</td>	US-10-440-464-155	Sequence 155, App
27	189.5	4.6	4139	7 <td>US-10-734-564-53</td> <td>Sequence 53, Appl</td>	US-10-734-564-53	Sequence 53, Appl
28	189.5	4.6	4139	8 <td>US-10-775-920-80</td> <td>Sequence 80, Appl</td>	US-10-775-920-80	Sequence 80, Appl
29	189.5	4.6	4139	8 <td>US-10-775-920-85</td> <td>Sequence 85, Appl</td>	US-10-775-920-85	Sequence 85, Appl
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45	188.5	4.6	1721	9 <td>US-10-843-641A-6369</td> <td>Sequence 6369, Ap</td>	US-10-843-641A-6369	Sequence 6369, Ap

#### ALIGNMENTS

RESULT 1  
US-10-007-270-1

Sequence 1, Application US/10007270  
Publication No. US20020160954A1

GENERAL INFORMATION:  
APPLICANT: Hageman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
FILE REFERENCE: 020618-000120US  
CURRENT APPLICATION NUMBER: US/10/007,270  
CURRENT FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US 09/430,195  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 09/183,972  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1  
LENGTH: 3330  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA, isoform A

US-10-007-270-1

Alignment Scores:  
Pred. No.: 0  
Score: 4073.00  
Percent Similarity: 97.31%  
Best Local Similarity: 97.31%  
Query Match: 98.93%

Length: 3330  
Matches: 796  
Mismatches: 1  
Indels: 22

DB: 5 Gaps: 1  
US-10-007-270-2 (1-797) x US-10-007-270-1 (1-3330)  
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Db 131 ATGTATTGGAAACATAGAAAGACCTATTTTGTGTTTGGATTTTCTCCAAGTTCAGGA 190  
Qy 21 ThrIysAspIleSerIleAsnIleTyrHisSerGluThrIysAspIleAspAspProPro 40  
Db 191 ACCAAAGATATCTCAATTAACATATACCTTCTGAAACTTAAGACATAGACATCCCCCA 250  
Qy 41 ArgAsnGluThrThrGluSerThrGluIysMetYrIysMetSerThrMetArgArgIle 60  
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Db 311 TTCGATTGGCAAAACATCGAACAAAAGATCCGATTTTTCCTCAACGGGGTTTAAAGTC 370  
Qy 81 CysProGlnGluSerMetIysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
Db 371 TGTCACAGGAATCCATGAAACAGATTTTACAGATCTTCAAGCTTATTATAGATTGAGA 430  
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Qy 121 GlyIuTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
Db 491 GGGGAATATCAGAGATCGGGTCAGCATCTGCCAGCAGAGACCTTCGCTTTTGACATT 550  
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Qy 181 GluThrIleValIleSerThr----- 187  
Db 671 GAAACCATGTGATTTCAC-AGCAATCTACATTTCAAAGACTTGGGCGAGTATCTAAGA 729  
Qy 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
Db 730 AAACCTCAGAAAGCAAAATTCAGAGATGTGCCAAGCTCTCACTTGCGGCTTTCCCTGTC 789  
Qy 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrIysMet 219  
Db 790 ACTCCTGATGACACCTCTCTCAATGAAATCTCGATTAATACCTCAGACACCAAGATG 849  
Qy 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSer 239  
Db 850 CCTACACAGAAAGAGAAACAGAAATTCGCTGTGTGGAGAGACAGAGGGGTGAGCTCAGC 909  
Qy 240 ValSerLeuValAsnGluIysPheIysAlaGluIuAlaAspSerGlnSerProTyrTyr 259  
Db 910 GCTCTCTGGTAAACCAAGATTCAAGGAGAGCTGCTGACTCCAGCTCCCATATTAAC 969  
Qy 260 GlnGluLeuAlaGlyIysSerGlnLeuGlnMetGlnIysIlePheIysIysLeuProGly 279  
Db 970 CAGGAGCTAGCAGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAACTTCCAGGA 1029  
Qy 280 PheIysIysIleHisValLeuGlyPheArgProIysIysGluIysAspGlySerSerSer 299  
Db 1030 TTCAAAAAATCCATGTGTAGATTAGACCAAGAAAGAAAGAAAGATGGCTCAAGCTCC 1089  
Qy 300 ThrGluMetGlnLeuThrAlaIlePheIysArgHisSerAlaGluAlaIysSerProAla 319  
Db 1090 ACAGAGATGCAACTTAACGGCCATCTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGGA 1149  
Qy 320 SerAspLeuLeuSerPheAspSerAsnIysIleGluSerGluGluValTyrHisGlyThr 339

Db 1150 AGTACCTCTCTGCTTTTGGATTCCAACAAATTTGAAATGAGAGAGTATCATGGAACC 1209  
Qy 340 MetGluIysAspIysGlnProGluIleTyrLeuThrAlaThrAspLeuIysArgLeuIle 359  
Db 1210 ATGGAGAGAGCAACAGCAACAGAAATCTATCTCAGCTACAGACCTCAAAAGCTGATTC 1269  
Qy 360 SerIysAlaLeuGluGlnGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
Db 1270 AGCAAGACCTAGAGAGAAAGAACATCTTGGATGTGGGAGACATTCAGTTCACTATGAA 1329  
Qy 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
Db 1330 ATTGCTGATCACTGCCAGCTTTGTGTCTGACACCCATCAGAGCTCCCAACATCTTTT 1389  
Qy 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
Db 1390 GCTGTTATACAGAGAGATGCTTATGATCCAGAACTTCTCTGTTGAACCCCAAGCTT 1449  
Qy 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProProAlaMet 439  
Db 1450 GAGACAGTGAACGAGACAGACATGTCTTACCTGACATCTTGTGCTCCACTGCTATG 1509  
Qy 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
Db 1510 GCTCTTACTCTCCGTCAAGAAAGCTCACTTTCTTTATGGATCAAGCATCTTCTCTG 1569  
Qy 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
Db 1570 ACTGATCAAGGACACACAGATACATGCGCACTGCCAGCAATGCTGATACAGAGGCTC 1629  
Qy 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
Db 1630 ACCATCCCACAGAGATTAATTCGCAATCAAGCAACTGGGCTTGGGAATTCACATCCA 1689  
Qy 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyIysAspMetValArgHisLeu 519  
Db 1690 CCTGATCTTCAGATGACAGCGCATCAAGTCAGAGTGGCGAAAGATGTGTGACACCTTA 1749  
Qy 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlyIyr 539  
Db 1750 GATGAATAGATCTGTCTGACACATCTCCCATCTGAGGTACCAAGACTCAGCAAAATAT 1809  
Qy 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
Db 1810 GTTCTGTCCAGATCATTTCTTGGAGATACCACTCTGTCTCAGCTTTACAGTATATC 1869  
Qy 560 ThrThrSerSerMetThrIleAlaProIysGlyArgGluLeuValIlePhePheSerLeu 579  
Db 1870 ACCACTAGTTCATGACCAATGGCCCCCAAGGGCGAGAGCTGTGTGTCTTCAGTCTG 1929  
Qy 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnIysSerSerLeuGlyIyrArg 599  
Db 1930 CGTGTGTCTTAACATGGCTCTTCCCAACGCTGTTCACCAAGAGCTCTCTGGAGTACCGA 1989  
Qy 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuAspSerAsnLeuThrGly 619  
Db 1990 GCTCTGGACAACAATTCACACAGCTGCTGTTCATATCTACATCCAAITTTACAGGA 2049  
Qy 620 PheIysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerIysMet 639  
Db 2050 TTTTAAGCAACTTGAATATCTTACTTCAGAAACGGAGATGTGTGTAATGCAAAATG 2109  
Qy 640 LysPheAlaIysSerValProTyrAsnLeuThrIysAlaValHisGlyValLeuGluAsp 659  
Db 2110 AAGTTTCTAAGTCTGTGCCGATATACCTCAACAGGCTGTGCAAGGGGCTTTCAGAGAT 2169  
Qy 660 PheArgSerAlaAlaIleGlnGlnLeuHisIleGlnIleAspSerTyrSerLeuAsnIle 679  
Db 2170 TTTGTTGTGTGACGCCCAACACTCATCTGGAAATAGACAGTACTCTCTCAACATT 2229  
Qy 680 GluProAlaAspGlnAlaAspProCysIysPheLeuAlaCysGlyGluPheAlaGlnCys 699



Db 2230 GAACACGATGATCAAGACAGATCCCTGCAAGTTCCTGGCCCTGGCGGAATTTGCCCAATGT 2289  
Qy 700 VallylaAsnGluArgThrGluGluAlaGluCysArgCysArgProGlyTyrAspSerGln 719  
Db 2290 GTAAACAGCAAGAGCTGAGAGCGAGTGTGCTGCACCAACAGAAATATGACACCCAG 2349  
Qy 720 GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyTyrArgGluVal 739  
Db 2350 GGGAGCTTGACGGCTTGGACACAGCGCTCTGTGGCCCTGGACCAAGAAATCGAGGTC 2409  
Qy 740 LeuGlnGlyArgGlyValaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLys 759  
Db 2410 CTCACGAGAAAGGAGCTCATGACAGTTGCCAGATCAGTCAAAATCAAGCATCAAA 2469  
Qy 760 ThrSerVallylaArgPheGlnAsnGlnGlnAsnAsnLysValIleSerLysArgAsnSer 779  
Db 2470 ACTAGAGTTAAAGAAAGTTCCAAATTCACAAATACAAAGATATCGTAAAGAAATTC 2529  
Qy 780 GluLeuLeuThrValaGluTyrGluGluPheAsnHisGlnAspTyrGluGluAsn 797  
Db 2530 GAATTACTGACCTAGAAATATGAAATTTTACCATCAAGATTGGAGAGAAAT 2583

RESULT 2  
US-10-007-270-27  
; Sequence 27, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hegeman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-00012005  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 3261  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IPM 150 isoform A variant cDNA sequence  
; NAME/KEY: CDS  
; LOCATION: (128)..(2440)  
US-10-007-270-27

Alignment Scores:  
Pred. No.: 0 Length: 3261  
Score: 4024.50 Matches: 793  
Percent Similarity: 99.62% Conservative: 1  
Best Local Similarity: 99.50% Mismatches: 3  
Query Match: 97.75% Indels: 3  
DB: 5 Gaps: 0

US-10-007-270-2 (1-797) x US-10-007-270-27 (1-3261)

Qy 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTyrIlePheLeuGlnValGlnGly 20  
Db 128 ATGTATTGTGAAACTGAAAGAGCTATTGTTGTTTGTGATTTTCTCCAAAGTTCAAGCA 187  
Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
Db 188 ACTAAAGATATCTCCATTACATATACCATTCGAAACTAAGACATAGCAATCCCA 247  
Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
Db 248 AGAAATGAAACAACTGAAAGTACTGAAAAATGTATCAAAATGTCACTATGAGACGAAT 307

Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
Db 308 TTCGATTGGCAAGATCTGAACAAAGATCCGCAATTTTCCCAAGCGGGGTAAAGTC 367  
Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
Db 368 TCTCCACAGGAATTCATGAAACAGATTTTATAGACAGCTTCAAGCTTATATGATTGAGA 427  
Qy 101 ValCysGlnGluAlaValaTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
Db 428 GTGTGCAGGAAGCAGATATGGAGACATATCCGATCTTCTGATTCGACCTGCACACA 487  
Qy 121 GlyGluTyrGlnAspTyrValaSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
Db 488 GGGAAATACAGACATGGGTCAAGATCTGCACAGAGAAACCTTGCCTCTTTCACATT 547  
Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLysAspLeuLeuGlnArgIleLysGln 160  
Db 548 GGAAGAAATCTCAGCAATTCAGAGGACCTCGATCTTCTCAGACAGAAATTAAGACG 607  
Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
Db 608 AGAAGTTTCCCTGACAGAAAGATGAAATATCTGCAGAGAAACATTTGGAGAGCCTGCT 667  
Qy 181 GluThrIleValIleSerThrAspValaAsnValSerLeuGlyProPheProLeuThr 200  
Db 668 GAACCATTTGTCATTTCAACAGATGTTCACAGTCTCACTTGGGCTTTTCTCTCAGCT 727  
Qy 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAspAspThrLysMetPro 220  
Db 728 CCGATGACACCTCTCTCATTAATTTCTCGAATACCTACAGACACCAAGATGCT 787  
Qy 221 ThrThrGluArgGluThrGluPheAlaValLeuGlnGluGlnArgValaGluLeuSerVal 240  
Db 788 ACAACAGAAAGAGAAACAGAAATTCCTGTGTGAGAGACAGAGGTGAGCTCAGCGTC 847  
Qy 241 SerLeuValaAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGln 260  
Db 848 TCTCTGTAAACCAAGAAAGTTCAAGGACAGCTGCTGATCTCCAGTCCCAATTAACCG 907  
Qy 261 GluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPhe 280  
Db 908 GAGCTGACAGAAATCTCCAACTTCAGATGCAAAAGATTTTAAAGAACTTCAGAGATTC 967  
Qy 281 LysLysIleHisValLeuGlyPheArgProLysGluLysAspGlySerSerSerThr 300  
Db 968 AAAAAAATCCATGTGTATGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACA 1027  
Qy 301 GluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSer 320  
Db 1028 GAGATGCAACTTACCGCCATCTTTAAGAGACACAGTGCAGAAACAAAGCCCTCCAGT 1087  
Qy 321 AspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValaTyrHisGlyThrMet 340  
Db 1088 GACCTCTGCTCTTTGATTCACAAATTTGAATGAGAGAGCTTATCATATGAACCATG 1147  
Qy 341 GluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSer 360  
Db 1148 GAGAGAGCAACAGCAACGAAGATTTATCTCACAGCTACAGACTCAAAAGGCTGATCACG 1207  
Qy 361 LysAlaLeuGluGluGlnGlnSerLeuAspValaGlyThrIleGlnPheThrAspGluIle 380  
Db 1208 AAGACACTAGAGAGAAAGAACTTTGATGGAGGAGCAATTCAGATTCATGATGAAT 1267  
Qy 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
Db 1268 GCTGATCACTCCAGCTTGTGCTCTGACACCCCAATCAAGCTGCCCAATCTTTTGT 1327  
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValaGluProGlnLeuGlu 420  
Db 1328 GTTATTAACAGAGAGATGATCTTGAATCCAGAACTTCTCTGTTGAACCCCAAGCTTGA 1387  
Qy 421 ThrValaAspGlyAlaGluHisGlyLeuProAspThrSerTyrPheProProAlaMetAla 440

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Db      1388  ACAGTGAAGGAGCAGAGCATGCTTACCTGACACTTCTGTGCTCCACCTGCTATGACC 1447
Qy      441  SerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThr 460
Db      1448  TCTACTCCCTGTCGAGAAAGCTCCACCTTCTTATAGGACATCAAGATCTTCTCTGACT 1507
Qy      461  AapGlnGlyThrThrAspThrMetAlaThrAapGlnThrMetLeuValProGlyLeuThr 480
Db      1508  GATCAAGGACCAACAGATACATAGGCTGACCTGACCAACATCTTGTACAGAGGCTCACC 1567
Qy      481  IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500
Db      1568  ATCCCAACAGATGATATTCTGCAATCAGCCAACTGGCTCTGGAAATTTCAATCCACT 1627
Qy      501  AlaSerSerAspAspSerAspSerSerAlaGlyGlyGluAapMetValArgHisLeuAap 520
Db      1628  GCATCTTCAGATGACAGCCGATCAAGATGACAGGTGGCGAAGATATGCTCAGACCTAGAT 1687
Qy      521  GluMetAapLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540
Db      1688  GAAATGATCTGTCTGACACTCTGCTGCCATCTGAGTACCAAGCTCAGCAATATGTT 1747
Qy      541  SerValProAspHisPheLeuGluAapThrThrProValSerAlaLeuGlnTyrIleThr 560
Db      1748  TCTGTCCCAAGATCATTTCTTGAGAGATACCACTCCTGCTCAGCTTTACAGATATCACC 1807
Qy      561  ThrSerSerMetThrIleAlaProlyArgIuArgGluLeuValValPhePheSerLeuArg 580
Db      1808  ACTAGTCTTATATACCAATTCGCCCCCAAGGCGCAGAGCTGGTGTCTTCTCAGTCTGCT 1867
Qy      581  ValAlaAspMetAlaPheSerAspAapLeuPheAapLeuSerSerLeuGluTyrIleArgAla 600
Db      1868  GTTGTCTAATAGGCTTCTTCCAAAGCACTGTTCAACAAAGCTCTCTGAGATACCGAGCT 1927
Qy      601  LeuGlnGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAspLeuThrGlyPhe 620
Db      1928  CTGGAGCAACAATTCACACAGCTGCTGTTCCATATCTACATTCACATTTACAGATTT 1987
Qy      621  LysGlnLeuGlnIleLeuAapPheArgAapGlySerValIleValAapSerIleMetLys 640
Db      1988  AAGCAACTTGAATATCTTAATCTTGAAACCGGAGAGTGATGATGTAATGCAAAATGAAAG 2047
Qy      641  PheAlaLysSerValProTyrAapLeuThrIleValAlaHisGlyValLeuGluAapPhe 660
Db      2048  TTGTCTAAGTCTGTGCGTATACCTCACCAAGGCTGACAGGAGCTCTGAGAGATTTT 2107
Qy      661  ArgSerAlaAlaAlaGlnIleLeuHisLeuGlnIleAapSerTyrSerLeuAapIleGlu 680
Db      2108  CGTTCTGCTGACGCCCAACAATCTCATCTGAAATGACAGCTACTCTCAACATTTGAA 2167
Qy      681  ProAlaAapGlnAlaAapProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700
Db      2168  CCAAGCTGATCAAGCAAGATCTCTGCAAGTTCCTGGCTGCGGCAATTTCCCAATGCTGTA 2227
Qy      701  LysAapGlnArgThrGlnGlnAlaGluCysArgCysLysProGlyTyrAapSerGlnGly 720
Db      2228  AAGAAAGAAAGGAGCTAGAGAGGAGAGTTCGCTGCAACCAAGATATACAGCCAGGGG 2287
Qy      721  SerLeuAapGlyLeuGluProGlyLeuCysGlyProGlyThrLysGlnCysGluValLeu 740
Db      2288  AGCTGGAAGCGTCTGGAACCAAGGCTCTGTGG-CTGGGCAAAAGGAATGCGAGGCTCTC 2346
Qy      741  GlnGlyLysGlyAlaProCysArgLeuProAapHisSerGluAapGlnAlaTyrIleThr 760
Db      2347  CAGGGAAGAGAGCTCCATGCG--GTTCCAGATCACTTGAAATCAACACATACAAAACT 2404
Qy      761  SerValLysPheGlnAapGlnGlnIleAapAapValIleSerLysArgAapSerGlu 780
Db      2405  AGTGTTTAA-AAAGTTCAAAATCAACAATAACAAAGATATCAGTAAAGAAATTTCTGAA 2463
Qy      781  LeuLeuThrValGluTyrGlnGluPheAapHisGlnAapTyrGluIleValAan 797

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Db      2464  TTAGTACCGTAGATATGAAGAAATTTAACCATCAAGATTGGGAAGAAAT 2514
RESULT 3
US-10-007-270-3
; Sequence 3, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2887
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IPW 150 cDNA sequence, isoform B
US-10-007-270-3
Alignment Scores:
Pred. No.: 0 Length: 2887
Score: 3619.00 Matches: 711
Percent Similarity: 90.00% Conservative: 0
Best Local Similarity: 90.00% Mismatches: 1
Query Match: 87.90% Indels: 78
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US-10-007-270-2 (1-797) x US-10-007-270-3 (1-2887)
Qy      8  AlaIlePheValPheThrIlePheLeuGlnValGlnGlyThrLysAapIleSerIleAan 27
Db      5  GCTATTTTGTGTTTGTGATTTTCTCCAAAGTTCAGGAACCAAA----- 49
Qy      28  IleTyrHisSerGluThrLysAapIleAapAapProAaGlaGlnIuThrThrGluSer 47
Db      49  ----- 49
Qy      48  ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAapLeuAlaLysHisArg 67
Db      49  ----- 49
Qy      68  ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87
Db      49  ----- 49
Qy      88  GlnIleAapSerLeuGlnAlaTyrTyrArgLeuAaGValCysGlnGlnIleValIleTyr 107
Db      50  -----GTCGTCAAGAAAGCAATATG 70
Qy      108  GluAlaTyrArgIlePheLeuAapArgIleProAapThrGlyGluTyrGlnAapTyrVal 127
Db      71  CAAGATATCGGATCTTCTGATGATCCCTGACACAGGAGGAATATCAGGACTGGGTTC 130
Qy      128  SerIleCysGlnGlnGlnIuThrPheCysIleAapPheAapIleGlyLysAapPheSerAan 147
Db      131  AGCATCTCCAGCAAGAAACCTTCTGCTCTTTCATTTGAAATAAATCTTCAGCAATTTCC 190
Qy      148  GlnGlnIleAapSerLeuLeuGlnGlnIleArgIleLysGlnArgSerPheProAapArgLys 167
Db      191  CAGAGCAACCTGATCTTCTCCAGCAAGAAATAAACAGAAAGATTTCCCTGACAGAAA 250
Qy      168  AapGlnIleSerAlaGlnLysThrLeuGlnGluProGlyGlyIuThrIleValIleSerThr 187
Db      251  GATGAATATCTGCAGAGAAAGACATTTGGAGAGCTGTGTGAAACCATTTGTCTTCAACA 310

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QY 188 ASDValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
 DB 311 GATGTGGCAAGCTCTCAGCTTGGGCTTTCCCTCTCAGCTCTGATACACCTCCCTCAAT 370  
 QY 208 GIUlleLeuAspAsnThrLeuAsnAspThrLyMetProThrThrGluArgGluThrGlu 227  
 DB 371 GAAATTTCTGATTAATCACTCAACGACACCAAGATCTTACACAGAAAGAAACAGAA 430  
 QY 228 PheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLySph 247  
 DB 431 TTCGCTGTGTGGAGAGACAGAGGGGTGAGCTCAGGCTCTCTCTGTTAAACCAAGATTCC 490  
 QY 248 LySAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLySergln 267  
 DB 491 AAGGCAAGAGCTGCTCACTCCAGTCCCATATTACAGAGCTACAGAAAGTGTCCAA 550  
 QY 268 LeuGlnMetGlnLysIlePheLySlyLeuProGlyPheLySlyValIleValLeuGly 287  
 DB 551 CTTCAATGCAAAAGATATTAAAGAACTTCCAGATTCAGAAATAAATCCATGTGTAGGA 610  
 QY 288 PheArgProLySlySgluLyAspGlySerSerSerThrGluMetGlnLeuThrAlaIle 307  
 DB 611 TTTAGCCAAAGAAAGAAAAGATGGCTCAGCTCCACAGAGATGCACTTACGGCCATC 670  
 QY 308 PheLyAspGlnSerAlaGluAlaLySerProAlaSerAspLeuLeuSerPheAspSer 327  
 DB 671 TTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAGAGTACCTCTGTCTTTGATCTCC 730  
 QY 328 AsnLySlyLeuSerGluGluValTyrHisGlyThrMetGluGlnAspLySglnProGlu 347  
 DB 731 AACAAATTTGAAGAGAGAGATCTATCATGGAACATGAGAGAGAGCAAGCAACAGAA 790  
 QY 348 IleTyrLeuThrAlaThrAspLeuLyAspGlyLeuIleSerLyAlaLeuGluGluGln 367  
 DB 791 ACTATCTCAGAGCTACAGACCTCAAAAGCTGATCAGCAAAAGCACTTAAGAGAAAGCA 850  
 QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
 DB 851 TCTTTGAGATGTGGGGCAATTCAGTTCACGTGATGAATTCGTGATCCTGCGACAGCTTT 910  
 QY 388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
 DB 911 GGTCCTGAGACCCAAATCAGAGCTGCCACATCTTTGCTGTTATTAACAAGAGATGCTACT 970  
 QY 408 LeuSerProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlnHis 427  
 DB 971 TTGAGTCCAGAACTTCTCTCTGTAACCCAGCTTGAGACAGTGGACGAGACAGACAT 1030  
 QY 428 GlyLeuProAspThrSerTyrSerProProAlaMetAlaSerThrSerLeuSerGluAla 447  
 DB 1031 GGTCTACCTGACACATCTTGGTCTCCACCTGCTATAGCTCTACCTCCCTGCAGAAAGCT 1090  
 QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467  
 DB 1091 CCACTCTTTTATGACATCAAGACATCTTCTCTGACATCAAGAGCCACACAGATACA 1150  
 QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
 DB 1151 ATGGCCACATGACCAAGACATGCTAGTACCAAGGCTTACCAATCCCAACGATATTATCT 1210  
 QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArg 507  
 DB 1211 GCAATTCAGCAACTGGCTCTGGGAATTTTCAATCCACCTGCATCTTCAATACAGCCGA 1270  
 QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGlnMetAspLeuSerAspThr 527  
 DB 1271 TCAAGTGCAGGTGGCAAGATATGTCACACACCTAGATGAATGATGTGCTGACACT 1330  
 QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
 DB 1331 CCGGCCCATCTGAGGTATCAGGGGCTCAGGAATAGTTTGTGTCCAGATCATTTCTTG 1390

QY 548 GIUAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567  
 DB 1391 GAGATATCACCTCCGTCTCAGCTTATACAGTATATACACATGATTTATGACATTTGCC 1450  
 QY 568 ProLySglYArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587  
 DB 1451 CCCAAGGGCCGAGACTGGTATGTTCTTCACTTCGCGTGGTCTTAACATGGCTTCTCC 1510  
 QY 588 AsnAspLeuPheAsnLySergSerLeuGlnTyrArgAlaLeuGluGlnGlnPheThrGln 607  
 DB 1511 AACGACCTGTTCAACAAAGAGCTCTCGAGATCCAGAGCTCTGAGCAACATATTCACAG 1570  
 QY 608 LeuLeuValProTyrLeuArgSerLeuLeuThrGlyPheLySglnLeuGluIleLeuAsn 627  
 DB 1571 CTGCTGTGTTCATATCTACGATCTTACAGATTTTAAACCACTTGAAATACTTAAC 1630  
 QY 628 PheArgAsnGlySerValIleValAsnSerLySmetLyPheAlaLySerValProTyr 647  
 DB 1631 TTCAGAAACGGAGTGTGATGTGATGCAAAATGAAGTTGTGAATCTGTGCTGTGAT 1690  
 QY 648 AsnLeuThrLySAlaValHisGlyValLeuGluAspPheArgSerAlaAlaAlaGlnGln 667  
 DB 1691 AACCTCACCAAGGCTGTGACAGGGGCTTTGAGAGATTTTCTGTGCTGACCCACAAACA 1750  
 QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687  
 DB 1751 CTCATCTGGAATATGACAGCTACTCTCTCAACATTTGAACCCAGTATCAACAGATCCC 1810  
 QY 688 CysLySphLeuAlaCysGlyGluPheAlaGlnCysValLySAsnGlnAspArgThrGln 707  
 DB 1811 TGCAAGTCTTGCGCTGGCGCAATTTGCCAATGTGTAAGAAAGAACGGAGCTGAGAA 1870  
 QY 708 AlaGluCysArgCysLySProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727  
 DB 1871 GCGAGTGTGCTGCAAAACAGATATGACAGCCAGGGAGGCTGAGCGGTCTGGAACCA 1930  
 QY 728 GlyLeuCySgLyProGlyThrLySgLucysGluValLeuGlnGlyLySgLyAlaProCys 747  
 DB 1931 GCCCTCTGTGGCCCTGGGCAAAAGAAATGCGAGTCTCCACAGGAAGGAGCTCATATC 1990  
 QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLySThrSerValLySphPheGlnAsn 767  
 DB 1991 AGTTGTCAGATCACTCTGAAATATCAAGATATCAAAACTAGTGTAAAGATTCCAAAT 2050  
 QY 768 GlnGlnAsnAsnLySValIleSerLySArgAsnSerGluLeuLeuThrValGluTyrGlu 787  
 DB 2051 CAACAAATTAACAAGTAAATCAGTAAAGAAATTTGAAATTAATCACTAGAAATATGAA 2110  
 QY 788 GIUAspAsnHisGlnAspTyrGluGlyAsn 797  
 DB 2111 GAATTTAACATCAAGATGGGAGAAAT 2140  
 RESULT 4  
 US-10-007-270-5  
 ; Sequence 5, Application US/10007270  
 ; Publication No. US20020160954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hageman, Gregory S.  
 ; APPLICANT: Kuehn, Markus H.  
 ; APPLICANT: University of Iowa Research Foundation  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ; FILE REFERENCE: 020618-000120US  
 ; CURRENT APPLICATION NUMBER: US/10/007.270  
 ; PRIOR FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/430,195  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 2244  
 ; TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..  
OTHER INFORMATION: n is a, c, g, or t.  
US-10-007-270-5

## Alignment Scores:

Pred. No.:	5,97e-312	Length:	2244
Score:	3323.00	Matches:	667
Percent Similarity:	95.56%	Conservative:	0
Best Local Similarity:	95.56%	Mismatches:	10
Query Match:	80.71%	Indels:	23
DB:	5	Gaps:	1

US-10-007-270-2 (1-797) x US-10-007-270-5 (1-2244)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
DB 151 ATGTATTGGAACTGAAAGAGCTATTTTGTGTTTGGATTCTTCCAAAGTTCAAGGA 210  
QY 21 ThrIlyAspIleSerIleAsnIleTyrHisSerGluThrIlyAspIleAspAsnProFro 40  
DB 211 ACCAAGATATCTCCATTACATATACCATCTGAAGACTTAAGACATGACATGCCCA 270  
QY 41 ArgAsnGluThrThrGluSerThrGluIlyMetTyrIlyMetSerThrMetArgArgIle 60  
DB 271 AGAAATGAAACCACTGAAAGTACTGAAAAATGTCAAAATGTCAACTATGAGAGAAATA 330  
QY 61 PheAspLeuAlaIlyHisArgThrIlyArgSerAlaPhePheProThrGlyValIlyVal 80  
DB 331 TTCGATTGGCAAGATGAAAGATGAAAGATCCGATTTTCCCAAGGGGTTAAAGTC 390  
QY 81 CysProGlnGluSerMetIlyGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
DB 391 TGTCACAGAGATTCATGAAACAGATTTTAGACAGCTTCAAGCTTATATGATTGAGA 450  
QY 101 ValCysGlnGlnAlaValTrrGlnAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
DB 451 GTGTCTCAGGAAGCAGCATGGAGCATATTCGATCTTCTGATCGCATCCCTGACACA 510  
QY 121 GlyIlyTyrGlnAspTrrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
DB 511 GGGGAATACAGACTGGGTCAGCATCTGCCAGCAGAGACCTTCTGCTCTTTGACATT 570  
QY 141 GlyIlyAsnPheSerAsnSerGlnGlnIlyIleuAspLeuLeuGlnAlaArgIleIlyGln 160  
DB 571 GGAATAAACTTCAGCAATCCCAAGAGCAGCTGATCTTCTCCAGACAGATTAACAG 630  
QY 161 ArgSerPheProAspArgIlyAspGlnIlyIleSerAlaGlnIlyThrLeuGlnGluProGly 180  
DB 631 AAAAAATTTCTCCAGCAAGAAAGATGAAATATCTGAGAGAGACATTTGGAGAGGCTGGT 690  
QY 181 GluThrIleValIleSerThr----- 187  
DB 691 GAAACCATTTGTCAATTTCAAC AGCAATCTACATTTCAAAAGACTTGGGCGATTTCTAAGA 749  
QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
DB 750 AAACCTCAGAGAGCAATTCAGATGTGCAAGTCTCACTTGGGCTTTCCCTGTC 809  
QY 200 ThrProAspAspThrIleuLeuAsnGlnIleLeuAspAsnThrIleuAspThrIlyMet 219  
DB 810 ACTCTGATGACACCTCTCTCAATGGAATTTCTGATATACACTCAACACACCAAGATG 869  
QY 220 ProThrThrGluArgGluThrGluPheAlaValIleuGlnGluGlyArgValGluLeuSer 239  
DB 870 CTTACACAGAAAGAGAAACAGATTCGCTGTGTGTGGAGAGACAGGGTGGAGCTCACG 929  
QY 240 ValSerIleuValAsnGlnIlyPheIlyValGlnIleuAlaAspSerGlnSerProTyrTyr 259  
|||||

DB 930 GTCTCTGTGTAACCAAGATTCAAGCAGAGCTCGCTGACTCCAGTCCCATATTATAC 989  
QY 260 GlnIlyLeuAlaGlyIlySerGlnLeuGlnMetGlnIlyIlePheIlyLeuProGly 279  
DB 990 CAGAGGCTAGCAGGAAAGTCCCAACTCAGATGCAAAAGATATTAAAGAACTTCCAGGA 1049  
QY 280 PheIlyIlyIleHisValIleuGlyPheArgProIlyIlyGlnIlyAspGlySerSerSer 299  
DB 1050 TTTCAAAAAATCCATGTGTTAGATTTTAGACCAAGAAAGAAAGATGGCTCAAGCTCC 1109  
QY 300 ThrGluMetGlnLeuThrAlaIlePheIlyArgHisSerAlaGlnAlaIlySerProAla 319  
DB 1110 ACAGAGATGCAACTTACCGCATCTTTAAGAGACACGTGACAGAAAGCAAAAGCCCTGCA 1169  
QY 320 SerAspLeuSerPheAspSerAsnIlyIleGluSerGlnGluValIlyHisGlyThr 339  
DB 1170 AGTACCTCTGTCTTTGATTTCACAAATTAAGATGAGAAAGTATCATCTGAAACC 1229  
QY 340 MetGluGluAspIlyGlnProGlnIleTyrLeuThrAlaThrAspLeuIlyArgLeuIle 359  
DB 1230 ATGAGAGAGGACCAAGCAACCAAGATCTATCTCAGCTACAGACTCAAAAGGCTGATC 1289  
QY 360 SerIlyAlaLeuGlnGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
DB 1290 AGCAAGCAGCTAGAGGAAGAAACAATCTTGATGTGGAGACAAATTCAGTTCACTGATGA 1349  
QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
DB 1350 ATTCTGATACAGCCAGCTTGTGCTTACACCCCATGAGAGCTGCCACATCTTT 1409  
QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
DB 1410 GCTGTATTAACAGAGAGATGCTACTTTGAGTCCAGAACTCTCTCGTTGAACCCAGCTT 1469  
QY 420 GluThrValAspGlyAlaGlnHisGlyLeuProAspThrSerTrrPserProProAlaMet 439  
DB 1470 GAGACAGTGGACGAGACAGACATGTCTACCTTCTGCTGCCACCTGCTATG 1529  
QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheAlaSerSerIlePheSerLeu 459  
DB 1530 GCCCT-ACCTCCGTGCAAGAGCTCCACCTTTCTTATGGATCAAGCATCTTCTCTG 1588  
QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
DB 1589 ACTGATCAAGCACCAAGATATCAATGCGCACTGACCAAGACATGCTGACAGGGCTC 1648  
QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
DB 1649 ACCATCCCAAGATGATTTATCTGCAATCAGCCAACTGGCTGGGAATTTCAATCCA 1708  
QY 500 ProIleSerSerAspAspSerArgSerSerAlaGlyGlyIlyAspMetValArgHisLeu 519  
DB 1709 CTTGATTTTCAAGATGACAGCGCATGACAGTGGCGAAGGTATGACAGACCTTA 1768  
QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGlnValProGluLeuSerGlnTyr 539  
DB 1769 GATGAATGATCTGTCTGACACATCTGCCCATTTGAGTACCAAGACTCAGGCAATAT 1828  
QY 540 ValSerValProAspHisPheLeuGlnAspThrThrProValSerAlaLeuGlnTyrIle 559  
DB 1829 GTTCTGTCCCAAGATCATTTCTTGAGAGATCCCACTCGTCTCAGCTTTCAGATATATC 1888  
QY 560 ThrThrSerSerMetThrIleAlaProIlyGlyArgIlyLeuValValPhePheSerLeu 579  
DB 1889 ACCACTAATTTATATACCATTTGCCCCCAAGGCGCAGAGCTGTGATTTCTTCAAGTGTG 1948  
QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnIlySerSerLeuGlnTyrArg 599  
DB 1949 CGTGTGTTACATAGGCTTTCTTCCACGACCTGTTCAACAAAGAGATATTGGAGTACGA 2008  
QY 600 AlaLeuGlnGlnIlyPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGly 619  
DB 2009 GCTGTGAGCAACATTCACACAGCTGTGTTTCATATCAAGATCCAACTTACAGAGA 2068  
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Qy      620 PheylGlnLeuGluIleLeuAsnPhaArganglySerValIleValIleSerlyMet 639
Db      2069 TTTAAGCACTGGAATACTTAATCTTCAAAAAGGAGGTGTATGTGTAATGCAAAAAG 2128
Qy      640 LysPheAlaIleSerValProTyrAsnLeuThrIleValIleValIleGlyValIleuGluuap 659
Db      2128 AGTTTGTCTGACGTGCGGTATTAACCTTCAACCAAGGCGTGTGACGCGGTCTTGGAGGAT 2188
Qy      660 PheArgSerAlaAlaIleGlnLeuIleuHileuGluIleAspSerTyrSerleu 677
Db      2189 TTTGTTGTCTGACGAGCCCAACACTCCATCTGGAATATGACAGCTACTCTC 2242

RESULT 5
US-10-007-270-8
/ Sequence 8, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ APPLICANT: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-000120US
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ PRIOR FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ PRIOR FILING DATE: 1998-10-29
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 3668
/ TYPE: DNA
/ ORGANISM: Mus sp.
/ FEATURE:
/ OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform A
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(3668)
/ OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-8

Alignment Scores:
Pred. No.: 2,25e-236 Length: 3668
Score: 2548.50 Matches: 528
Percent Similarity: 75.12% Conservative: 79
Best Local Similarity: 65.35% Mismatches: 180
Query Match: 61.90% Indels: 21
DB: 5 Gaps: 9

US-10-007-270-2 (1-797) x US-10-007-270-8 (1-3668)
Qy      1 MetTyrLeuGluThrArgArgAlaIlePheValIlePheThrIlePheLeuGlnValGlnGly 20
Db      136 ATGAATTTTCAATTAACATGCTATCTTGTGTTGGATTTTCTCAAGTTCAGGA 255
Qy      21 ThrIleAspIleSerIleAsnIleTyrIleSerGluThrIleAspIleAsnPropio 40
Db      256 ATCAAAAGATACCTCTATTAATATTCAGTTCGAAATTAATAACATACAAAACCCCA 315
Qy      41 ArgAsnGluThrThrGluSerThrGluIuIuMetTyrIleMetSerThrMetArgArgIle 60
Db      316 AATAATCGAAACATGAAAGTACTTCACAGATGCAACAAAGTGTCAACCATGAAACGAATA 375
Qy      61 PheAspLeuAlaIleHisArgThrIleArgSerAlaPhePheProThrIleValIleVal 80
Db      376 TTCGATTTCCAAAGCTTGAACCAAAATCAGCATCTTTCCCA---GCTGCTAACATC 432
Qy      81 CysProGlnIuSerMetIleGlnIleLeuAspSerIleGlnAlaIleTyrIleArgLeuArg 100
Db      433 TGTCCACAGAAATCCTTGAGACAGATTTTAGCAAGTCTTCAGAAATATATATAGACAGAA 492

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Qy      101 ValCysGlnGluAlaValITrGluAlaIleTyrArgIlePheLeuAspArgIleProAspThr 120
Db      493 GTATGTCAAGAGTGTGTGGAGAACATATCTATCTTCTGACCGAATTCCTACACA 552
Qy      121 GlyIuIuTyrGlnAspTrpValSerIleCysGlnGlnGlnIuThrPheCysLeuPheAspIle 140
Db      553 GAGGAATATCAAGATCTGGGTACGCTCTCCGAAAGAAACCTTGTGCTCTTTAGCAT 612
Qy      141 GlyIuAsnPheSerAsnSerGlnIuHileuAspLeuLeuGlnGlnArgIleIleArgin 160
Db      613 GGGAAAACTTCAGCAATCCGAGAGCACCTAGATCTTCTCAGACAGAAATTAACAG 672
Qy      161 ArgSerPheProAspArgIleAspGluIleSerAlaGluIuIuThrLeuGlnGluIuProGly 180
Db      673 AAGACCTTCCCTGGAGGAAAGATAGACAGCTCCATGAGACACTGGAACACCTACT 732
Qy      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db      733 GAAGCCCTGTGTGTACCAAGATGTTTCCAGAGATGTCCTGGGCTCTCCCATCTCCT 792
Qy      201 ProAspAspThrLeuLeuAsnGlnIleLeuAsnAsnThrLeuAsnAspThrIleMetPro 220
Db      793 TCTGATGACACAGACCTCAAGAGATTTCTAGTGTCACTCAAGGACATTCAAAAGCCC 852
Qy      221 ThrThrGluArgGluThr-----GluPheAlaValLeuGlnGluGln 234
Db      853 ACAACAGAAAGTAAACAGAACCTATTCACTGTGTGAATTTCA-----TCAAGAGAG 906
Qy      235 ArgValGluLeuSerValSerLeuValAsnGlnIuIuPheIleValGluLeuAlaAspSer 254
Db      907 AAGTGGAATTCAGATCTCTGTCCAAACCAAGATTCAGGAGAGCTCCAACTCT 966
Qy      255 GlnSerProTyrTyrGlnGlnIuLeuAlaGlyIuSerGlnLeuGlnIleMetGlnIlePhe 274
Db      967 GGGTACCACTACTACAGGAAGTGTGGGACAGTCCCAACTGACAGTCAAAAGATATT 1026
Qy      275 LysIleValProGlyIlePheIleValIleHileuGlyPheArgProIleValIleGlyIu 294
Db      1027 AAGAACTTCCAGGATTCGGAAGAAATCCGTGTATTAGATTTAGACCAAAAGAAAGAA 1086
Qy      295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheIleArgHisSerAlaGlu 314
Db      1087 GATGATCAAGCTCCAGAAATATACAGCTTATGCGCATCTTTAAGGAGGACCATGACAA 1146
Qy      315 AlaIleSerProAlaSerAspLeuLeuSerPheAspSerAsnIleIleGluSerGluGln 334
Db      1147 GCAAAAGCCCTGAAATGATCATCTACTGTCTCTGTAATCCAAATAATGAAGTGAAGA 1206
Qy      335 ValTyrHileGlyThrMetGlnGluIuAspIleProGluIleTyrIleuThrAlaThrAsp 354
Db      1207 ATCCATCATGAGTCATA---GAAACAAACAAACAGAAACCTTACCTCCACACTACAG 1263
Qy      355 LeuIleAspGlnIleSerIleValLeuGlnGluGlnGlnIuSerLeuAspAlaIleThrIle 374
Db      1264 CTCAAAATCATCATATACACTACTAGATGAGACCTGTCTCTGTAGAGGAGAAAT 1323
Qy      375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGln 394
Db      1324 CCATTCCGGATGAAATGATTAACGAGACCTC-----TTCAGACCTGTCACTGAACAGAT 1377
Qy      395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414
Db      1378 CTGCCCAAGCCCTTGTGATGATGTCAAGAGATGCACTTTGAGATGCCAATCTCTTC 1437
Qy      415 ValGluProGlnIleGluIuThrValAspGlyAlaGluHileGlyLeuPro----- 430
Db      1438 GTTAGCCTTAGCTTAGGAGCTGAGACAGAGAGATCTGACCTCTCGAAATGCTCC 1497
Qy      431 --AspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGlnAlaProPro 449
Db      1498 AAAGACAGTTCGTGTCTCCACTGTATCAGCTCAATTTCCGATCAGAAATCTACCT 1557
Qy      450 PhePheMetAlaSerSerIlePheSerIleuThrAspGlnGlyThrThrAspThrMetAla 469

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Db      1558 TCGT---ACACCTAGCATCTTCTCTAGATGCTCAAGCCCTTCCTTGATGACC 1614
Qy      470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThSerAspThrSerIle 489
Db      1615 ATGGCCCCAAGCACTCATCCCAAGCCCACTCTCCCACTGATTAATCTCAATC 1674
Qy      490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerSerSer 509
Db      1675 CGCCATATGCTCTGGAAATGTCACATTTGGCTGCATCTCCAGTACAGAAAGCTGATC 1734
Qy      510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
Db      1735 ACAAGACGCATGACACATCCGAGACCTAGATGCGATGATGTCCTGACACGCACGCC 1794
Qy      530 ProSerGluValProGluLeuSerGluThrValSerValProAspHisAspLeuGluAsp 549
Db      1795 TTGTCAAGAAATATCAAGACTGAGTGGATCGAATTCGCTCGCGTCAATGCGCTTGAAGATG 1854
Qy      550 ThrThrProValSerAlaLeuGlnThrIleThrThrSerSerMetThrIleAlaProLys 569
Db      1855 ACCACACCCATCCCAAGCACTAGCGTTTCATCACACAGCTCCGAGACCATTTGCCACCAAG 1914
Qy      570 GlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp 589
Db      1915 GGCACGAGCTAGTGGTATTCTTCAAGCTCGCGTGTCTAACAATGCGCTTCTCTATGAC 1974
Qy      590 LeuPheAsnLysSerSerLeuGluThrArgAlaLeuGlnGlnPheThrGlnLeu 609
Db      1975 CTGTTCACAAAGATCTCTGAGATCAAGCCCTGGAAACAAGATTCACAACTCGTGG 2034
Qy      610 ValProTyrLeuArgSerAsnLeuThrGlyPheGlyLeuGlnIleLeuAsnPheArg 629
Db      2035 GTTCCCTATCTACGATCGAATCTTACGGGATTTAAGCACTGGAATATCTCAGCTTCAGA 2094
Qy      630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649
Db      2095 AACGGAAGTGATCTGTGAACAGCAAGCGGTTTGAAGCGGTTACCTTCAACACTTC 2154
Qy      650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669
Db      2155 ACCCAGGCGGTGGCGGAGCTTGGAGATCTTGGTCCACCGCAGCTCAAGGCGTCAAT 2214
Qy      670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
Db      2215 CTGGAATCGAAAGCACTCCCTCCGACATTGAACCAAGCTGACGGCGGATCCCTGCAAA 2274
Qy      690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709
Db      2275 CTCTAGACTGTGGCAATTTGCCAGTGTGAAGAAATGAGTGGACAGAGAGAGAGAG 2334
Qy      710 CysArgCysLeuProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729
Db      2335 TGTGCTGACAGACAGGAGACATGAGAGCCACGGGACCTTGACTCAACAGACCTTGAACCTC 2394
Qy      730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyValAspProCysArgLeu 749
Db      2395 TGTCCCTCGGA---AAGACTGTGTGGCGCGCGGAGCAAGCAACTCATGACGGCCA 2451
Qy      750 ProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsnGlnGln 769
Db      2452 CCAGATCACTCTAACAACCAAGCTCAGAACCTGTGTTAAAAAGCTA-----CGTCAG 2505
Qy      770 AsnAsnLeuValIleSerLysArgAsnSerGluLeuLeuThrValGluThrGluGluPhe 789
Db      2506 CAATAATAGGTAGTCAAGAAAGAAATTCATAACTATCAGCTATAGATTAAGAAATTT 2565
Qy      790 AsnHisGlnAspTyrGluGluAsn 797
Db      2566 GAAAGACCAAGACTGGAGGGAAT 2589

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; Sequence 10, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Mus sp.
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D
US-10-007-270-10

Alignment Scores:
Pred. No.: 1,1e-119 Length: 1726
Score: 1342.50 Matches: 310
Percent Similarity: 44.96% Conservative: 51
Best Local Similarity: 38.61% Mismatches: 99
Query Match: 32.61% Indels: 343
Gaps: 9
DB: 5

US-10-007-270-2 (1-797) x US-10-007-270-10 (1-1726)
Qy      1 MetTyrLeuGlnThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
Db      140 ATGAATTTCAATTAACATGATCTATCTTTGTTGGATTTTCTCCAACTTCAAGGA 199
Qy      21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
Db      199 ----- 199
Qy      41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60
Db      199 ----- 199
Qy      61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
Db      199 ----- 199
Qy      81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
Db      200 -----ATCAAA 205
Qy      101 ValCysGlnGluAlaValIleProGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
Db      206 GATATCAAGAAAGTGTGTGGGAGACATATGATCTTCTTCCAGACCAATTCCTGACACA 265
Qy      121 GlyIleTyrGlnAspTyrValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle 140
Db      266 GAGGAATATCAAGACTGGGTGAGCTCGCTCGCGAAGAAACCTTGTGCTCTTTACACTT 325
Qy      141 GlyLysAsnPheSerAsnSerGlnGlnIleLeuAspLeuLeuGlnGlnArgIleLysGln 160
Db      326 GGGAAATCTTCAAGCACTCCAGAGACCTTAGATCTTCTTCAACAGAAATTAACAAG 385
Qy      161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
Db      386 AGAAGCTTCCCTCGGAGGAAAGATGACACAGCTCCATGAGAGACACTGGAACACACTACT 445
Qy      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db      446 GAAGCCCTGTGTATCCACAGATGTTCACAGATGTTCCTGGGGCCATTTCCACCTTCTCT 505

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QY 201 ProAspArgThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrIleMetPro 220
DB 506 TCTGATGACAGACCTCAAGAGATTTCTACGTGTCACTTCAAGACCAATTTAAAAAGCCC 565
QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln 234
DB 566 ACAACGAAAGATATAACAGAACCTATTCACGTCTGAAATTTCTCA-----TCAGAGGAG 619
QY 235 ArgValGluLeuSerValSerLeuValAsnGlnIlePheValAsnGluLeuAlaAspSer 254
DB 620 AAGGTGAGATTACAGATCTCTGCAAAACACAGGTTCAAGAGACAGATCCCAACTCT 679
QY 255 GlnSerProTyrTyrGlnGluLeuAlaGlyIleSerGlnLeuGlnMetGlnIlePhe 274
DB 680 GGGTACCATATCTACAGAGAACTGGTGGACAGTCCCACTCAGTTGCAAAAGATATTT 739
QY 275 LysIleValLeuProGluPheIleValIleValLeuGluPheArgProIleValGluIle 294
DB 740 AAGAACTTCCAGATTCGAGAGAAATCCGTGATTAAGATTAGACCAAGAAAGAGAGA 799
QY 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheIleArgHisSerAlaGln 314
DB 800 GATGTTCAAGCTCCACAGAAATACAGCTTATGCCATCTTTAAGAGGAGCATCCAGAA 859
QY 315 AlaIleSerProAlaSerAspLeuLeuSerPheAspSerAsnIleGluSerGluGln 334
DB 860 GCAAAAGCCCTGATGATCATCTACTGCTCTTGATTTCCAAATTTAAAGTAAAGAA 919
QY 335 ValTyrHisGlyThrMetGluGluIleAspIleProGluIleTyrLeuThrAlaThrAsp 354
DB 920 ATCCATCATGAGTCACTA---GAGACAAACAAACCAAGAACTTACCTCCACACTCAAGC 976
QY 355 LeuIleValGluIleSerIleValLeuGluGlnGlnSerLeuAspValGlyThrIle 374
DB 977 CTCAAAACATCATATACAACTACTAGATGAGACCTGCTCTGTTGTAAGAGGAAATTT 1036
QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394
DB 1037 CCATTTCGGTGAATTAAGTACCTGAGACACTC-----TTCAGACCTGTCTCAACACAGAT 1090
QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414
DB 1091 CTGCCCAAGCCCTTGTGATGTCAAGAGATGCACTTGAATTCAGAACTTCCCTTTC 1150
QY 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrp 434
DB 1151 GTTAGGCTAGGCTTGAGGCACTGAC----- 1177
QY 435 SerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPheMetAlaSer 454
DB 1177 ----- 1177
QY 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474
DB 1177 ----- 1177
QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494
DB 1177 ----- 1177
QY 495 GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGluAsp 514
DB 1177 ----- 1177
QY 515 MetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGluValPro 534
DB 1177 ----- 1177
QY 535 GluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThrProValSer 554
DB 1177 ----- 1177

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QY 555 AlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProIleGlyArgGluLeuVal 574
DB 1177 ----- 1177
QY 575 ValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnIleSer 594
DB 1177 ----- 1177
QY 595 SerLeuGluTyrArgAlaLeuGlnGlnGlnPheThrGlnLeuLeuValProTyrLeuArg 614
DB 1177 ----- 1177
QY 615 SerAsnLeuThrGlyPheIleGlnLeuGluIleLeuAsnPheArgAsnGlySerValIle 634
DB 1178 -----AGAAAGGATCTAGCTG 1195
QY 635 ValAsnSerIleMetIlePheAlaIleSerValProTyrAsnLeuThrIleValHis 654
DB 1195 ----- 1195
QY 655 GlyValLeuGluAspPheArgSerAlaAlaIleGlnIleuHisLeuGluIleAspSer 674
DB 1195 ----- 1195
QY 675 TyrSerLeuAsnIleGluProAlaAspGlnAlaAspProGlyValPheLeuAlaCysGly 694
DB 1196 -----CTGCTGATCATGCGGAGATCCCTGCAAACTTCTAGACTGTGCG 1237
QY 695 GluPheAlaGlnCysValIleAsnGluIleAspGluGluAlaGluCysArgCysIlePro 714
DB 1238 AATTTGCCCATGTGTAAAGATATGATGACAGACAGAAAGAGATGTGCTGCGACAGC 1297
QY 715 GlyTyrAspSerGlnGlySerLeuAspGlyLeuGlnProGlyLeuCysGlyProGlyThr 734
DB 1298 GACATCATGAGACGACAGGAGCCTGGACTTACAGACCTGAACTGTGTCCTGCGA--- 1354
QY 735 LysGluCysGluValLeuGlnGlyIleValAlaProCysAspLeuProAspHisSerGlu 754
DB 1355 AAGACTTGTGGCCGCGCGAGAACAACTCATGACAGGCGCAACAGATCATCTTCA 1414
QY 755 AsnGlnAlaTyrIleThrSerValIleValIlePheGlnAsnGlnAsnIleValIle 774
DB 1415 AACCAAGCTCAGAACTCGGTGTTAAAGCTA-----CTCAGCAAAATTAAGTAGTC 1468
QY 775 SerIleValAsnSerGluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTrp 794
DB 1469 AAGAAAGAAATTTCTAAACTATCAGCTATAGGATTTGAAGAAATTTGAAGACAGACTGG 1528
QY 795 GluGluAsn 797
DB 1529 GAGGGAAT 1537

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RESULT 7  
 US-10-007-270-12  
 ; Sequence 12, Application US/10007270  
 ; Publication No. US20020160954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hageman, Gregory S.  
 ; APPLICANT: Kuehn, Markus H.  
 ; APPLICANT: University of Iowa Research Foundation  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ; FILE REFERENCE: 020618-000120US  
 ; CURRENT APPLICATION NUMBER: US/10/007,270  
 ; CURRENT FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/430,195  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; PRIOR FILING DATE: 1998-10-29  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 1321  
 ; TYPE: DNA



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/ ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform E
US-10-007-270-12

Alignment Scores:
Pred. No.: 9,93e-80 Length: 1321
Score: 929.50 Matches: 185
Percent Similarity: 79.41% Conservative: 31
Best Local Similarity: 68.01% Mismatches: 53
Query Match: 22.58% Indels: 3
DB: Gaps: 2

US-10-007-270-2 (1-797) x US-10-007-270-12 (1-1321)

QY 526 AapThrProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHis 545
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 320 GAAAGCGCAGCCTTGTGAGAAATATCAGAACTGAGTGAATGATTCGCTCGGATCAG 379

QY 546 PheLeuGluAapThrTherProValSerAlaLeuGlnTyrIleThrTherSerSerMetThr 565
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 380 TTCTTGAGATATACACACCCATCCCAACAGTACGGTTCATACCAACGCTCCAGAC 439

QY 566 IleAlaProLysGlyArgGluLeuValAlaPhePheSerLeuArgValAlaAsnMetAla 585
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 440 ATTGCACCAAGGCGCAGGAGCTAGTGATCTTCAGCTCGCTGCTGTTTAACATGCGG 499

QY 586 PheSerAsnAapLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPhe 605
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 500 TTCTCTTATGACTGTTCACCAAGAGTCTCTGAGATACCAACCCCTGGAACAGCAATTC 559

QY 606 ThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheIleGlnLeuGluIle 625
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 560 AAGAGACTGCTGCTGCTCCATCMACGATGATCTTACGGGATTTAAGCACTGAAATA 619

QY 626 LeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerVal 645
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 620 CTCACCTTCAGAAACGAGAGTGTGATCGTGAACAGCAAGTGCAGTTTCAGAAAGCGGTA 679

QY 646 ProTyrAsnLeuThrIleValAlaHisGlyValLeuGluAapPheArgSerAlaAla 665
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 680 CCTCAACACTCACCACCGCGCGGCTCTGAGAGATCTTCGCTCCACCCCACT 739

QY 666 GlnGlnLeuIleLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAla 685
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 740 CAAGGCTCAATCTGGAATCGAAAGCTACTCTCGACATTTGAACCACTGATCAGGCG 799

QY 686 AapProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThr 705
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 800 GATCCCTGCAAACTTCTAGACTGTGGCAAAATTGCCCACTGTGTAAAGATGAGTGAACA 859

QY 706 GlnGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeu 725
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 860 GAGGAGACGAGAGTGTGCTGACAGACAGGACATGAGACGACGACCTGACCTACACAG 919

QY 726 GlnProGlyLeuCysGlyProGlyTyrThrLysGluCysGluValLeuGlnGlyLysGlyAla 745
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 920 ACCCTGAACCTCTGCTCCCTTGA---AAGACTGTGTGTGCGCGCGGACCAACCAACT 976

QY 746 ProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPhe 765
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 977 CCATGAGGCGCACACAGATCACTTACAAACCAAGCTCAGGAACCTGTGTTAAAGACTA 1036

QY 766 GlnAsnGlnGlnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGlu 785
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1037 -----CGTCAGCAAAATAGGTAGTCAAGAAACGAATTTCTTAACATCACTATAGGA 1090

QY 786 TyrGlnGluPheAsnHisGlnAapTyrGlnGlyAsn 797
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1091 TTTGAAAAATTTGAAAGACCAAGACTGGAGGAAAT 1126

RESULT 8
US-10-783-528-9
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/ Sequence 9, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Glsh, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4165
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4076)..(4076)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (4091)..(4091)
; OTHER INFORMATION: n is a, c, g, or t
US-10-783-528-9

Alignment Scores:
Pred. No.: 9,79e-79 Length: 4165
Score: 927.00 Matches: 297
Percent Similarity: 39.71% Conservative: 145
Best Local Similarity: 26.68% Mismatches: 267
Query Match: 22.52% Indels: 405
DB: Gaps: 36

US-10-007-270-2 (1-797) x US-10-783-528-9 (1-4165)

QY 2 TyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThr 21
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 202 TTCTCTTTTGGGAAAGATTTCTCTGAGTATTTTG-AATTTGCTCTGATAGAAAGAGAC 260

QY 22 --LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro--- 39
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 261 TTTTCATATTTAACAAGCAAAACCTACTATCT--ATAAGAGAGATTCAGAACCAAG 317

QY 40 -----ProArgAsnGluThr-----ThrGluSer 47
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 318 AGTGCAGTTCTTTTCTCTGCTGCGAAGATCAACAGACCTTCTCTAGCTACCAAAAAG 377

QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 378 AAACGCTCTGAGCCGACGAGAAAGCTGAAGACAGTGCTTA-----ATCGAA 425

QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 426 AGCGGAGATCATATCTGTTCTTCTTAATGAGTGAAGAAATCTGCCAGATGAAGAGTGTGA 485

QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValIleTrp 107
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 486 GAGGCTGTGGCAATCATGATGTAAGTATTTAAAGCCAGAGTGTGCAGAAAGCTGTCTGG 545

QY 108 GlnAlaTyrArgGlyIlePheLeuAspArgIleProAspThrGlyLysGlnAspTrpVal 127
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 546 GAAAGCTTCAGAGACTTTTGGATGAGCTTCTCTGCGCGGTGAGAAATCATTACTGAGATG 605

QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 606 AATTGTGTGAGAGATGAGTCAACAAGTATATTTGAATGGGCAAAATTTTAGTAATCT 665

QY 148 GlnGlnLysLeuAspLeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 666 GTGAAACATAGAAAGCTTATCATGTAAGAAAGCACTTAT-----GCAAAAG 710
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QY 168 AaPgluIleSerAlaGluThrLeuGluPro-----GlyGluThrIleVal 184  
 Db 711 GAAAGCTGAAGAGCTCTGAA---CTGCTTCTCCAGCTTCGTGGTGAATCTTCAACA 767  
 QY 185 ILeSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200  
 Db 768 TTGGAGACACACTACTCTCAGTGT-----CCACATCCAGAGGTGAGCGCTTATGAA 818  
 QY 201 -----ProAspSerThrLeuLeuGluIleLeuAsp 211  
 Db 819 GGTGCTCAGAGAGCAGCTTGGAAAGCCGAGAGAGATATTGATGCAATTAAT---GAG 875  
 QY 212 AaPThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeu 231  
 Db 876 AATGTCATTAAGAAAGACCAAAACACAGCAGGTGAACAGATTGCAAGAAATTC----- 926  
 QY 232 GluGluGluArgValGluLeuSerValSerLeuValAsnGluLysPheLysAlaGluLeu 251  
 Db 927 -----AGTATCCACCTTTGGGGAGAGTACAGGAGAAAGACTA 965  
 QY 252 AlaSerSerGlnSerProGlyTyrGlnGluLeuAlaGlyLysSerGlnLeuMetGln 271  
 Db 966 CAGGATTCCTCCAGCTTTCACCCACAGCCTTGAAGAAGAAATTATTTCAGAGGTTGAA 1025  
 QY 272 LysIlePheLysLeuProGluPheLysIleIleValLeuGlyPheArgProLys 291  
 Db 1026 AATGCATTAATCTGGGTACAGGCTACAGAAATTCGTGTACTTAATTAATAGTCCCC 1085  
 QY 292 LysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHis 311  
 Db 1086 AAGGAAATATGAC-----AGTGCCTGAAGTGTATTACTATGCACTTACCTTC----- 1130  
 QY 312 SerAlaGluAlaLysSerProAlaSer---AspLeuLeuSerPheAspSerLeuLysIle 330  
 Db 1131 AATGTGAGAGCCCATCGCAATACCACTGGACCTTATGACTTACCTTCAACAAGATG 1190  
 QY 331 GluSerGluGluValLysIleGlyThrMetGluGluAspLysGluProGluIleTyrLeu 350  
 Db 1191 GAAAC-----CATGGCTTGGGAACGTGATGATMAACCACTGTGTATTAT 1238  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerLysValLeuGluGlu----- 365  
 Db 1239 ACAATCAGTAATCTTCAGAGATATATTGCTGAGACATTCGACGAGAAATTTTGTGGG 1298  
 QY 365 ----- 365  
 Db 1299 AACTCTTCTGTAATCCAGATCCGTATCTCCCTGACGTTATCAATGAGAGAGTTTG 1358  
 QY 366 ---GluGlnSerLeuAspVal-----GlyThrIleGlnPheThr--- 377  
 Db 1359 CCGTCAACAACTGAAGATCTAGTTTGAAACACCAAGTTCAAGTCTTCAGGCAAGCCG 1418  
 QY 378 -----AspGluIleAla 381  
 Db 1419 TCATCTATTCTGGATAATACCTTTCAGCTGCAATGCGCCCTCAGCAGATGAATCATCAC 1478  
 QY 382 GlySerLeuPro-----AlaPheGlyProAspThr 391  
 Db 1479 ACAGATATTCACACACTGATATTTCAGCTGTGCTCCCTCAGCCACTGCGAGGAAATC 1538  
 QY 392 GlnSerGluLeuPro----- 396  
 Db 1539 TGGTCAAAAGTCTTGGGTGATTAAGTCTTACACACAAATTAGCTTTCCTGGAAG 1598  
 QY 396 ----- 396  
 Db 1599 ATGGGCTCAGCTCTTCCCAAGGTTTAAAGGTTAAAGAGCTTGAAGCTTCAATTCGTGC 1658  
 QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 Db 1659 ACCCGGAGAGTCTTCAAGACTGGCTTGCTGTGGCTTCTGAGGAAAGACTTCTGATCT 1718  
 QY 411 GluLeuProProValGluProGluLeuGluThrValAspGlyAlaGlu----- 426

Db 1719 CACTTG-----GTGAAGATGATTAAGCAATGTTGAAGAGTCGAAAGATTTTCTTCT 1772  
 QY 427 ---HisGlyLeuProAspThrSerThrSerProProAlaMetAlaSerThr----- 442  
 Db 1773 ATTTGATTAATTCCTTCAAGTTCACTTACTCAACCTGTGCCAAAGAAACAATACATCC 1832  
 QY 443 -----SerLeuSerGluAlaPro-----ProPhe 450  
 Db 1833 ATGGAAGACTGATGATGTGCTTAAACATCTGCACCATATGACCTTCTATACCTTTT 1892  
 QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
 Db 1893 GCGTGGACTCTTGAACCTTCAAAAGCAAAAGCAATTAAGAGCCCTTCTCGCA 1952  
 QY 471 AaPThrMet----- 474  
 Db 1953 GATGCATCCATGAAAGAGTTAATATTGACGGTGTATTAGTTCAAGGTCTGGGCA 2012  
 QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
 Db 2013 AAGGTAGATCTGATTAATTCGGCCATGAGAGTGAAGACTTCATCA---GAGAAAGCCCGGA 2069  
 QY 495 GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGlyIleAsp 514  
 Db 2070 CCACTGTCCAGCCGTGGCTTGAAGATGAATGATCTTTTCCAGCTGAGATTGAAGAC 2129  
 QY 515 MetValArgHisLeu---AspGluMetAspLeuSerAsp----- 526  
 Db 2130 AAGAAACTAGTTTGTGTTGACAAATGATTCACAGACCAAAATTAGTAAGACTCAAA 2189  
 QY 527 -----ThrProAlaProSerGluValPro----- 534  
 Db 2190 TATGAACATGATGACAGATCCACACTTTCAGAGAAAGACCTTTAGTGGCCTGTCT 2249  
 QY 535 -----GluLeuSerGluTyrValSerValProAspHisPhe 546  
 Db 2250 GTGCCCATCTTGCAGATATCTGACGTGAATCTGCTCTTAACCTCCCAAGCAGATA 2309  
 QY 547 LeuGlu-----AspThr 550  
 Db 2310 TCAGAAAGTACCTGGTGTGATGATGATTCCTGACTTACCAAGACACTTATACGATCT 2369  
 QY 551 ThrProValSerAla----- 555  
 Db 2370 GTAGCAATCTGCTCTTACTGATTAATCAGATCAGCAGATGCATCTTAAGAGAGAT 2429  
 QY 556 LeuGlnTyrIleThrThrSerSer----- 563  
 Db 2430 ATGGAACAATTAATCGATGATCCAACTATGAATGTTTGAAGAGGTTCAATGTGA 2489  
 QY 564 -----MetThrIleAlaProLysGlyArgGlu----- 572  
 Db 2490 AAGCAGATATGCCAAACTTGTGACATATATTGCCAGAAATCAGAGAGATTGGACAA 2549  
 QY 572 ----- 572  
 Db 2550 ACTTCTCCCTAGAGAAATTGTCAGAGACATATTGGCAATGACACACAGAGTGTGAC 2609  
 QY 572 ----- 572  
 Db 2610 AGGCTGTGTTATCTGTGACACAGTCTACAAATTGCTCCAAACCAATTCACACCTTG 2669  
 QY 572 ----- 572  
 Db 2670 CTAGAGATGAAGTAATTAATGGGTGATACAGATATTGTGTTAAGTGAACCGGATAGGC 2729  
 QY 572 ----- 572  
 Db 2730 ACAGATTAATACAGCTGAGCAAGTCCAAAGCAAAATGCAAGGTTGTAGTTATGTG 2789  
 QY 572 ----- 572

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Db      2790 GAAATGTCAACAAGTGTTCATCCACAGAGATGTTAGTGCTGGCCACAGAAAGGA 2849
Qy      573 -----LueValValPhePheSerLeuArg 580
Db      2850 GAGAGATGACTTGAATTATACCCAGACTTGAAGACCTTGTTGTGTTTCTTCAGCCCTCGGA 2909
Qy      581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600
Db      2910 GTGACTTAACATGATGTTTTCAGAGATGCTGTTTAATATAAAACTCCCTGGAGATATAAGCC 2969
Qy      601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620
Db      2970 CTGGAGCAAAAGATCTTCAAGATTTGCTGTTCCCTATCTCCAGTCAATCTCAAGCGGCTTC 3029
Qy      621 LysGlnLeuGluLileuAsnAspPheArgAsnGlySerValIleValAsnSerLysMetLys 640
Db      3030 CAGAACTTGAAATCTTCAACTTCAGAAATGGCAGCATTTGTGTGTAACAGTCGAATGAAG 3089
Qy      641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValIleGlyValLeuGluAspPhe 660
Db      3090 TTGGCAATTCCTGCTCCCTCAACGTCACAAATGGGTTGATGATGATTCCTGGAAGCTTT 3149
Qy      661 ArgSerAlaAlaIleGlnLeuLysLeuGluIleAspSerTyrSerLeuAsnIleGlu 680
Db      3150 TGTACACACTGCTACAAATACCAATGAACTGGCTATTGATTAATACCTCTTGATGTGAA 3209
Qy      681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700
Db      3210 TCAGCTGATGAAGCCCAACCTTGCAAGTTTCAGGCTGTGAATGAATTTTCAAGAGTCTG 3269
Qy      701 LysAsnGluArgThrGlnGluAlaGluCysArgCysLysPheProGlyTyrAspSerGln 719
Db      3270 GTCAACCCCTGGAGTGAAGAAAGCAAGTGCAGATGTTCCCTGGATACCTGAGTGTGAA 3329
Qy      720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735
Db      3330 GAACGGCCCTGTCAAGGTCTCTGTGACCTACAGCCGACTTCTGCTTGATGATGAAG 3389
Qy      736 GluCysGluValLeuGlnGlyLysGlyAlaProCysArg 748
Db      3390 ---TGTGACATTATGCTGTGGCAGCGGGCCATTGTAGG 3425

RESULT 9
US-10-007-270-16
/ Sequence 16, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hegeman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ APPLICANT: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-000120US
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ CURRENT FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ PRIOR FILING DATE: 1998-10-29
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 4166
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Human IPM 200 (Isoform A) cDNA
US-10-007-270-16

Alignment Scores:
Pred. No.: 9,8e-79 Length: 4166
Score: 927.00 Matches: 297
Percent Similarity: 39.71% Conservative: 145
Best Local Similarity: 26.68% Mismatches: 267

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Query Match: 22.52% Indels: 405
DB: 5 Gaps: 36
US-10-007-270-2 (1-797) x US-10-007-270-16 (1-4166)

Qy      2 TyrLeuGlnThrArgArgAlaIlePheValPheThrPilePheLeuGlnValGlnGlyThr 21
Db      202 TTCCCTCTTTGGGAAGATTCTCTGGGTATTTTG-AATTTGCTGATGAAGAGAC 260
Qy      22 ---LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro--- 39
Db      261 TTTTCATCATTAACAGACAAACCTACTTATCT--ATAGAGAGATCCAGAAACCCAG 317
Qy      40 -----ProArgAsnGluThr-----ThrGlnSer 47
Db      318 AGTCAGATTCTTTTCTCTGCTGTAAGATCAACAGACCTTTCTTGCTACCAAAAG 377
Qy      48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67
Db      378 AAACAGCCTCGAACCGCAGAGAACTGAAGACAGTGCTTA-----ATCAGA 425
Qy      68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGlnSerMetLys 87
Db      426 AGCGGAGATCTATTTGTTCTTAATGAGATGAATAATCTGCCAGATGAAGAAGTGTCA 485
Qy      88 GlnIleLeuAspSerLeuGlnAlaIleTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107
Db      486 GAGCCTGTGGCAATCATGTGAATTTTAAGTCCAGATGTGTGACGAACTGTCTGG 545
Qy      108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127
Db      546 GAAGCTTCAAGACCTTTTGGATGATGACCTCTCGGCGGTGAGAAATATCATTAAGTGA 605
Qy      128 SerIleCysGlnGlnGlnThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147
Db      606 AATTGTGTGAGATGAGTGAAGTCAAGATATTTTGAAGGCGCAAAATTTTAAGTAATCT 665
Qy      148 GlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167
Db      666 GTGGAACATTAAGACTTAATCATGAAGAACTGACTTAT-----GCANA 710
Qy      168 AspGluIleSerAlaGluLysThrLeuGlyGluPro-----GlyGluThrIleVal 184
Db      711 GAACCTGAAGAGCTTGAA---CTGTCTTCCAGATTCCTGTGGATGATCTTCAACA 767
Qy      185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200
Db      768 TTGGAGACACTTACTCTCAGTGT-----CCACATCCAGAGGTGACGCTATGAA 818
Qy      201 -----ProAspAspThrLeuLeuAsnGluIleLeuAsp 211
Db      819 GGTGCTCAGAGAGAGCTTGGAAGGCGCAGAGAGATATTAGCAATGAATTT---GAG 875
Qy      212 AsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeu 231
Db      876 AATGATTAAGAAGAACCAAAACCAAGAGTGAACGATTGACGAATTC----- 926
Qy      232 GluGlnGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeu 251
Db      927 -----AGTATCCACCTTTGGGAGAGACATACAGGAAACACTA 965
Qy      252 AlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGln 271
Db      966 CAGGATTCCTCCAGCTTTCACACACAGACCTTGAAAGAAATTTATTTTCAGAGGTTGA 1025
Qy      272 LysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLys 291
Db      1026 AATGATTTACCTGGGTTTACAGAGCTACAGAGAAATTCGTGTAATTTAGTCCCCC 1085
Qy      292 LysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHis 311
Db      1086 AAGGAAATATGAC-----AGTGGCTGATGATGTTTACTATGACGATTACCTTC----- 1130

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QY 312 SerAlaGluAlaIysSerProAlaSer-----AspLeuLeuSerPheAspSerAlaIysIle 330  
 Db 1131 AATGGAGGCGCTTACGCAATACCACTGGAGCTCAATTAAGCTTCACTCAACAAAGGTG 1190  
 QY 331 GluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeu 350  
 Db 1191 GAAAC-----CATGGCTTGGGAACCTGAGATGAATAAACCACTGTGTTAT 1238  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGlu----- 365  
 Db 1239 ACAATCAGTAACCTTCAGATATATATGTGTGAGACATGACAGAAATTTTGTCTGGG 1298  
 QY 365 ----- 365  
 Db 1299 AACTTCTCTTGAATCAGATCCTGATTCCTCGACCTTATCATGATGAGAGATTG 1358  
 QY 366 ---GluGlnSerLeuAspVal-----GlyThrIleGlnPheThr--- 377  
 Db 1359 CGTCAACCAACTGAATATCTAGTTTGGAAACACCAAGTTCAAGTCTTCAGGCAACGGCG 1418  
 QY 378 -----AspGluIleAla 381  
 Db 1419 TCATCATTTCTGGATATATACCTTCAAGCTGACGACCTCGACAGATGATCATCAC 1478  
 QY 382 GlySerLeuPro-----AlaPheGlyProAspThr 391  
 Db 1479 AGCAGATTTCCACCACTGATTTACAGCTGTGCTCTCCCTCAGCCACTGGCAGGAATC 1538  
 QY 392 GlnSerGluLeuPro----- 396  
 Db 1539 TGTCTGAAGAAGCTTTGGGTATTTAGTGTCTACACAAATTAAGCTTCCCTCGAAG 1598  
 QY 396 ----- 396  
 Db 1599 ATGGGCTCAGCTCTCCACAGAGTTTAAAGGTAGACAGCTTGACTCTTCACTGTGTC 1658  
 QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 Db 1659 ACCCGGCGAGTCTTCAGACTGTGCTGCTGTGGCTTGTGAGAAAGAAAGACTTGTGATCT 1718  
 QY 411 GluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlu----- 426  
 Db 1719 CACTTG-----GTAAAGATGATTAAGCAATGTTGAAGAGCAGAAATTTCTTCT 1772  
 QY 427 ---HisGlyLeuProAspThrSerThrProProAlaMetAlaSerThr----- 442  
 Db 1773 ATGTATTCATGTGCTTCAAGTTCATTCATCAACCTGTGCACAAAGAAACAAATACATCC 1832  
 QY 443 -----SerLeuSerGluAlaPro-----ProPhe 450  
 Db 1833 ATGGAAGACTGTGATGTGCTTAAACATCTTCACCATCTGACCTTCTTATACCTTT 1892  
 QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
 Db 1893 GCGTTGACTCTCTTCACTCCAAAGTCAAAAGCAATTAAGTAGACCCCTTCTCGCA 1952  
 QY 471 AspGlnThrMet----- 474  
 Db 1953 GATGATCATGTGAAGAAAGATTAAATATTGACCGGTGTTAGGTTGAGGCTGTGGGCA 2012  
 QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
 Db 2013 AAGGATGATCTGATTACTTGGCCATGAGTGAAGACTTCATCA---GAGAAGACCGCGCA 2069  
 QY 495 GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGlyIuAsp 514  
 Db 2070 CCACCTTCCAAAGCCGGGCTTGAAGATGATGATTCATTTGCCAGCTGAAGTTGAAGAC 2129  
 QY 515 MetValArgHisLeu---AspGluMetAspLeuSerAsp----- 526  
 Db 2130 AAGAAACTAGTTTATGTTGACAAATAATGATTCACAGACCAATATAGTAAGACATCAAA 2189  
 QY 527 -----ThrProAlaProSerGluValPro----- 534

Db 2190 TATGAATGATGACAGATCCACACTTTCCAGAGAAAGAGCTTTATGTGGCTGCT 2249  
 QY 535 -----GluLeuSerGluTyrValSerValProAspHisPhe 546  
 Db 2250 GTGCCATCTTGCAGATATCTGACGTGAATCTGGGTCTTAACCTCCCAAGACATTA 2309  
 QY 547 LeuGlu-----AspThr 550  
 Db 2310 TCAGAAAGTACCTGTGTGATGATGATTCAGTTACCAAGACACTTATTAAGTCACTCT 2369  
 QY 551 ThrProValSerAla----- 555  
 Db 2370 GTAGCAATCTCTGCTCTTAATGATTAATCAGATCAGGACAGATCCATCTTAAGAGAT 2429  
 QY 556 LeuGlnTyrIleThrThrSerSer----- 563  
 Db 2430 ATGGAACAAATTAAGTCAATCCAACTAATGATGTTGACAGTGAAGTTCAATGTA 2489  
 QY 564 -----MetThrIleAlaProLysGlyArgGlu----- 572  
 Db 2490 AAGCAGATATCAAACTTTGTGACTATATTCAGAAATCAGAGAGATTGACACAGA 2549  
 QY 572 ----- 572  
 Db 2550 ACTTCTCCCTAGAGAAATTTGCCAGACATATTTGGCAAGTACACACAGATGCTGAC 2609  
 QY 572 ----- 572  
 Db 2610 AAGCTCTGTATCTGTGACACAGTCTACCAATTTGCTTCAACCAATCTCCACCTTG 2669  
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 Db 2670 CTAGAGATGAATTAATATGGGTGTACAGATATTTGTTAGAACTGACCGGATAGGC 2729  
 QY 572 ----- 572  
 Db 2730 ACAGATTAATCAAGCTGAGCAAGTCCAGAGCAAAATGGCAAGTTGATTAATGTG 2789  
 QY 572 ----- 572  
 Db 2790 GAATGTCAACAAGTTCATCTCCACAGAGATGTTAGTGTGGCTTGCCCAAGAGAA 2849  
 QY 573 -----LeuValValPhePheSerLeuArg 580  
 Db 2850 GGAGATGACTGATTAATACCAAGACTTCAGAGAGCTTGTGTGTTCTTCAAGCTCCGA 2909  
 QY 581 ValAlaAspMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGlnTyrArgAla 600  
 Db 2910 GTGACTTAACATGATGTTTCAAGAAATCTGTTTAATTAAMACCTCTTGAAGTAAAGCC 2969  
 QY 601 LeuGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
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 QY 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
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 QY 641 PheAlaLysSerValProTyrAsnLeuThrIleValIleGlyValLeuGluAspPhe 660  
 Db 3090 TTTGCCAATTTGTCCTCTCAACCTCAACATGCGGTACATATCTTGGAACAACCTT 3149  
 QY 661 ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680  
 Db 3150 TGTACACTGCTCAACAAATCAATGAATGCTGTGATTAATTAATCTCTTGAATGGA 3209  
 QY 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
 Db 3210 TCAGGTGATGAAGCAACCTTGCAAGTTTCAGGCTGTAAATGAATTTTCAGAGTGTCTG 3269  
 QY 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln--- 719

Db 3270 GTCAACCCCTGGAGTGGAGAACCAAGTCAGATCTTCCCTGATACCTGAGTGGAA 3329  
Qy 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCyGlyProGlyThrIys 735  
Db 3330 GAACGGCCCTGTCAAGGCTCTGTGACCTCAAGCCTGACTTCTGCTTGAATGAGAAAG 3389  
Qy 736 GluCyGluValLeuGlnGlyLeuGlyAlaProCyAspArg 748  
Db 3390 ---TGTGACATTATGCTGGGCAAGGGGCAATTGTGAG 3425  
RESULT 10  
US-10-007-270-14  
/ Sequence 14, Application US/10007270  
/ Publication No. US20020160954A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Hageman, Gregory S.  
/ APPLICANT: Kuehn, Markus H.  
/ APPLICANT: University of Iowa Research Foundation  
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
/ FILE REFERENCE: 020618-000120US  
/ CURRENT APPLICATION NUMBER: US/10/007,270  
/ PRIOR FILING DATE: 2001-11-08  
/ PRIOR APPLICATION NUMBER: US 09/430,195  
/ PRIOR FILING DATE: 1999-10-29  
/ PRIOR APPLICATION NUMBER: US 09/183,972  
/ PRIOR FILING DATE: 1998-10-29  
/ NUMBER OF SEQ ID NOS: 37  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 14  
/ LENGTH: 555  
/ TYPE: DNA  
/ ORGANISM: Unknown Organism  
/ FEATURE:  
/ OTHER INFORMATION: Monkey IPM 150 cDNA (partial)  
/ US-10-007-270-14  
/ OTHER INFORMATION: Description of Unknown Organism: Monkey species  
US-10-007-270-14  
Alignment Scores:  
Pred. No.: 5 676-76 Length: 555  
Score: 885.00 Matches: 167  
Percent Similarity: 95.65% Conservatve: 9  
Best Local Similarity: 90.76% Mismatches: 8  
Query Match: 21.50% Indels: 0  
Gaps: 0  
DB: 5 0  
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Qy 73 PhePheProThrGlyValIysValCyProGlnGluSerMetIysGlnIleLeuAspSer 92  
Db 4 TTCTTCCGAAAGGGGTTAAAGTCTGTCCACAGAAATCCATGAACAGATTTTTACGCACT 63  
Qy 93 LeuGlnAlaIyTyTrArgLeuArgValCyGlnGlnAlaValIyTrpGlnAlaIyTrArgIle 112  
Db 64 CTTCAAGCTTATTATGATTGAGAGTGTCTCAGAGCAAGCATGAGGAACATATCGCATC 123  
Qy 113 PheLeuAspArgIleProAspThrGlyGluIyTrpGlnAspTrpValSerIleCyGlnGln 132  
Db 124 TTCTGAGATCGATCCCTCAACAGGGGAAATACAGAGCTGGGTCTGCTTGCACGAG 183  
Qy 133 GluThrPheCyLeuPheAspIleGlyIyAsnPheSerAsnSerGlnIuhIleuAsp 152  
Db 184 GAGACTTCTGCTCTTTTACATCGCAAAACTTACGCAATTTCCAGAGAGCACTGGAT 243  
Qy 153 LeuLeuGlnGlnArgIleIysGlnAlaIySerPheProAspArgIyAspGluIleSerAla 172  
Db 244 CTTCTCCACAGAGAAATAAAGAGAGATTTCCCTGAGAGAAAGATGAAGTATCTACA 303  
Qy 173 GluIySerThrLeuGlyGluProGlyGluIyTrpIleValIleSerThrAspValAlaAsnVal 192  
Db 304 GAGAAACATTTGGAGAGCTTACTGTAACCATTTGTGTTCACACAGATTTGCGCAGCTC 363  
Qy 193 SerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsn 212

Db 364 TCACCTGGGCTTTCCCTGCTACCTCTGATGACACCCCTCCCAATGAAATTCGTGATAT 423  
Qy 213 ThrLeuAsnAspThrIySerMetProThrThrGluArgGluIyTrpGlnAlaValLeuGlu 232  
Db 424 GCACCTCAACGACACCAAGATGCTTACACAGAAAGAGAAAGAACTGCTGTGTCTGAG 483  
Qy 223 GluGlnArgValGluLeuSerValSerLeuValAsnGlnIyPheIyAlaGluLeuAla 252  
Db 484 GAGCAGAGGGGTGGAGCTGACATCTCTGTATAAACAGAGGTTCAAGGAGGCTCCCT 543  
Qy 253 AspSerGlnSer 256  
Db 544 GACCTCACTGCA 555  
RESULT 11  
US-10-007-270-18  
/ Sequence 18, Application US/10007270  
/ Publication No. US20020160954A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Hageman, Gregory S.  
/ APPLICANT: Kuehn, Markus H.  
/ APPLICANT: University of Iowa Research Foundation  
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
/ FILE REFERENCE: 020618-000120US  
/ CURRENT APPLICATION NUMBER: US/10/007,270  
/ PRIOR FILING DATE: 2001-11-08  
/ PRIOR APPLICATION NUMBER: US 09/430,195  
/ PRIOR FILING DATE: 1999-10-29  
/ PRIOR APPLICATION NUMBER: US 09/183,972  
/ PRIOR FILING DATE: 1998-10-29  
/ NUMBER OF SEQ ID NOS: 37  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 18  
/ LENGTH: 2964  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ OTHER INFORMATION: Human IPM 200 cDNA sequence, isoform C  
US-10-007-270-18  
Alignment Scores:  
Pred. No.: 3 896-71 Length: 2964  
Score: 846.50 Matches: 274  
Percent Similarity: 41.81% Conservatve: 142  
Best Local Similarity: 27.54% Mismatches: 256  
Query Match: 20.56% Indels: 325  
Gaps: 32  
DB: 5 32  
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Qy 2 TyrLeuGluIyTrpArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnIyThr 21  
Db 100 TTCCCTCTTTTGGAGAAATTTCTCTGGGTATTTTG-ATAATTTGCTCTGATGAAGAGAC 158  
Qy 22 ---LysAspIleSerIleAsnIleTyTrIserGluIyTrpLysAspIleAspAsnPro--- 39  
Db 159 TTTCATCATTTACAGCAACAACTCTTATCT---ATAGAGAAATTCAGAAACCCAG 215  
Qy 40 -----ProArgAsnGluIyTrp-----ThrGluSer 47  
Db 216 AGTGACGTTTCTTTCTCTGCTGAGAGAAATCAACAGACCTTCTAGCTACCAAAAG 275  
Qy 48 ThrGluIySerMetTyTrIySerSerThrMetArgArgIlePheAspLeuAlaIySerIleArg 67  
Db 276 AAACAGCTCTGAGACCGAGAGAAACTGAAGACAGTGTTA-----ATCAGA 323  
Qy 68 ThrIyAspSerAlaPhePheProThrGlyValIyValCyProGlnGluIySerMetIyS 87  
Db 324 AGCGGAAATCTATTCTGTTCTTAATGAGAGAAATCTGCCAGATGAAGTGTGCA 383  
Qy 88 GlnIleAspSerIleGlnAlaIyTyTrArgLeuArgValCyGlnGlnIyAlaValIyTrp 107  
::: :::

Db 384 GAGCTGTGGCAAAATCATGTGAAATATTTAAAGTCGAGTGTGTGTCAGGAAGCTGTCTGG 443  
Qy 108 GUAUATYrArgllIephelueApargllIeproAspThrGlylulYrGlnAspTrpVal 127  
Db 444 GAAGCCTTAGAGACTTTTGGATGTCACCTTCCTGGCGCTGAGAAATATCATTAACCTGGAGT 503  
Qy 128 SerIleCyseGlnGlnIulThrPheCyseIuePheAspIleGlyIueAsnIlePheSer 147  
Db 504 AATTGTGTGAGGAGTGAAGTCAACAGTATATTTGAAATGGCAAAATTTTAgTGAATCT 563  
Qy 148 GlnGlnHileuAspIleuAspIleuGlnIulArgIleGlnArgSerPheProAspArgLys 167  
Db 564 GTGGAACATAGAAGCTTATCATGAAGAAAGTCACTTAT-----GGAAG 608  
Qy 168 AspGluIleSerAlaGluIulYrThrLeuGlyGluPro-----GlylulThrIleVal 184  
Db 609 GAACCTGTAAAGCAGCTGTAAA---CTGTCTTCCTCCAGTTCCTGTGGTATCTTCACACA 665  
Qy 185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProIleuThr----- 200  
Db 666 TTGGAGAGACATACTCTCAGTGT-----CCACATCCAGAGGTGACCGCTATGAA 716  
Qy 201 -----ProAspAspThrLeuIleuAsnGluIleuAsp 211  
Db 717 GGTGCCTCAGAGCAGCTTGGAAAGCCAGAGAGATTAAGCAATGAAATT---GAG 773  
Qy 212 AantThrIleuAsnAspThrIlysmecProThrThrGluArgIulThrGluPheAlaValLeu 231  
Db 774 AATGTGATAGAAAGAACCCAAACACAGAGGTGAACAGATTGCAGAAATTC----- 824  
Qy 232 GlnGlnGlnArgValGluIleuSerValSerIleuValAsnGlnIulYrPheLysAlaGluIleu 251  
Db 825 -----AGTATCCACCTTTTGGGAGAGAGTACGGAGAAAGACTA 863  
Qy 252 AlaAspSerGlnSerProIlyrGlnGlnIleuAlaGlyLysSerGlnIleuGlnIleuMetGln 271  
Db 864 CAGGATTCCTCCAGACTTTCACCAACAGCAGCCTTGAAGAAGAAATTTATTCAGAGGTGAA 923  
Qy 272 IylIlePheLysLysLeuProGlyPheLysLysIleHisValIleuGlyPheArgProLys 291  
Db 924 AATGCATTACTGGGTACTACAGGCTCAAGAAATTCGTGACTGAATTTAGTCCCCC 983  
Qy 292 LysGlnLysAspGlySerSerSerThrGlnIleuGlnIleuThrAlaIlePheLysArgHis 311  
Db 984 AAGGAAATATGAC-----AGTGGCTGAGATGTTACTATGACGTTACCTTC----- 1028  
Qy 312 SerAlaGlnAlaLysSerProAlaSer---AspIleuLeuSerPheAspSerAsnLysIle 330  
Db 1029 AATGTGAGGCCATCAGCAATACCACTGGAGCTCATTAAGCTTCACCTCAACAGAGTG 1088  
Qy 331 GluSerGlnGluValIlyrHisGlyThrMetGlnGluAspLysGlnProGluIleYrIleu 350  
Db 1089 GAAAC-----CATGGCTTGTGGAACCTGATGATTAACCCACTTGTGTTAT 1136  
Qy 351 ThrAlaThrAspLeuLysArgIleuIleSerIylAlaIleuGlnGlnIleuIleuSerLeu--- 369  
Db 1137 ACAATCAGTAACCTTCAGAGATTAATATGCTGAGACATTCAGAGAAATTTTGTCTGGG 1196  
Qy 370 -----AspValGlyThrIleGlnPhe----- 376  
Db 1197 AACTCTCTTGATCCAGATCTGATTCCTGACGACTTATCAATGTAGAGAGATTG 1256  
Qy 377 -----ThrAspGluIle-----AlaGlySerLeuProAlaPheGly 388  
Db 1257 CGTCAACCAACTGAATCTAGTTTGAACACCCAAAGTTCAAGTCTTCAGGCA---ACG 1313  
Qy 389 ProAspThrGlnSerGluIleuProThrSerPheAlaValIleThrGlnAspAlaThrIleu 408  
Db 1314 CGGTACATCAT-TCGTGCTTCARACTGGCTTGGCTGTGCTTGAAGAAAGACTTCT 1372  
Qy 409 SerProGluIleuProProValGluProGlnIleuGluThrValAspGlyValIleu----- 426  
Db 1373 GGATTCACCTTG-----GTAGAAGATGATTAAGCAATGTGTAAGAGTCAGAAAGTTT 1426

Qy 427 -----HisGlyIleuProAspThrSerTrpSerProProAlaMetAlaSerThr--- 442  
Db 1427 CTTTCTATTGATTCATGCTTCCTTCAAGTTCATTCACCTCAACCTGTGCCAAAGAAACAATA 1486  
Qy 443 -----SerLeuSerGlnAlaPro----- 448  
Db 1487 CCATCATGGAAGACTGTCGATGTGTCCTTACATCTTCACCATTCGATCTCTTCTATA 1546  
Qy 449 PropheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMet 468  
Db 1547 CCTTTGGCTTGAGCTCTTCGACCTCCCAAGTCAAAGACCAATTAAGAGACCCCTTTC 1606  
Qy 469 AlaThrAspGlnThrMet----- 474  
Db 1607 CTGCCAGATGCACTGCATGAAAAAGATTAAATTTGACGTCGTTTAGTTCAAGGCTCT 1666  
Qy 475 -----LeuValProGlyIleuThrIleProThrSerAspTrpSerAlaIleSerGlnIleu 492  
Db 1667 GGGCAAAAGTATGATCTGATTTACTTGGCCATGAGTGAAGACTTCATCA---GAGAAAGC 1723  
Qy 493 AlaIleuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGly 512  
Db 1724 GCTGAACACGTGTCAGAGCCGTGGCTTGAAGATGATGATTCATTTTGCCACCTGATTT 1783  
Qy 513 GluAsp-----MetValArgHisIleuAspGluMetAsp----- 523  
Db 1784 GAAGACAAAGAACTAGTTTACTGTGACAAATGATTCACAGACCAATTAAGTAAGCAC 1843  
Qy 523 ----- 523  
Db 1844 TCAAAATATGAACATGATGACATCCATACCTTCCAGAGAAAGCCTTTAGTGGG 1903  
Qy 524 -----LeuSerAspThrProAlaPro----- 530  
Db 1904 CCTGCTGTGCCATCTTCGACAGATCTGAGCTGAATCGCGTCTTAAACCTCCCAAG 1963  
Qy 531 -----SerGluValProGluIleuSerGluIlyrValSerValProAspHisPheIleuGln 548  
Db 1964 CACATATAGAAAGTACCTGGTGTGATGATTAATCTGATTAACCAAGACCTCTTATACG 2023  
Qy 549 AspThrThrProValSerAla----- 555  
Db 2024 ACATCTGTAGCAATCTGCGCTCTACTGATTAATCAGATCAGGACAGTCCATCTTAAG 2083  
Qy 556 -----LeuGlnIlyrIleThrThrSerSer----- 563  
Db 2084 GAGGATATGAAACAATTAATTAAGTCAATCCATGATGATGTTGACAGTGAAGTTGCA 2143  
Qy 564 -----MetThrIleAlaProLysGlyArgGlu----- 572  
Db 2144 ATGTAAAGCCAGATATGCAAACTTTGTGAGACTATATTCGCAAGATCAGAGAGATTGG 2203  
Qy 572 ----- 572  
Db 2204 ACAAGAACTTCTCCCTAGAGAAATTTGCCAGAGACATATTGGCAAGTACCAACAGAGT 2263  
Qy 572 ----- 572  
Db 2264 GCTGACAGGCTGTGTTATCTGTGACAGAGTCAACAAATTGCTCAACACAAATTCCTC 2323  
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Db 2324 ACCCTGTAGAGATGAAGTAATTAATGGGTGTAAGATATTTGTTAGAACTGACCGG 2383  
Qy 572 ----- 572  
Db 2384 ATAGGACAGATTAATCAAGCTGACAGTCAAGTCAAGACAAATGCGAAGTTGTAAGT 2443  
Qy 572 ----- 572  
Db 2444 TATGTGAATATGTCAACAAAGTGTTCATCTCAAGAGATGTTAGTGTGGCTTGCCCA 2503

QY 573 -----LeuValValPhePheSer 578  
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 Db 2864 GTGGAATCAGGTGATGAAAGCAACCTTCAGAGTTTCAGGCTGTATGATTAATTCAGAA 2923  
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## RESULT 12

us-10-007-270-23  
 / Sequence 23, Application US/10007270  
 / Publication No. US20020160954A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Hageman, Gregory S.  
 / APPLICANT: Kuehn, Markus H.  
 / APPLICANT: University of Iowa Research Foundation  
 / TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 / FILE REFERENCE: 020618-000120US  
 / CURRENT APPLICATION NUMBER: US/10/007,270  
 / PRIOR FILING DATE: 2001-11-08  
 / PRIOR APPLICATION NUMBER: US 09/430,195  
 / PRIOR FILING DATE: 1999-10-29  
 / PRIOR APPLICATION NUMBER: US 09/183,972  
 / NUMBER OF SEQ ID NOS: 37  
 / SOFTWARE: Patentin Ver. 2.1  
 / SEQ ID NO 23  
 / LENGTH: 4204  
 / TYPE: DNA  
 / ORGANISM: Mus sp.  
 / FEATURE:  
 / OTHER INFORMATION: Mouse IPM 200 cDNA sequence (partial)  
 / NAME/KEY: misc feature  
 / LOCATION: (1)..(4204)  
 / OTHER INFORMATION: n is a, c, g, or t.  
 / us-10-007-270-23

## Alignment Scores:

Pred. No.: 2,266-70 Length: 4204  
 Score: 841.00 Matches: 261  
 Percent Similarity: 41.20% Conservative: 123  
 Best Local Similarity: 28.00% Mismatches: 238  
 Query Match: 20.43% Indels: 310  
 DB: 5 Gaps: 34

us-10-007-270-2 (1-797) x us-10-007-270-23 (1-4204)

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Db 21 TATTTAAAGCCAGGTGTGCAGAGAACCATCTCGAAGCCTTCAGACGTTTGGAT 80  
 QY 116 ArgIleProAspThrGlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPhe 135  
 Db 81 CGACTTCTGGCCGTGATGAATATCTGTCATCGAATGAATTTATGTGAGATGAGATCA 140  
 QY 136 CysLeuPheAspIleGlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuGln 155  
 Db 141 AGCTGATTTGAATAGGCGCCCATTTTGTAGTCTGTGGAACATAGAACTTAATCATG 200  
 QY 156 GlnArgIle-----LysGlnArgSerPheProAspArgLysAspGluIleSerAla 172  
 Db 201 AAGAAATCGGCTTACACAAGGAGACGTGAGACGCTCCTGAAAGATCAG---TCGTGT 257  
 QY 173 GluLysThrLeuGlyGluPro-----GlyGluThrIleValIleSerThrAspVal 189  
 Db 258 GGGCCTGAGTTGTCTTTCAGATTCCTATTTGTGTGAGCC-----TCAACACTGACA 308  
 QY 190 AlaAsnValSerLeuGlyProPhePro-----LeuThrPro 201  
 Db 309 GGTGCTGTCTCCAGTCTTCTTATCCAGAGTTGGCTTGAGAGCGCAGCGCTACCG 368  
 QY 202 AspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetProThr 221  
 Db 369 CAGAGAGTATCAGCAATGAATTT---GAGATGTGACAGAGAGCCACCAACACAGCT 425  
 QY 222 ThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSer 241  
 Db 426 GCTGAACAGATTCGGAATTC-----AGCATCAAA 455  
 QY 242 LeuValAsnGlnLysPheLysAlaGluLeuLeuAlaAspSerGlnSerProTyrTyrGlnGlu 261  
 Db 456 CTTCTGGGAAAGCATATACATGAAAGACTCGGAGATCTCCTCCAGCGCCCTTACCGGCTC 515  
 QY 262 LeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLys 281  
 Db 516 CTCGTGAAGAAGATTATTTACAGAGGTGAAAAAGCATTCACAGGGTTACTCGGTACAAAG 575  
 QY 282 LysIleHisValLeuGlyPheArgProLysGlyLysAspGlySerSerSerThrGlu 301  
 Db 576 GGCATCCGTGTTCTGGAATTCAGGGCCCCCGGAGAAATGACAGTGGATGATGTTGAC 635  
 QY 302 MetGlnLeuThrAlaIlePheLysArgHisSerAlaGlnAlaLysSerProAlaSer--- 320  
 Db 636 TATGCAATTAC-----TTCAATGCCAAGCATACAGCAATACCACTCGG 680  
 QY 321 AspLeuLeuSerPheAspSerAsnLysIleGlnSerGlnGluValTyrHisGlyThrMet 340  
 Db 681 GACCTCATAGCCTTCACCTCCCAAGAGTAGAAAC-----CATGGCCTTGTA 728  
 QY 341 GluGluAspLysGlnProGluLysIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSer 360  
 Db 729 GAGATGATGATTAACCCACTGCTGTATACATTAATTAATTAATTAATTAATTAATTCCT 788  
 QY 361 LysAlaLeuGluGluGlu-----GlnSerLeuAspVal----- 366  
 Db 789 GAGACGCTGCACCAAGAACTTTTATGATGGAAATTCCTTTGATCCAGATCCCAAGCCT 848  
 QY 367 -----GlnSerLeuAspVal----- 371  
 Db 849 CTCGACGTCATCATATGTAGAGAGATTTTGTCCCCCAAGCAAGACATGATTTGGAAC 908  
 QY 372 -----GlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGly 388  
 Db 909 ACCCAAGTTCAAGTCTTCAAGGTGACA-----ACATCCTCTATTATTTGCTTGAG 959  
 QY 389 ProAsp-----ThrGlnSerGluLeuProThrPhePheAlaValIleThrGluAspAla 406  
 Db 960 CTTGACCTGCTGCTGCTCTGAGGAAAGACTCTTGATCTGATCTTATTAAGAAATGGG 1019  
 QY 407 ThrLeuSerProGlu----- 411

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Db 1020 TTAGCAGACCTGAAGATTAGAGTACTCTGATTGATGATGTGGCTTCAAGCCATTAA 1079
QY 412 -----LeuProValGlu----- 416
Db 1080 ATTCAACCTGTGCCAAMAGAAACAGTACCACTATGGAAGACTGACACGGCTCTCTTG 1139
QY 417 -----ProGlnLeuGlu-----ThrValAsp---GlyAlaGlu 426
Db 1140 TCCACACCAACATCTGACCTCTTCTGCTATAGAAACCTTACTTAAGACATAGGACACCT 1199
QY 427 HlsGlyLeu----- 429
Db 1200 TCTGGCTTGAGTCCCTGGCTTCAAAACATCTCAGACCACTTGGAGTAGATCCCATGCTTT 1259
QY 430 ProAspThrSer----- 433
Db 1260 CCAGACACCTCTGTGGAAAAAGCTTCATTTTGAAGAGCTGGCTTGGGCTTCTGGG 1319
QY 434 -----TyrSerProAlaMetAlaSerThr----- 442
Db 1320 AAAAGATTGATGATGATTGATGGCCATGAGTGAAGACTTCATTGAGAAACCACTAAA 1379
QY 443 -----SerLeuSerGlnAlaPro----- 448
Db 1380 CCAGTGTCAAAAGTCAATGCTGTGAAGAACAGATGACATTATACCACTGAGGGTAGAGAA 1439
QY 448 ----- 448
Db 1440 AAATTACATATAGATGCGAGAGTAGATTCACAGAACAAATTATTGAATCATCAGAACAT 1499
QY 448 ----- 448
Db 1500 AGATATGAGATAGAGCCCATACATTTTATAGAGAAAGANTCCCATGTAGATCTACTATA 1559
QY 449 ProPheMetAlaSerSer-----IlePheSer-----LeuThr 460
Db 1560 CCCATCTTTGTAGAGTCGCGCACTCCACCTACATCTCCATCTTTTCAAAAACACTTCA 1619
QY 461 AapGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValPro---GlyLeu 479
Db 1620 GATGTACACGACATTTGATTTCTTACTCACTAACCAACCCCTTCTTACCGGTAATACTATA 1679
QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499
Db 1680 GCAATCCCTGCTTCCATTAAGAAAACAGATGAGTCTTAAGAGAAATGTGTACTATACA 1739
QY 500 ProAlaSerSerAsp-----AspSerArgSerSerAlaGlyGlyIleAspMet--- 515
Db 1740 GAATCATCTCACTCAAAAGAACTTGACAGTGAAGTTCCAGTGTCAAGGCCAAGATTGCA 1799
QY 516 -----ValArg 517
Db 1800 CCTGTGTGACCATGTGTGCCAGAAATCAGATACAGTTTGGACAAGAACTTCTCTTAAGG 1859
QY 518 HlsLeuAspGlnMetAspLeuSerAspThrPro----- 528
Db 1860 AAATTGTCCAGACACATTTGGCAAGTACACAGAGAGACATGACAGACTCTGTGTGAAA 1919
QY 529 -----AlaProSerGlnValPro-----GlnLeuSerGln 538
Db 1920 GCTTCATGACACAGTCCACTGAAATGTGCTTCAACCAACCCACTCCACCGAGCTAGAGAG 1979
QY 539 TyrValSerVal----- 542
Db 1980 GAAATTAATAATGCGGTCCAGATATTTGATTAGAACTAGATCAGGTAGGACAGATTAT 2039
QY 543 -----ProAspHisPheLeuGlnAspThr 550
Db 2040 TATCAGTCCGAGCTAATGAAAGAACATGCGAAGCGCTGATGAGCAATGTGGAATGTCT 2099
QY 551 ThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProGlyGly 570
Db 2100 ACCAGTGT-----CACTACACAGAGATGCTTATTTGTGCTCTGCCCAAAAAGAA 2150

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QY 571 -----ArgGlnLeuValValPhePheSerLeuArgVal 581
Db 2151 GGTGTTCTGAGTACACCCAGACCTGACAGAGAGCTGGTGTCTTCTTCAAGCTCCGCGG 2210
QY 582 AlaAsnMetAlaPheSerAsnAspLeuPheAsnTyrSerSerSerLeuGlnTyrArgAlaLeu 601
Db 2211 ACMAACATGTTGTTTACGAAAGACTTGTTTAAACAAAACCTTTGGAATATTAAGCCCTG 2270
QY 602 GlnGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheIys 621
Db 2271 GAACAAAGATTCTTGAAGACTGCTGCTCCATCTCCAGTCAAAATCTGACAGGTTCCAG 2330
QY 622 GlnLeuGlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerIleMetLeuPhe 641
Db 2331 AACCTGAAATCTCTGAGTTTCAAGAAACGCGACATTTGGTGTAACGCGAGTGAAGTTC 2390
QY 642 AlaIysSerValProTyrAsnLeuThrIleValAlaHisGlyValLeuGlnAspPheArg 661
Db 2391 GCCGAGTCTGCCCTCTCTTAATGTCAACAAAGCCCATGTATGAGATTTCTGAAAGACTTTGT 2450
QY 662 SerAlaAlaAlaGlnGlnLeuHisLeuGlnIleAspSerTyrSerLeuAsnIleGlnPro 681
Db 2451 ACCACTGCTTACCAAAACCATGACATGATATGATAGTACTCCCTGAGCGTAGAATCA 2510
QY 682 AlaAspGlnAlaAspProCysIlePhePheLeuAlaCysGlyGlnPheAlaGlnCysValIys 701
Db 2511 GGTGATGAGGCCCAACCTTGGCAAGTTTCAAGCTGTATATGAAATTTCTGAGGTTGGTA 2570
QY 702 AsnGlnIleGlnGlnIleGlnIleCysArgCysIysProGlyTyrAspSerGlnIle--- 720
Db 2571 AATTCATGAGTGAAGGAAAGCAAAAGTCAACCTCGGTATACCTGAGTGTGATGAA 2630
QY 721 -----SerLeuAspGlyLeuGlnIleProGlyLeuCysGlyProGlyThrIysGln 736
Db 2631 CTGCTTGTCAAAAGCTCTGTGATCTTACAGCTGATCTTCTGTTGAAGATGAAAG--- 2687
QY 737 CysGlnValLeuGlnGlyIleGlyAlaProCysArg 748
Db 2688 TGTGACATTATGCCCTGGGACATGAGCCATTGTGTAGA 2723

RESULT 13
US-10-972-079-61156/C
; Sequence 61156, Application US/10972079
; Publication No. US2005015317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISER, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61156
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Chicken 19866894321451_5
US-10-972-079-61156

Alignment Scores:
Pred. No.: 4,39e-14 Length: 592
Score: 248.50 Matches: 51
Percent Similarity: 69.89% Conservative: 14
Best Local Similarity: 54.84% Mismatches: 23
Query Match: 6.04% Indels: 5

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2006, 04:07:16 ; Search time 350 Seconds

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Title: US-10-007-270-2

Perfect score: 4117  
Sequence: 1 MYLERRRAFWVFIRLQVQ.....NSELTVEYEFHNDWEN 797

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-CGN2\_1/USPTO.spool/US10007270/runat.11012006.110807.10791/app.query.fasta.1.967  
-DB=Published Applications NA New -OPMT=fastcap -SUFFIX=rnbn -MINMATCH=0.1  
-LOOPEXT=0 -UNIT5-bits -START=1 -END=1 -MATRIX=blonum62  
-TRANS=human0.cdi -LIST=45 -DOCALLIGN=200 -THR.SCOR=bpct -THR.MAX=100  
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USRR=US10007270.0CGN.1.122.0runat.11012006.110807.10791  
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-LONGLOG -DEV.TIMEOUT=120 -MARN.TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

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10: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	6.2	1219	US-10-750-185-30474	Sequence 30474, A
2	257	6.2	1219	US-10-750-623-30474	Sequence 30474, A
3	188.5	4.6	6245	US-10-401-386B-61	Sequence 61, Appl
C 4	168	4.1	1288	US-10-750-185-46240	Sequence 46240, A
C 5	168	4.1	1288	US-10-750-623-46240	Sequence 46240, A
C 6	162	3.9	554	US-10-750-185-30481	Sequence 30481, A
C 7	162	3.9	554	US-10-750-623-30481	Sequence 30481, A
C 8	143.5	3.5	3741	US-11-044-899-1	Sequence 1, Appl

9	140.5	3.4	2358	US-10-995-561-485	Sequence 485, App
10	140.5	3.4	2338	US-10-995-561-483	Sequence 483, App
11	140.5	3.4	3207	US-10-995-561-487	Sequence 487, App
12	140.5	3.4	3303	US-10-995-561-486	Sequence 486, App
13	140.5	3.4	3373	US-10-995-561-481	Sequence 481, App
14	140.5	3.4	3442	US-10-995-561-480	Sequence 480, App
15	140.5	3.4	3538	US-10-995-561-484	Sequence 484, App
16	138	3.4	10170	US-11-136-527-1817	Sequence 1817, Ap
17	137.5	3.3	2156	US-11-000-688-1488	Sequence 1488, Ap
C 18	136.5	3.3	2244	US-10-467-657-7103	Sequence 7103, Ap
19	136.5	3.3	8035	US-10-467-657-8035	Sequence 8035, Ap
20	135.5	3.3	2748	US-10-821-234-662	Sequence 662, App
21	133	3.2	4834	US-11-077-712-1	Sequence 1, Appl
22	133	3.2	9286	US-11-136-527-578	Sequence 578, App
23	131.5	3.2	7748	US-11-136-527-3397	Sequence 3397, Ap
24	131.5	3.2	7872	US-11-136-527-2235	Sequence 2235, Ap
C 25	130.5	3.2	5506	US-10-821-234-277	Sequence 277, App
26	130.5	3.2	5510	US-11-150-406-1	Sequence 1, Appl
27	129.5	3.1	5286	US-10-955-054A-61	Sequence 61, Appl
28	128.5	3.1	5085	US-11-052-554A-67	Sequence 467, App
29	127.5	3.1	921	US-10-401-386B-30	Sequence 30, Appl
30	127.5	3.1	3343	US-11-136-527-3157	Sequence 3157, Ap
31	127	3.1	5795	US-11-136-527-3157	Sequence 3157, Ap
32	126.5	3.1	14770	US-10-821-234-268	Sequence 268, App
33	126	3.1	10211	US-11-000-688-98	Sequence 98, Appl
34	125.5	3.0	3656	US-10-947-249-138	Sequence 198, App
35	125	3.0	5054	US-10-821-234-123	Sequence 123, App
36	123	3.0	4070	US-11-000-688-134	Sequence 134, App
37	123	3.0	6900	US-11-000-688-1142	Sequence 1142, Ap
38	123	3.0	8512	US-11-124-368A-46	Sequence 46, Appl
39	123	3.0	10300	US-10-947-249-122	Sequence 122, App
40	122	3.0	6266	US-10-955-054A-24	Sequence 24, Appl
41	121	2.9	6035	US-11-136-527-3751	Sequence 3751, Ap
42	121	2.9	11598	US-11-124-368A-137	Sequence 137, App
43	121	2.9	11602	US-11-124-368A-136	Sequence 136, App
44	121	2.9	12678	US-11-124-368A-135	Sequence 135, App
45	120.5	2.9	3644	US-11-136-527-2438	Sequence 2438, Ap

#### ALIGNMENTS

RESULT 1  
US-10-750-185-30474  
; Sequence 30474, Application US/10750185  
; Publication No. US2005026063A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: Denise Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFEID, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: PANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30474  
; LENGTH: 1219  
; TYPE: DNA  
; ORGANISM: Bovine 1986688067526  
US-10-750-185-30474  
Alignment Scores:  
Pred. No.: 1.38e-13  
Score: 257.00  
Percent Similarity: 96.00%  
Best Local Similarity: 90.00%  
Query Match: 6.24%  
Length: 1219  
Matches: 45  
Conservative: 3  
Mismatches: 2  
Indels: 0

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DB: 6 Gaps: 0
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QY 99 LeuAaGValCyGgInGluAaValTTPGluAaIaTTPGluAaIaPheLeuAaPArgIlePro 118
DB 1070 CTTCCAGTGTGCAGAGAGCGGTGTGGAGGCTTACCGGATCTTCTGGATGCTCCCT 1129
QY 119 AaPThGluGluTyrGlnAaPTrPaValSerIleCyGgInGluGluThrPheCysLeuPhe 138
DB 1130 GAGCCGGGGGAATCCAGAGACTGGGTGACGCTGTGCCAGAGAGACCTTCTGCTCTTT 1189
QY 139 AaPileGlyLyAsnAaPheSerAaSerAaSerAa 148
DB 1190 GACATCGGGAAAAATTTCAGCAACTCCGAG 1219

RESULT 2
US-10-750-623-30474
/ Sequence 30474, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMT GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: M11100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30474
/ LENGTH: 1219
/ TYPE: DNA
/ ORGANISM: Bovine 19866880607526
US-10-750-623-30474

Alignment Scores:
Pred. No.: 1,38e-13 Length: 1219
Score: 257.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 6.24% Indels: 0
DB: 6 Gaps: 0

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QY 99 LeuAaGValCyGgInGluAaValTTPGluAaIaTTPGluAaIaPheLeuAaPArgIlePro 118
DB 1070 CTTCCAGTGTGCAGAGAGCGGTGTGGAGGCTTACCGGATCTTCTGGATGCTCCCT 1129
QY 119 AaPThGluGluTyrGlnAaPTrPaValSerIleCyGgInGluGluThrPheCysLeuPhe 138
DB 1130 GAGCCGGGGGAATCCAGAGACTGGGTGACGCTGTGCCAGAGAGACCTTCTGCTCTTT 1189
QY 139 AaPileGlyLyAsnAaPheSerAaSerAaSerAa 148
DB 1190 GACATCGGGAAAAATTTCAGCAACTCCGAG 1219

RESULT 3
US-10-401-386B-61
/ Sequence 61, Application US/10401386B
/ Publication No. US20050261213A1
/ GENERAL INFORMATION:
/ APPLICANT: Patrick Branigan
/ APPLICANT: Theresa J Goletz
/ APPLICANT: David M Knight
/ APPLICANT: Stephen G McCarthy

```

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/ APPLICANT: Bernard J Scallion
/ APPLICANT: Linda A Snyder
/ TITLE OF INVENTION: Nucleic Acid Compositions and Methods
/ TITLE OF INVENTION: for Use
/ FILE REFERENCE: GEN 310CIP
/ CURRENT APPLICATION NUMBER: US/10/401,386B
/ PRIOR FILING DATE: 2003-03-28
/ PRIOR APPLICATION NUMBER: 10/247,203
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR APPLICATION NUMBER: 60/328,371
/ PRIOR FILING DATE: 2001-10-10
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 61
/ LENGTH: 6245
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (2767)...(3521)
/ OTHER INFORMATION: HCMV\ promoter
/ FEATURE:
/ NAME/KEY: polyA_signal
/ LOCATION: (47)...(241)
/ OTHER INFORMATION: SV40 PolyA
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (3525)...(4422)
/ OTHER INFORMATION: HCMV\IE\Introna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (4453)...(6241)
/ OTHER INFORMATION: MUC1\CDNA
/ FEATURE:
/ NAME/KEY: rep origin
/ LOCATION: (1589)...(2540)
/ OTHER INFORMATION: ori1
US-10-401-386B-61

Alignment Scores:
Pred. No.: 3.74e-06 Length: 6245
Score: 188.50 Matches: 85
Percent Similarity: 40.84% Conservative: 51
Best Local Similarity: 25.53% Mismatches: 126
Query Match: 4.58% Indels: 71
DB: 6 Gaps: 16

US-10-007-270-2 (1-797) x US-10-401-386B-61 (1-6245)
QY 385 ProAaPheGly-----ProAaPThGlnSerGluLeuProThrSerPheAa 400
DB 4753 CCAAGCCACGGGTGTCACTCGGCGCCGAGACACAGG---CCGAGCCCGGCTCCACCGCC 4809
QY 401 ValIleThGlnAaPalaThrLeuSerProGluLeuProPro-----ValGlu 416
DB 4810 CCCCAGCCACGGGTGTCACTCGGCGCCGAGACACAGGCGGCGGCTCCACCGAA 4869
QY 417 ProGlnLeuGluThrValAaPglValAaGluHsGlyLeuProAaPThSerTyrSerPro 436
DB 4870 CCCCAGCCACGGGTGTCACTCGGCG---CCGAGACACAGGCGGCGGCG 4917
QY 437 -----ProAaMetAlaSerThrSerLeuSerGluAaProProPhePheMetAa 453
DB 4918 GGCTCCACCCCGGCGCGGCTCCAC---GCCCCCA-----GCC 4956
QY 454 SerSerIlePheSerLeuThrAaPglGluThrThrAaPThMetAlaThrAaPglThr 473
DB 4957 CACGGTGTCACTCGGCGCGGAC-----ACC 4983
QY 474 MetLeuValProGlyLeuThrIleProThrSer-----AaPThSerAlaIleSer 490
DB 4984 AGCGCGCCCGGCGCTCCACCGCCCGGAGCCAGGTGTCACTCGGCGCGGAGAAC 5043

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Db      94 GACATCATGCTGTGACATGGGCGCATTTGTAG 62
RESULT 6
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/ Sequence 30481, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: BATES, Stephen
/ APPLICANT: HOLM, Tom
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30481
/ LENGTH: 554
/ TYPE: DNA
/ ORGANISM: Bovine 19866881169584
US-10-750-185-30481
Alignment Scores:
Pred. No.: 2,88e-05 Length: 554
Score: 162.00 Matches: 35
Percent Similarity: 75.00% Conservative: 7
Best Local Similarity: 62.50% Mismatches: 10
Query Match: 3.93% Indels: 4
DB: 6 Gaps: 1
US-10-007-270-2 (1-797) x US-10-750-185-30481 (1-554)
QY      221 ThrThrgluArgGluThrhglupheAlaValLeuGlu-----GluGlnArgVal 236
Db      416 ACACAGGAAAGAAAATAATGAATTCACGAGATGCTGCTGAGAGATGCACTGGAGCAAGAAAGTA 357
QY      237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256
Db      356 GAGCTAAGTATCTCTCTGCGAAACCAAGAGTTCAAGTCAAGCTGATATACCTCCAGTCC 297
QY      257 ProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLys 272
Db      296 CCGTATTACCAAGAGGTCCAGCCAAAGTCTCAGCTTCAGGTGAGCAAA 249
RESULT 7
US-10-750-623-30481/C
/ Sequence 30481, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30481
/ LENGTH: 554
/ TYPE: DNA
```

```
/ ORGANISM: Bovine 19866881169584
US-10-750-623-30481
Alignment Scores:
Pred. No.: 2,88e-05 Length: 554
Score: 162.00 Matches: 35
Percent Similarity: 75.00% Conservative: 7
Best Local Similarity: 62.50% Mismatches: 10
Query Match: 3.93% Indels: 4
DB: 6 Gaps: 1
US-10-007-270-2 (1-797) x US-10-750-623-30481 (1-554)
QY      221 ThrThrgluArgGluThrhglupheAlaValLeuGlu-----GluGlnArgVal 236
Db      416 ACACAGGAAAGAAAATAATGAATTCACGAGATGCTGCTGAGAGATGCACTGGAGCAAGAAAGTA 357
QY      237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256
Db      356 GAGCTAAGTATCTCTCTGCGAAACCAAGAGTTCAAGTCAAGCTGATATACCTCCAGTCC 297
QY      257 ProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLys 272
Db      296 CCGTATTACCAAGAGGTCCAGCCAAAGTCTCAGCTTCAGGTGAGCAAA 249
RESULT 8
US-11-044-899-1
/ Sequence 1, Application US/11044899
/ Publication No. US20050260616A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, M.
/ APPLICANT: Schwab, M.
/ TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
/ FILE REFERENCE: 10200-017-999
/ CURRENT APPLICATION NUMBER: US/11/044,899
/ CURRENT FILING DATE: 2005-01-26
/ PRIOR APPLICATION NUMBER: 09/830,972
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: PCT/US99/26160
/ PRIOR FILING DATE: 1999-11-05
/ PRIOR APPLICATION NUMBER: 60/107,446
/ PRIOR FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 3741
/ TYPE: DNA
/ ORGANISM: Rattus sp.
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (253)...(3741)
US-11-044-899-1
Alignment Scores:
Pred. No.: 0.0265 Length: 3741
Score: 143.50 Matches: 158
Percent Similarity: 35.17% Conservative: 123
Best Local Similarity: 19.77% Mismatches: 283
Query Match: 3.49% Indels: 236
DB: 7 Gaps: 41
US-10-007-270-2 (1-797) x US-11-044-899-1 (1-3741)
QY      139 AepIleGlyLysAenPheSerAnSerGlnGlu---HleLeuAepLeuLeuGlnGlnArg 157
Db      1111 GAATGGGATCATCTTTAAAGGCTCCCAAAAGAGAGTCAGCATATTAGTAAAGAAC 1170
QY      158 IleLysGlnArgSerPheProAspArgLysAsp-----GluLleSerAlaGluLysThr 175
Db      1171 ACTAAGAGAAAGTAATGTGTGAGAGTAAGCAAGAGAGATTGTGTGATGTCAGCC 1230
QY      176 LeuGlyGluProGlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGly 195
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Db      1231 CTTCAAGTCCACAGAAATCACCTGTGGTTAAAGAGACAGGT----- 1275
Qy      196  ProPheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsn 215
Db      1276 -----GTCCTCCAGAAAAGACAAATG-----GACATTTTAAATCAATGACAGATG 1320
Qy      216  AspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGlu----- 232
Db      1321 TCAGTAGTAGACACCTGTAGGAGAGATGACACTTAAAGCCATTGAAACAGACATG 1380
Qy      233 -----GluGlnArgValGluLeuSerValSerLeuValAsnGlnLys 246
Db      1381 GAAAGTAAAGATACCTTATAGGAGAGTAGGAGATGCTGCTGCTAGAGCTAATGTGAA 1440
Qy      247  PheValAlaGlu-----LeuAlaAspSerGlnSerProTyrrGlnGluLeuAla 263
Db      1441 AGTAAAGTCGACGAAAATGCTTGAAGATAGC----- 1473
Qy      264  GlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysIle 283
Db      1474 -----CTGAGACAAAAGTCTTGGAAAGATAGTAAAGCGAAGATGAGAT 1521
Qy      284  HisValLeuGlyPheArgProLysArgLysAspGlySer----- 297
Db      1522 GCTTCTTCCCAAGTACCAGAACCTGGAAGACAGCTCCAGAGCATATATACCTGT 1581
Qy      298 -----SerSerThrGlnMetGlnLeuThrAlaIlePheLysArg 310
Db      1582 GCTTCTTACTCTACGAAACCGAAAGCACACAGAAACACTTCCCTGTTAGTAAGAT 1641
Qy      311  HisSerAlaGluAlaLysSerProAlaSerAspLeuSerPheAspSerAsnLysIle 330
Db      1642 CATACTTCAGAAAATTAACA-----GATGAAAAAAAATA 1677
Qy      331  GluSerGlnLys-----ValTyrrHisGlyThrMetGlnGluAspLysGlnProGlu 347
Db      1678 GAAAGAAAGAGAGCCCAATTTAACAAGAGACATGAGCCCAAAACGTCAAAATCCTTTC 1737
Qy      348  Ile-----TyrLeuThrAlaThrAspLeuLysArg--- 357
Db      1738 CTTGAGCAGTAGACGATTCGTGAGCAGATATATGTTACAAAGATACCTTACAAAGGTG 1797
Qy      358 -----LeuIleSerLysAla 362
Db      1798 ACTGAGGACGACGTCAAAACATGCTGAGAGGTCTGACGCCAGATTAGTTCAGAGACGA 1857
Qy      363  LeuGlnGlnGlnSerLeuAspValGlyThr----- 373
Db      1858 TGTGAAGTGAAGTGAAGACCAAGGTACAAAGATTGCTTATGAAACAAAGTGAAC 1917
Qy      374  ---IleGlnPheThrAspGluIleAlaGlySerLeu---ProAlaPheGlyProAspThr 391
Db      1918 TTGGTCAAAACATCAGAAAGCTATACAGATCATTTACCCACA----- 1962
Qy      392  GlnSerGlnLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGlu 411
Db      1963 ---GCACAGCTTGGCCATCATTTGAG-----GAGCTGAAGCAACTCCGTCACACATTT 2013
Qy      412  LeuProValGluProGlnLeuGlnThrValArgValAlaGlnHisGlyLeuProAsp 431
Db      2014 TTGCTGTGATTT-----GTTATGAAAGACCACTTAATTTCTCTCTTCCA 2058
Qy      432  ThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePhe 451
Db      2059 AGCGCTGGCTTCTGTAGTGCAGCCAGTGTATCCCACTGGAAGACCTCT----- 2112
Qy      452  MetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAsp 471
Db      2113 -----CCAGTTAGTTATGAC 2127
Qy      472  GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491

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Db      2128 AGTAAAGCTTGAGCCTGAAGACCCCCACCATATGAAAGCAGCATGATGACACTA 2187
Qy      492  LeuAlaLeu-----GlyTyrSerHisProProAlaSerSerAspSerArg 507
Db      2188 AAAGCTTTGGACAAAGAGAAATAAAGACCT-----GAAAGTTT 2232
Qy      508  SerSerAlaGlyGlyGlu-----AspMetValArg 517
Db      2233 AATGCACTGTTCAGGAAACAGAAAGCTCTTATATATTCATTCGCTGTGATTTAATAA 2292
Qy      518  HisLeuAspGlnMetAspLeuSerAspThrProAlaPro-----SerGluValProGlu 535
Db      2293 -----GAAACAAGCTCTCCACTGAGCAAGTCCAGATTCTTAATTTACAGA 2343
Qy      536  LeuSerGluTyr---ValSerValProAspHis-----PheLeuGluAspThrThrPro 552
Db      2344 ATAGCAAAATTCGAGAAAGTCCGTCGCCGACAAACGCTGAGTACGAGTACGATTCCTCACT 2403
Qy      553  ValSer---AlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArg 571
Db      2404 GAATCTGAACAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCACAAACACAA 2463
Qy      572  GluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591
Db      2464 GAGGAGCGCTG-----ATGCTCATGAAGAGAGAGTCTCACT 2499
Qy      592  AsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThr-----Gln 607
Db      2500 GAAGTGCTGACAGATGAGCCAGCACAAAGAGAGAGACTTAGGCTTCACCTCAGAGAG 2559
Qy      608  LeuLeuValProTyrLeuArgSer-----AsnLeuThrGlyPheLys----- 621
Db      2560 CTAGGAAGCCATTTTAAAGTCTTTTCAGCCCAATTTACATAGTACAAAGATGCTGCA 2619
Qy      622 -----GlnLeuGluIleLeu 626
Db      2620 TCTATATGACTTCCACACTTGAACAAAGAGAAATTTCTTGCCAAATGGAAGAGTTT 2679
Qy      627  Asn-----PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLys 643
Db      2680 AATACGTCAATTTATTCAAATGATGACTTACTTCTTCAAGAAACAAATTAATAAGAA 2739
Qy      644  SerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSer--- 662
Db      2740 AGTAAACATTTTCAGATTCATCTCCGATTGAG---ATAATAGATGAATTTCCACGTTT 2796
Qy      663 -----AlaAlaIleGlnGlnLeuHisLeuGlnIleAsp 673
Db      2797 GTCACTGTCAAAAGATGATTTCTCTTAATTTAGCCAAAGAGTACACTGATCTGAAAGTATCC 2856
Qy      674  SerTyrSer-----LeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeu 691
Db      2857 GACAAAGTGAATTTGCAATATATCCAAAGCGGGCAGATTGATTCCTGCTTGAAATTTG 2916
Qy      692  AlaCysGly---GluPheAlaGlnCys-----ValLysAsnGlu 703
Db      2917 CCGTGTGACCTTTCTTCMAAATATATATATCTTAAGATGAAGTACATGTTTCAGATTA 2976
Qy      704  ArgThrGlnGluAlaGlnCysArgCysLysAspProGlyTyrAspSerGlnGlySerLeuAsp 723
Db      2977 TTCTCCGAAATATAGTCCAGTGTATCTTAAGGCATCCAT---TGCCTTCAAAATGCTCT 3033
Qy      724  GlyLeuGlnProGlyLeuCysGlyProGlyThrLysGlnCysGluValLeuGlnGlyLys 743
Db      3034 GCTTTGGA-----CTTCAGACAGAAATGGCAGCATAGTTAAATCCAAA 3078
Qy      744  Gly-----AlaProCysArgLeuProAspHisSerSerGluAsnGlnAlaTyrLys 759
Db      3079 TCACCTTAGAAAGAGAGAAATAAATCTTCTTCTGACAGAGAAA----- 3126
Qy      760  ThrSerValLysPheGlnAsnGlnAsnAsnLysValIleSerTyrArgAsnSer 779
Db      3127 -----GAGGACAGATCCCTGTACAGTGTATTTGTACAGAGACTGAGT 3168

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Qy 780 GluLeuLeuThrValGlu-----TyrGluGluPheAsnHISGlnAspTyrGluGly 796
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 3169 AAAAATTGAGTTGTTGACCTCTCTACTG-GAGAGACATTAAAGAACTGAGAGTGT 3224

RESULT 9
US-10-995-561-485
; Sequence 485, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 2358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-485

Alignment Scores:
Pred. No.: 0.0252 Length: 2358
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conservative: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
DB: 6 Gaps: 19

US-10-007-270-2 (1-797) x US-10-995-561-485 (1-2358)

Qy 171 SerAlaGluLeuThrLeuGluGluProGluGluThrIleValIleSerThrAspValAla 190
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 171 ACTGGGATCTCAGCAGAAAGGAAACCGAGGAG-----CTAGGGCCAGGAGATGGCG 224

Qy 191 AsnValSerLeuGluProPheProLeuThrProAspAspThrLeuLeuAsnGluLeu 210
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 225 GACGAGGCTTAACTGCTGGGCTG-----GATGAGGAGAGCCCTTCGAAAGCTGGTG 272

Qy 211 AspAsnThrLeuAsnAspThrIleMetProThrThrGluArgGluThrGluPheAlaVal 230
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 273 GAGGTCAACGACGATCTGGCAGAG-----CGCGCGGATCCGCTCAGCCATC 320

Qy 231 LeuGluGluGlnArgValGluLeu-----SerValSerLeuValAsnGlnIlePhe 247
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 321 CGGGAATGACAGCGGAGAGAGCTGAGCGGAGAGAGAGGCGCTTCGATCCAGCGTTTC 380

Qy 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyr-----GlnGluLeuAlaGlyLys 265
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 381 CGTCCGACGCGGAGAGCAACAAAGAACTGGCTGCACTCTCAGCAGCGGAGAGCTGAG 440

Qy 266 SerGlnLeuGlnMetGlnIlePheLeuLysLeuPheGluPheIleIleVal 285
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 441 CAGCGGCGCTGCTGGCAGCGCTGGCAGGCGCAGCTGAGTCCATGAAGATGTGGAGAA 500

Qy 286 LeuGluPheArgProLysLeuGluLysAspArgLysSerSerSerThrGlnMetGlnLeuThr 305
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 501 TTG-----ACTGCACTGTTCGAAAGCGCTGTGATGATGAGAGCGGAGCTATCCGA 554

Qy 306 AlaIlePheLysArgHisSerAla-----GluAlaLysSerProIleSerAspLeu 322
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 555 GCTGCACATCCGCGGTGATGACGGCTCAGAGATTTGAGGCTCCAGCTTGGCTGGAGTTTG 614

Qy 323 LeuSerPheAspSerAsnLysIleGlnSerGluGluValTyrHisGlyThrMetGlnGlu 342
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 615 TACAGCGGCGCTCCCAACAGT-----GGCTCAAGAGAGAGAC 650

Qy 343 AspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeu---IleSerLys 361
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
```

```
Db 651 AGCAAGGG-----CTAGCGGACACAGAGCTGGAAACAGTGTAGTCCAGAG 698
Qy 362 AlaLeuGluGluGluGlnSerLeuAspVal-----GlyThr 373
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 699 CGAGAGGAAACAGAAACAGAGGAGGAGGTTTCAAGCCAAACCCCACTGAAAGGACCC 758
Qy 374 IleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSer 393
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 759 AGCCAGGATGTGACCAAGTGAACATCTCTGTCGAGACC---CCACTGGAGAGCATTC 815
Qy 394 GluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuPro 413
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 816 AGCTCACTCTCTCACCACCAAGTTCACCAACCCCTCTCTCTGAGCTCCATTCAGAG 875
Qy 414 ProValGluProGlnLeuGluThrValAspGlyValGluIleGlyLeuProAspThrSer 433
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 876 CTTGCCAGGCGCCAGTCTTACAGCTGAG-----GTTCCAGGAGAGCCCAAGACCC 929
Qy 434 TrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaPropPhePheMetAla 453
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 930 CCCAGCCCAACCAAGACACCAAGCCCTGAGCCCTCAGAGATCTCA----- 974
Qy 454 SerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThr 473
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 974 ----- 974
Qy 474 MetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAla 493
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 975 -----ACGCTCCAGACATGAGGCGCAAGTGTCAACAACTTCTG 1016
Qy 494 LeuGlyIleSerHisProProAlaSer-----SerAspAspSer 506
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1017 TCTGGCCCCAAAGAGACCTCTGCTCCAGAGCCCAAGCCCAAGAGCCCTGTGACCAAG 1076
Qy 507 ArgSerSer---AlaGlyGlyGluAspMetValArgHisLeuAspGluMet----- 522
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1077 AGAACAGACATGTGTGAGCCCGACCTGCCAAGCTCTCTGTGCGGTCTCAGCCCGC 1136
Qy 523 -----AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu 538
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1137 CAACCAAGCCCAAGAACCGAGAGTCCACCCCTTGCAGAGGACCTTCTCATTCAGCGG 1196
Qy 539 TyrValSerValProAspHisPhe----- 546
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1197 GCTGCTCTGTGGCGGATCGGTCCACAAATCATGTGATTCCTCATAGCTGCTAGG 1256
Qy 547 LeuGluAspThrThrProValSerAlaLeuGlnIleThrThrSerSerMetThrIle 566
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1257 CTCAGGATGTGACACACCCAGGCTGCTTAAGTCCCTGACCCCGCAAGGCTC---CTG 1313
Qy 567 AlaProLysGlyArgGluLeuValAlaPheSerLeuArgValAlaAsnMetAlaPhe 586
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1314 GGCCTCTCTCCACACAGACCAACCCCTGCTCTCTCCAGAGGCTCTCTCTGAGGAC 1373
Qy 587 SerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThr 606
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1374 CCCAGTATACCTCTCTCCGCTTCAAGAGAGCAAGAGAGTACGCCAGCCCTGAGCC 1433
Qy 607 GlnLeu 608
  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1434 CAGCTT 1439

RESULT 10
US-10-995-561-483
; Sequence 483, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
```









```

Db      792 GCTGCATCGCGCTGACGGCTCAGAGATTGAGGCTGCACCTTGCTGGAGTTG 851
Qy      323 LeuSerPheAapSerAsnIleIleGluSerGluGluValIleThiIleGlyThrMetGlu 342
Db      852 TACAGCGGGCGTCCCAACAGT-----GGCTCAAGAGAGAGAG 887
Qy      343 AapIleGluProGluIleIleThiLeuThrAlaThrAapIleValArgLeu---IleSerIys 361
Db      888 AGCAAGGGG-----CTAGCGGCACACAGGCTGGAACAGTGAAGTGCACAG 935
Qy      362 AlaleuGluGluGluGluSerLeuAapVal-----GlyThr 373
Db      936 CGAGAGAAACAGAAACAGCAGGAGAGTTTCAAAAGCAACCCCAAGCCCTGAAGGAC 995
Qy      374 IlegInPheThrAapGluIleAlaGlySerLeuProAlaPheGlyProAapThrGlnSer 393
Db      996 AGCCAGAGATGTGACCAAGTGAACCTCTGCTGCGAGCC---CCACTGGAGCACTCC 1052
Qy      394 GluLeuProThrSerPheAlaValIleThrGluAapAlaThrLeuSerProGluLeuPro 413
Db      1053 AGCTCACTGCTGCTCACCAGCAAGTTCAACCACTGCTGCTGCTGAGCTTCATTTGAG 1112
Qy      414 ProValGluProGluIleGluIleThrValAapGlyAlaGluIleGlyLeuProAapThrSer 433
Db      1113 CTGCGCAGAGGCCAGTGGCTTACAGTGAAG-----GTTCAAGGAGCCCAAGGACACC 1166
Qy      434 TrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPheMetAla 453
Db      1167 CCAGGCCCAACCCCAAGCAACCAAGCCCTGAGCTCAGAGTCTCA----- 1211
Qy      454 SerSerIlePheSerIleThrAapGluIleThrThrAapThrMetAlaThrAapGluThr 473
Db      1211 ----- 1211
Qy      474 MetLeuValProGlyLeuThrIleProThrSerAapIleSerAlaIleSerGluLeuAla 493
Db      1212 -----ACGCTCCCAAGCATGAGGGCGAGTGTCAACAAGCTTTC 1253
Qy      494 LeuGlyIleSerIleProProAlaSer-----SerAapSer 506
Db      1254 TCTGGCCCCAAGAGACCCCTGCTGCGCAGAGCCCAAGAGCCCTCTTCAACCAAG 1313
Qy      507 ArgSerSer---AlaGlyGlyGluAapMetValArgHisLeuAapGluMet----- 522
Db      1314 AGAGCAGAGTGTGATGACCCCAAGCCCTGCAACGCTCTGCTGCTGCTGAGCCCGCC 1373
Qy      523 -----AapLeuSerAapThrProAlaProSerGluValProGluLeuSerGlu 538
Db      1374 CAACAGCCCAAGAACAGAGTGCACCCCTTGCAGAGGACCTTCTCATTTCAAGGG 1433
Qy      539 TyrValSerValProAapHisPhe----- 546
Db      1434 GCTGGCTCTGTGGGATCGTGTCCACAAGTTCACTGATTCTCTATGCTGTAG 1493
Qy      547 LeuGluAapThrThrProValSerAlaLeuGluIleThrThrSerSerMetThrIle 566
Db      1494 CTTCAGATGTGACCAACCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1550
Qy      567 AlaProIleGlyArgGluLeuValAlaPheSerLeuArgValAlaAlaMetAlaPhe 586
Db      1551 GGGCCCTCTGCAACAGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1610
Qy      587 SerAapLeuPheAapLeuValSerSerLeuGluIleThrAlaLeuGluGluIleThr 606
Db      1611 CCCAGATGTGCTCTCCGCTTCAAGAGAGCAACAGAGTGAAGCCAGCCCTGAGCC 1670
Qy      607 GlnLeu 608
Db      1671 CAGCTT 1676

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RESULT 14  
US-10-995-561-480

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; Sequence 480, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85/702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 3442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-480

Alignment Scores:
Pred. No.: 0.0444 Length: 3442
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conservative: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
DB: Gaps: 19

US-10-007-270-2 (1-797) x US-10-995-561-480 (1-3442)
Qy      171 SerAlaGluIleThrLeuGluProGlyIleValIleSerThrAapValAla 190
Db      408 ACTGGGATCTCACCAGAAAGAACCGACGAG-----CTAGAGCCAGCAGATGGCG 461
Qy      191 AsnValSerLeuGlyProPheProLeuThrProAapThrLeuLeuAsnGluIleLeu 210
Db      462 GACGAGGCTTAGCTGGGCTG-----GATGAGGAGACCTTTCGAGAGCTGCTG 509
Qy      211 AapAenThrLeuAapThrIleThrMetProThrThrGluArgGluThrGluPheAlaVal 230
Db      510 GAGGTCAACAGCAGATCTGCGCAGAG-----CGCCGGCGATCCGCTCAGCCATC 557
Qy      231 LeuGluGluIleArgValGluLeu-----SerValSerLeuValAenGluIlePhe 247
Db      558 CGGGAATCGACGGCGCAGAGACTGAGCGCAGAGAGAGGCGCTGCGATCCAAAGCTTTC 617
Qy      248 IysAlaGluLeuAlaAapSerGlnSerProIleIle-----GlnGluLeuAlaGlyIys 265
Db      618 CTTGCCAGCGCAGACCAAGAGAGTGGCTGCACTTCAGACAGCGGAGAGCTGAG 677
Qy      266 SerGlnLeuGluMetGlnIlePheLeuIleValSerLeuProGlyPheIleVal 285
Db      678 CAGCGGCTGCTGCGCAGCGCTGCGCAGGCTGAGTCCATGAAGATGTGAAGAA 737
Qy      286 LeuGlyPheArgProIleValSerGlyIleValSerSerSerThrGluMetGlnLeuThr 305
Db      738 TTG-----ACTGCACTGTGCGAAGCCGTGTGATGAGAGAGCGCAAGCTGATCCGA 791
Qy      306 AlaIlePheIleValArgHisSerIle-----GluAlaIleSerProAlaSerAapLeu 322
Db      792 GCTGCATCGCGCTGTAAGGAGTGAAGATTGAGTGCACCTGCTGCTGCTGCTGCTG 851
Qy      323 LeuSerPheAapSerAsnIleIleGluSerGluGluValIleThiIleGlyThrMetGlu 342
Db      852 TACAGCGGGCGTCCCAACAGT-----GGCTCAAGAGAGAGAG 887
Qy      343 AapIleGluProGluIleIleThiLeuThrAlaThrAapIleValArgLeu---IleSerIys 361
Db      888 AGCAAGGGG-----CTAGCGGCACACAGGCTGGAACAGTGAAGTGCACAG 935
Qy      362 AlaleuGluGluGluGluSerLeuAapVal-----GlyThr 373
Db      936 CGAGAGAAACAGAAACAGCAGGAGAGTTTCAAAAGCAACCCCAAGCCCTGAAGGAC 995
Qy      374 IlegInPheThrAapGluIleAlaGlySerLeuProAlaPheGlyProAapThrGlnSer 393

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Db      996 AGCAGAGATGTGACACAGTACACTCTGCTGCGAGCC---CCACTCTGGAGACATCC 1052
Qy      394 G|L|E|U|E|P|R|O|T|H|S|E|P|H|E|A|I|A|V|A|I|E|T|H|G|U|A|P|A|L|T|H|I|E|U|S|E|P|P|R|O|G|L|E|U|P| 413
Db      1053 AGCTCACTGCTCCCTCACCGACATTTCACCCACCCCTGCTCTCTGAGCTCCATTCATGGAG 1112
Qy      414 P|R|O|V|A|G|L|P|R|O|G|L|E|U|G|I|U|T|H|V|A|L|A|P|G|I|V|A|G|I|U|H|I|A|G|I|U|E|P|P|R|O|A|P|H|T|H|S|E| 433
Db      1113 CTGCGGAGGCCCTAGGCTTACAGCTAG---GTTCCAGAGGCCCGAGGCCACCC 1166
Qy      434 T|P|S|E|P|P|R|O|A|L|E|T|A|S|E|T|H|S|E|U|S|E|S|E|G|I|U|A|L|P|R|O|P|H|E|P|H|E|T|A| 453
Db      1167 CCCAGGCCACCCAGACACACACACCCCTGAGCCCTCAGAGCTTCA----- 1211
Qy      454 S|E|S|E|T|I|E|P|H|E|S|E|U|T|H|A|P|G|I|N|G|I|U|T|H|T|H|A|P|H|T|H|E|T|A|L|H|T|H|A|P|G|I|N|T|H| 473
Db      1211 ----- 1211
Qy      474 M|E|T|E|U|V|A|P|R|O|G|L|E|U|T|H|I|E|P|R|O|T|H|S|E|A|P|T|Y|S|E|R|A|I|L|E|S|E|G|I|N|E|U|A| 493
Db      1212 -----ACGCTCCCGACACTGAGGCGCAGTGTCAACAGCTTCTG 1253
Qy      494 L|E|U|G|I|L|E|S|E|T|I|A|P|R|O|A|L|A|S|E|-----S|E|A|P|A|P|S|E| 506
Db      1254 TCTGGCCCCAAGAGACCCCTGCTGCGCAGAGCCCGACACAGAGCCCTCTGACACCAAG 1313
Qy      507 A|P|G|S|E|S|E|-----A|A|G|I|G|L|G|I|U|A|P|M|E|T|V|A|A|A|G|I|U|E|U|A|P|G|I|U|E|T|----- 522
Db      1314 AAGAGCAGACGTGGCTGAGCCCGACCCCTGCGCAACGCTCCCTGCGGTGCTCAGCCCCCG 1373
Qy      523 -----A|P|E|U|S|E|A|P|H|T|H|P|R|O|A|L|P|R|O|S|E|G|I|U|A|L|P|R|O|G|L|E|U|S|E|G|I|U| 538
Db      1374 CAACAGCCCAAGAACGAGAGTCCACCCCTTGCCAGCGGACCTTCATTCACCGG 1433
Qy      539 T|Y|V|A|S|E|T|I|A|P|R|O|A|L|P|H|E|----- 546
Db      1434 GCTGGCTCTGTGGGATGCTGTCACAAAGTTACATGATTCCTGATGCTGCTAGG 1493
Qy      547 L|E|U|G|A|P|H|T|H|P|R|O|V|A|L|S|E|A|L|E|U|G|I|N|T|Y|I|E|T|H|T|H|S|E|S|E|T|H|I|E| 566
Db      1494 CTTCAAGATGACACACCCGAGCTGCTTAAGTCCCTCAGCCCGCAGAGCTC---CTG 1550
Qy      567 A|A|P|R|O|G|L|Y|A|G|I|U|E|U|A|I|A|P|H|E|S|E|U|T|H|A|A|A|A|A|P|H|E| 586
Db      1551 GGCCTCTCCCTCACGACACACCCCTGCTCTCTCCAGCGGCTCTCTCTCGGAGC 1610
Qy      587 S|E|A|A|P|L|E|U|P|H|E|A|N|L|Y|S|E|S|E|T|H|U|T|Y|A|I|A|L|E|U|G|I|N|G|I|N|P|H|E|T|H| 606
Db      1611 CCCAGTATACCTCTCCCGGTTACAGCAAGAGCAAGAGTACCCGAGCCCTGAGC 1670
Qy      607 G|I|N|E|U| 608
Db      1671 CAGCTT 1676

RESULT 15
US-10-995-561-484
; Sequence 484, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE. METHODS OF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 3538
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-10-995-561-484
Alignment Scores:
Pred. No.: 0.0463 Length: 3538
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conservative: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
DB: 6 Gaps: 19

US-10-007-270-2 (1-797) x US-10-995-561-484 (1-3538)
Qy      171 S|E|A|I|G|U|T|H|T|E|U|G|I|U|P|P|R|O|G|I|U|T|H|I|E|V|A|I|L|E|S|E|T|H|A|P|V|A|I|A| 190
Db      408 A|C|T|G|G|A|G|A|T|T|C|A|C|A|G|A|A|G|A|C|C|G|A|G|-----C|T|A|G|G|C|C|A|G|A|T|G|G|C|G| 461
Qy      191 A|E|N|V|A|S|E|U|E|U|G|I|P|R|O|P|H|E|P|R|O|U|T|H|P|R|O|A|P|S|T|H|E|U|S|E|U|A|N|G|I|U|E|U| 210
Db      462 G|A|C|A|G|G|C|T|T|A|G|C|T|G|G|G|C|T|G|-----G|A|T|G|A|G|G|A|G|C|C|T|T|G|A|A|G|C|T|G| 509
Qy      211 A|P|A|E|N|T|H|L|E|U|A|N|A|P|H|T|H|Y|S|E|T|P|R|O|T|H|T|H|G|U|A|G|I|U|T|H|S|I|U|P|H|E|A|I|A|V|A|I| 230
Db      510 G|A|G|T|C|A|C|A|G|A|G|A|T|G|G|C|A|G|A|G|-----C|G|C|G|C|G|C|A|T|C|G|C|T|C|A|G|C|A|T|C| 557
Qy      231 L|E|U|G|I|U|G|I|N|A|T|V|A|I|G|I|U|E|U|-----S|E|A|I|S|E|T|E|U|V|A|A|N|G|I|N|Y|S|P|H|E| 247
Db      558 C|G|G|A|A|C|T|G|C|A|G|G|G|A|G|A|G|C|T|G|A|G|C|G|C|G|A|G|A|G|G|C|C|T|G|C|A|T|C|A|A|G|C|T|T|C| 617
Qy      248 I|Y|A|I|A|G|I|U|E|U|A|A|P|S|E|G|I|N|S|E|P|R|O|T|Y|T|Y|-----G|I|N|I|U|E|U|A|I|G|I|U|Y|S| 265
Db      618 C|G|T|G|C|G|A|G|C|G|C|A|G|A|C|A|C|A|G|A|A|A|C|T|G|C|T|G|C|A|C|T|C|C|A|C|A|G|C|G|G|A|G|C|T|G|A| 677
Qy      266 S|E|G|I|N|E|U|G|I|E|U|S|I|L|E|P|H|E|U|Y|S|I|U|E|U|P|P|R|O|G|I|P|H|E|U|Y|S|I|L|E|I|U|A|I| 285
Db      678 C|A|G|C|G|G|C|T|C|C|T|G|C|A|C|G|C|T|G|C|A|G|G|C|A|G|C|T|G|C|A|G|T|C|C|A|T|A|A|C|A|T|G|T|G|A|G|A| 737
Qy      286 L|E|U|G|I|P|H|E|A|T|P|R|O|G|L|E|U|S|I|U|Y|A|P|G|I|Y|S|E|S|E|T|H|G|I|U|E|G|I|N|E|U|T|H| 305
Db      738 T|T|G|-----A|C|T|G|C|A|C|T|G|T|G|G|A|A|C|C|G|C|T|G|A|G|T|A|G|A|G|A|G|G|A|G|C|T|G|A|T|C|C|A| 791
Qy      306 A|A|I|E|P|H|E|U|Y|A|A|G|I|S|E|E|A|I|-----G|I|U|A|I|Y|S|E|P|R|O|A|L|A|S|E|A|P|H|E|U| 322
Db      792 G|C|T|G|C|A|T|C|G|C|G|G|T|A|C|G|G|C|T|C|A|G|A|G|A|T|T|A|G|G|C|G|C|C|A|C|T|G|C|T|G|G|A|G|T|T|G| 851
Qy      323 L|E|U|S|E|P|H|E|A|P|S|E|A|N|L|Y|S|I|L|E|U|S|E|G|I|U|A|I|T|Y|H|I|G|I|U|T|H|E|G|I|U|G|I| 342
Db      852 T|A|C|A|G|C|G|G|C|G|C|C|A|A|C|A|G|T|-----G|G|C|T|C|A|A|G|A|G|A|G|A|C| 887
Qy      343 A|E|P|Y|S|G|I|N|P|R|O|G|I|U|I|E|T|Y|I|E|U|T|H|A|L|H|T|H|A|P|L|E|U|Y|A|A|G|L|E|U|-----I|L|E|S|E|U|S| 361
Db      888 A|G|C|A|A|G|G|G|-----C|T|A|G|C|G|C|A|C|A|G|C|T|G|A|A|C|A|G|T|G|A|G|T|G|G|C|C|A|G|A|G| 935
Qy      362 A|A|L|E|U|G|I|U|G|I|N|S|E|U|E|A|P|V|A|I|-----G|I|Y|T|H| 373
Db      936 C|G|A|G|A|G|A|C|A|G|A|A|C|A|G|A|G|C|A|G|A|G|T|T|A|A|A|C|C|A|C|C|C|C|A|C|C|C|T|G|A|G|C|A|C| 995
Qy      374 I|L|E|I|N|P|H|E|T|H|A|P|G|I|U|I|E|A|I|A|G|I|S|E|U|E|P|R|O|A|L|A|P|H|E|G|I|P|P|R|O|A|P|H|T|H|S|E| 393
Db      996 A|C|C|A|G|A|T|G|T|A|C|C|A|C|A|G|T|C|C|T|G|C|G|A|G|C|-----C|C|A|C|T|G|A|G|C|A|C|A|T|C|C| 1052
Qy      394 G|U|L|E|U|P|R|O|T|H|S|E|P|H|E|A|I|A|V|A|I|E|T|H|G|U|A|P|A|L|T|H|I|E|U|S|E|P|P|R|O|G|L|E|U|P| 413
Db      1053 A|G|T|C|A|C|T|G|C|T|C|C|C|A|C|G|A|G|T|T|A|C|C|A|C|C|C|T|G|C|T|G|A|G|C|T|C|C|A|T|T|G|A|G| 1112
Qy      414 P|R|O|V|A|G|L|P|R|O|G|L|E|U|G|I|U|T|H|V|A|L|A|P|G|I|V|A|G|I|U|H|I|A|G|I|U|E|P|P|R|O|A|P|H|T|H|S|E| 433
Db      1113 C|T|G|C|G|A|G|G|C|C|A|G|C|C|T|T|A|C|A|G|T|A|G|-----G|T|T|C|A|G|G|A|G|C|C|A|G|C|C|A|G|C|C|A|C|C| 1166
Qy      434 T|P|S|E|P|P|R|O|A|L|E|T|A|S|E|T|H|S|E|U|S|E|S|E|G|I|U|A|L|P|R|O|P|H|E|P|H|E|T|A| 453
Db      1167 C|C|A|G|C|C|C|A|C|C|A|A|A|C|C|A|C|A|G|C|C|T|G|A|G|C|T|C|C|A|G|A|G|T|T|C|C|A|----- 1211
Qy      454 S|E|S|E|T|I|E|P|H|E|S|E|U|T|H|A|P|G|I|N|G|I|U|T|H|T|H|A|P|H|T|H|E|T|A|L|H|T|H|A|P|G|I|N|T|H| 473

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Db      1211 ----- 1211
QY      474 MetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAla 493
Db      1212 -----ACGGTCCCGCAGCAGTGGTGTCAACAAGCTTCG 1253
QY      494 LeuGlyIleSerHisProProAlaSer-----SerAspAspSer 506
Db      1254 TCTGGCCCAAGAAGACCCCTGCTGCCCCAGAGCCCAAGAGCCCTCTGACACCAAG 1313
QY      507 ArgSerSer--AlaGlyGlyGluAspMetValArgHisLeuAspGluMet----- 522
Db      1314 AAGAGCAGACGTGGCTGAGACCCGACCTGCAACGCTCCCTGCGGTCTAGCCCGCC 1373
QY      523 -----AspLeuSerAspThrProAlaProSerGluValProGlyLeuSerGlu 538
Db      1374 CAACCAGCCGAGAACCGAGAGTCCACCCCTTGGCCAGCGAATTCTCATTCACAGCG 1433
QY      539 TyrValSerValProAspHisPhe----- 546
Db      1434 GCTGGCTCTGTGCGGATGCTGCCAAGTTCACATCTGATTCTTAGCTGCTAG 1493
QY      547 LeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIle 566
Db      1494 CTCAGAGATGGCACACCCCGAGCTGCTAGTCCCTGACCCCGCAAGGCTC---CTG 1550
QY      567 AlaProLysGlyArgGlnLeuValAlaPheSerLeuArgValAlaAsnMetAlaPhe 586
Db      1551 GGCCCTCCCTCACCAGCACCACTGCTCTCTCCAGCGGCTCTCTCGGGGC 1610
QY      587 SerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThr 606
Db      1611 CCCAGTGAATACCTCTCCCGGTTCAGCAAGAGCAACAGAGTAGCCAGCCCTGGCC 1670
QY      607 GlnLeu 608
Db      1671 CAGCTT 1676
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Search completed: January 15, 2006, 07:40:26  
Job time : 401 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 16:58:56 ; Search time 1153 Seconds

(without alignment)  
4606.904 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117  
Sequence: 1 MYLERRALFFWVIFLQVQ.....NSELLTVYERFHDWEGN 797

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0 , Fgapext 7.0
	Delpop 6.0 , Delpext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame\_p2n.model -DEV=x1h  
-O=/cgn2.1/USPTO.spool/US10007270/runat.11012006.110802.10611/app.query.fasta\_1.967  
-DB=N.Geneseq -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -IDOPCL=0 -IDOPEXT=0  
-UNITS=bites -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR.SCOR=Pct -THR.MAX=100 -THR.MIN=0 -MODE=LOCAL  
-OUTFMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10007270\_@CGN\_1.1.805 @runat.11012006.110802.10611 -NCPU=6 -ICPU=3  
-NO.WMAP -LARGESUBQUERY -NEG.SCOR=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq\_21.\*

1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001s:\*  
5: geneseqn2001s:\*  
6: geneseqn2002s:\*  
7: geneseqn2002s:\*  
8: geneseqn2003s:\*  
9: geneseqn2003s:\*  
10: geneseqn2003s:\*  
11: geneseqn2003s:\*  
12: geneseqn2004s:\*  
13: geneseqn2004s:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4073	98.9	3330	9	ACCS7946 Human int
2	4073	98.9	3330	10	ADAI4840 Human int
3	4039.5	98.1	3263	3	AAA46205 Human enco
4	4024.5	97.8	3261	9	ACCS7960 Human int

5	4024.5	97.8	3261	10	ADAI4866 Human CDN
6	3619	87.9	2887	9	ACCS7947 Human int
7	3619	87.9	2887	10	ADAI4842 Human int
8	3526.5	85.7	2966	3	AAA46328 Interphot
9	3323	80.7	2244	3	AAA46329 Interphot
10	3323	80.7	2244	9	ACCS7948 Human int
11	3323	80.7	2244	10	ADAI4844 Human int
12	2548.5	61.9	3668	9	ACCS7950 Human int
13	2548.5	61.9	3668	10	ADAI4847 Human int
14	2192	53.2	3206	3	AAA46309 CDNA enco
15	1342.5	32.6	1726	9	ACCS7951 Mouse int
16	1342.5	32.6	1726	10	ADAI4849 Human int
17	929.5	22.6	1321	9	ACCS7952 Mouse int
18	929.5	22.6	1321	10	ADAI4851 Mouse int
19	927	22.5	4165	3	AAA46206 CDNA enco
20	927	22.5	4165	13	ADAI4859 Cancer-ab
21	927	22.5	4166	9	ACCS7954 Human int
22	927	22.5	4166	10	ADAI4855 Human int
23	885	21.5	555	3	AAA46204 CDNA enco
24	885	21.5	555	9	ACCS7953 Monkey in
25	885	21.5	555	10	ADAI4853 Monkey in
26	846.5	20.6	2964	9	ACCS7955 Human int
27	846.5	20.6	2964	10	ADAI4857 Human int
28	841	20.4	4204	3	AAA46310 CDNA enco
29	841	20.4	4204	9	ACCS7958 Mouse int
30	841	20.4	4204	10	ADAI4862 Mouse int
31	241	5.9	1094	3	AAA46321 Exon 13 o
32	201.5	4.9	3670	14	ADY84505 MUC-1::HS
33	201.5	4.9	3712	14	ADY84507 MUC-1::HS
34	196	4.8	1548	14	AEAI1045 DNA enco
35	196	4.8	1548	14	AEAI1738 Wobbled M
36	196	4.8	1548	14	AEBO0289 DNA enco
37	194.5	4.7	2026	11	ACN91439 Breast ca
38	193	4.7	3727	14	ADY84504 MUC-1::HS
39	193	4.7	3769	14	ADY84506 MUC-1::HS
40	192.5	4.7	1817	3	AAA46320 Exon 12 o
41	191.5	4.7	1805	12	ADQ83917 Human tum
42	191.5	4.7	1805	12	ADQ86329 Human tum
43	191.5	4.7	1805	12	ADQ85148 Human tum
44	191.5	4.7	1805	13	ADQ83237 Human tum
45	190.5	4.6	1800	13	ADT89853 Human muc

## ALIGNMENTS

RESULT 1  
ACCS7946  
ID ACCS7946 standard; CDNA, 3330 BP.  
ACCS7946;  
11-AUG-2003 (first entry)  
Human interphotoreceptor matrix IPM 150, isoform A, CDNA.  
Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
receptor; ophthalmological; gene therapy; gene; ss.  
Homo sapiens.  
Key Location/Qualifiers  
CDS 131..2586  
FT /product= "IPM 150"  
FT /transl\_except= (pos:668..756,aa:Thr-Asp)  
FT sig\_peptide 131..190  
FT /\*tag= b  
PN WO2003039346-A2.  
PD 15-MAY-2003.  
XX 08-NOV-2002; 2002WO-US036090.

XX 08-NOV-2001; 2001US-00077270.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX Hageman GS, Kuehn MH;  
 XX WPI: 2003-441440/41.  
 XX P-PSDB; ABR42342.  
 XX  
 XX New interphotoreceptor matrix proteins and polynucleotides, useful for  
 XX treating or preventing photoreceptor death or retinal detachment, or for  
 XX treating ocular disorders.  
 XX  
 XX Claim 1; Page 77; 105dp; English.

XX The present sequence is that of cDNA encoding isoform A of novel human  
 XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
 XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
 XX is located on chromosome 6q13-q15, a region that also contains loci for  
 XX progressive bilateral chorioretinal atrophy, autosomal dominant Stargardt's  
 XX -like macular dystrophy, North Carolina macular dystrophy and Salla  
 XX disease. Members of the IPMC gene family have been identified in humans,  
 XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
 XX Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
 XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
 XX antibodies that specifically bind the polypeptides, and vectors  
 XX comprising the polynucleotides. A claimed method of treating or  
 XX preventing photoreceptor death or retinal detachment involves  
 XX administering an IPMC polynucleotide, polypeptide or antibody. Also  
 XX claimed is a method for identifying a compound capable of modulating IPMC  
 XX gene expression

XX Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	0	Length:	3330
Score:	4073.00	Matches:	796
Percent Similarity:	97.31%	Conservative:	0
Best Local Similarity:	97.31%	Mismatches:	1
Query Match:	98.93%	Indels:	22
DB:	9	Gaps:	1

US-10-007-270-2 (1-797) x ACC57946 (1-3330)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 DB 131 ATGTAATTGGAAACTAGAAAGACTATTTTGTGTTTGGATTCTTCCAACTCAAGCA 190  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 DB 191 ACCAAGATATCTCCATTACATATACATCTTCGAAACTTAAGACATACATACATCCCA 250  
 QY 41 ArgAsnGluThrThrgIuSerThrgIuLysMetTyrLysMetSerThrMetArgArgIle 60  
 DB 251 AGAAATGAAACAACCTGAAAGTACTGAAAAATGTACAAAATGTCAACTATGAGAGCAATA 310  
 QY 61 PheAspLeuAlaIleHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 DB 311 TTCGATTTGGCAAGATCGAACAACAAATCCGCAATTTTCCCAACGGGGGTAAAGTC 370  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaIleTyrTyrArgLeuArg 100  
 DB 371 TGTCCACAGAAATCCATGAAACAGATTTTAGACAGCTTCACAGCTTATTAATGATTGACA 430  
 QY 101 ValCysGlnGluAlaValTyrGlnAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 431 GGTGTCAAGGAAGCACTATGGGAAGCATATCCGATCTTTCTGGATCGATCCCTGACACA 490  
 QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 491 GGGGAATATCAGGATCGGGTCAAGCATCTCCACAGCAGAGACCTTTCCTTTGACATT 550

QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgIleLysGln 160  
 DB 551 GGAAGAAATCTTCAACATTTCCCAAGAGCACTGGATCTTCTCCACAGACAAATTAACAG 610  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 DB 611 AGAAGTTTCCCTGCACAGAAAAGATGAAATATCTGCAGAGAGACATTGGAGAGCTGGT 670  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 671 GAAACCATTTGCATTTCAAC-AGCAATCTACATTTCAAGAAGCTTGGCGATATTCTAAGA 729  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 730 AAACCTCAGAGAGCAAAATTCAGATGTTCCACAGCTCTACCTTGGCCCTTCCCTTC 789  
 QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
 DB 790 ACTCCTGATGACACCTCTCCTCAATGAATTTCTCGATATATACATCAACAGACCAAGATG 849  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSer 239  
 DB 850 CCAACCAAGAGAGAGAGAAACGAATTCGCTGTGGAGAGCAGAGGGGTGAAGCTCAGC 909  
 QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
 DB 910 GTCTCTCGGTAAACCAAGATTTCAAGCAGACGCTCGTACCTCCAGTCCCATATTAC 969  
 QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGly 279  
 DB 970 CAGAGCTAGACAGAGAAAGTCCCAACTTCAGATGCAAAAAGATATTTAAAGAACTTCCAGAG 1029  
 QY 280 PheLysLysIleHisValLeuGlyPheAspProLysLysGlyLysAspGlySerSerSer 299  
 DB 1030 TTCAAAAAAATCCATGTGTGTAGATTAGACCAAGAAAGAAAGAGTGCCTCAAGCTCC 1089  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
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 DB 1270 AGCAAGACACTAGAGAGAAACAATCTTGGATGTGGGAGACAAATTCACTTCACTGATGA 1329  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
 DB 1330 ATTGCTGATACCTGACAGCTGCTTGTGCTCTACACCCATCAGAGCTCCCAACATCTTT 1389  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
 DB 1390 GCTGTTATTAACAGAGATGCTACTTGTAGTCCAGAACTTCTCTGTTGAACCCAGCTT 1449  
 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrSerProProAlaMet 439  
 DB 1450 GAGACAGTGGACGAGAGACAGATGCTTACTGACATTTCTTGCTCCACCTGCTATG 1509  
 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
 DB 1510 GCCTTACTCCTCCGTGCAAGAGCTCCACCTTTTATGAGATCAACAGATCTTCTCTG 1569  
 QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
 DB 1570 ACTGATCAAGGACCAACAGATACAAATGGCACCTGACGAGCAAAATGTGTAGTACAGAGGCTC 1629  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499

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Db      1630 ACCATCCCCACGAGTATTATTCTGCAATCAGCCAACTGGCTCTGGGAATTCACATCCA 1689
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Db      1690 CCTGACATCTTCAGATGACGACGATCAAGTGCAGGGGGAAGATATGTCTCAGACACCTTA 1749
Qy      520  AapGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539
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Qy      540  ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559
Db      1810 GTTTCGTGCCAGATCATTTCTTGGAGATACCACTCCGTCTCAGCTTTACAGTATATC 1869
Qy      560  ThrThrSerSerMetThrIleAlaProGlyGlyGluLeuValValPhePheSerLeu 579
Db      1870 ACCACTAGTTCATATGACCATTCGCCCAAGGGCCGAGAGCTGTGTCTTCAGTCTG 1929
Qy      580  AcGValAlaAsnMetAlaPheSerAspLeuPheAsnLeuPheAsnLeuSerLeuGlnTyrArg 599
Db      1930 CTTGTTGCTAACATGGCTTCTTCACAGACTGTTCACAAAGAGCTCTCGAGATACCA 1989
Qy      600  AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGly 619
Db      1990 GCTCTGGAGCAACAATTCACACAGCTGCTGTTCCATATCTACATCCATCTTACAGA 2049
Qy      620  PheGlyGlnLeuGlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerIleMet 639
Db      2050 TTTAAGCAACTTGAATATCTTAATCTCAGAAACGGGAGGTATGTAATGCAAAATG 2109
Qy      640  LysPheAlaLysSerValProTyrAsnLeuThrIleValHisGlyValLeuGlnLeuAsp 659
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Qy      660  PheArgSerAlaAlaAlaGlnGlnLeuHisLeuGlnIleAspSerTyrSerLeuAsnIle 679
Db      2170 TTTGTTGCTGCGACGCCCAACAATCTCCATCTGAAATATGACAGTACTCTCTCAACAT 2229
Qy      680  GluProAlaAspGlnAlaAspProCysGlyPheLeuAlaCysGlyGluPheAlaGlnCys 699
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Qy      700  ValLysAsnGluArgThrGlnGlnIleAlaGluCysArgCysLysProGlyTyrArgSerGln 719
Db      2290 GTAAGAACGAAACGACGAGAGACGGAGTGTCTGCGTGAACCAAGATATACAGCCAG 2349
Qy      720  GlySerLeuAspGlyLeuGlnIleProGlyLeuGlyGlyProGlyTyrThrLeuGluCysGluVal 739
Db      2350 GGGAGCTGGACGCTCTGGAACCAAGCCTCTGTGGCCTTGGCACAAAAGGAATGCCAGGTC 2409
Qy      740  LeuGlnGlyLysGlyAlaProCysArgLeuProAspHisAspSerGluAsnGlnAlaTyrLys 759
Db      2410 CTCACGGGAAAGGAGCTCATGCAAGGTTGCCAGATCACTCGAAATCAACACATACAAA 2469
Qy      760  ThrSerValLysLysPheGlnAsnGlnGlnAsnLeuValIleSerIleArgAsnSer 779
Db      2470 ACTAGTGTAAAGAAAGTTCAAAATCAACAAATTAACAAAGTATATCAGTAAGAAATCT 2529
Qy      780  GluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGlnIleValAsn 797
Db      2530 GAATATACGACCGTGAATATATGAATTTAAACATCAAGATTGGAGAGGAAT 2583

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RESULT 2
ADA14840
ID      ADA14840 standard; cDNA; 3330 BP.
XX
AC      ADA14840;
XX
DT      06-NOV-2003 (first entry)
XX
DE      Human Interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX

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KW      ss; gene; human; IPMC 150 isoform A; gene therapy;
KW      interphotoreceptor matrix component; IPMC; ocular disorder;
KW      macular degeneration; photoreceptor death; retinal detachment.
OS      Homo sapiens.
FH      Key
FT      CDS
FT      131..2586
FT      /*tag= b
FT      /*product= "IPMC 150 isoform A"
FT      /*transl_except= (pos:689..756,aa:Thr-Asp)
FT      sig_peptide
FT      131..150
FT      /*tag= a
FT      /*label= Signal_sequence
FT      mat_peptide
FT      191..2583
FT      /*tag= c
FT      /*label= Mature_IPMC_150_isoform_A
FT      misc_feature
FT      692..753
FT      /*tag= d
FT      /*note= "This region could represent intronic sequence not
FT      removed from the cDNA sequence."
PN      US2002160954-A1.
XX
PD      31-OCT-2002.
XX
PF      08-NOV-2001; 2001US-00007270.
XX
PR      29-OCT-1998; 98US-00183972.
PR      29-OCT-1999; 99US-00430195.
XX
PA      (IOWA ) UNITV IOWA RES FOUND.
XX
PI      Hageman GS, Kuehn MR;
XX
DR      WPI; 2003-238235/23.
XX
P      P-PsDB; ADA14841.
XX
PT      New isolated or recombinant interphotoreceptor matrix component
PT      polynucleotide and polypeptide, useful for diagnosing, preventing,
PT      treating or prognosticating ocular disorders, e.g. macular degeneration
PT      or retinal detachment.
XX
PS      Claim 3; Page 29-30; 76pp; English.
XX
CC      The invention relates to an isolated or recombinant interphotoreceptor
CC      matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC      comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC      gene operatively linked to the IPMC polynucleotide. The IPMC
CC      polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC      preventing, treating or prognosticating ocular disorders, e.g. macular
CC      degeneration, photoreceptor death or retinal detachment. They are also
CC      useful for identifying a compound capable of modulating IPMC gene
CC      expression in a cell. The present sequence represents cDNA encoding human
CC      interphotoreceptor matrix component, IPMC, 150 isoform A.
XX
SQ      Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;
XX

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## Alignment Scores:

```

Pred. No.:      0      Length:      3330
Score:          4073.00  Matches:      796
Percent Similarity: 97.31%  Conservative: 0
Best Local Similarity: 97.31%  Mismatches: 1
Query Match:      98.93%  Indels: 22
DB:              10      Gaps: 1

```

US-10-007-270-2 (1-797) x ADA14840 (1-3330)

```

Qy      1  MectyrLeuGluTutrrArGArGAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
Db      131  ATGTAATTTGAAACCTAGAAAGAGCTATATTTTCTTTTGGATTTTCTCCAGATTCAAGCA 190
Qy      21  ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40

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Db 191 ACCAAGATATCTCCATTACATATACCATCTGAAACTTAAGACATAGACATCCCCCA 250  
Qy 41 ArgAaNGlUThrThGluSerThrGluYsMetYrYsMetSerThrMetArgArgIle 60  
Db 251 AGAAATGAAACAACTGAAAGTACTGAAAAATGTCAAAATGTCAACTATGAGAGAAATA 310  
Qy 61 PheaPLeuAlaYsHhIeArGThrYsArgSerAlaPhePheProThrGlyValYsVal 80  
Db 311 TTCGATTTGGCAAGCATCGACATCAAAAGATCCGCATTTTCCCAACGGGGGTTAAAGTC 370  
Qy 81 CysPProGInGluSerMetYsGlnIleLeuAAsPserLeuGlnAlaYrYrYrArgLeuArg 100  
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Db 431 GTGTGTCAGGAAGCATGATGGAAGCATATCGGATCTTCTGGATCGCATCCCTGACACA 490  
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Db 551 GGAATAAACTTCAGCAATCCAGAGACACTGGATCTTCTCCAGACAGAAATAAACAG 610  
Qy 161 ArgSerPheProAspArgYsAspGluIleSerAlaGluYsThrLeuGluYsLeuProGly 180  
Db 611 AGAAGTTTCCCTGACAGAAAGATGAAATATCTGCAGAGAGACATGGGAAGGCTGGAT 670  
Qy 181 GluThrIleValIleSerThr----- 187  
Db 671 GAAACATTTGCTATTCAAC-AGCAATCTACATTTCAAAAGACTTGGGCGATTTCTAAGA 729  
Qy 188 -----AspValAlaAAsPValSerLeuGlyProPheProLeu 199  
Db 730 AAACCTCAGAAAGACAAATTCAGATGTGGCCACGCTCACTTGGGCTTTCCCTCTC 789  
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Db 790 ACTCTGATGACACCTCTCTCAATGAAATTCGAAATATCACTCAACACACCAAGAG 849  
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Db 850 CCTACACAGAAAGAGAAACAGAAATTCGCTGTGTGTGAGAGACAGAGGTGAGCTCAGC 909  
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Qy 280 PheYsYsIleHhIeValLeuGlyPheArGProYsLeuGluYsAAsPglySerSerSer 299  
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Qy 300 ThrGluMetGlnLeuThraIlePheYsArgHhIeSerAlaGluAlaYsSerProAla 319  
Db 1090 ACGAGATGCAACTTACGGGCATCTTTAAGAGACACAGTGCAGAAACAAAGCCCTGCA 1149  
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Qy 340 MetGluGluAspYsGlnProGluIleYrYrLeuThraIleThrAspLeuYsArgLeuIle 359  
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Qy 360 SerYsAlaLeuGluGluGluGlnSerLeuAAsPValGlyThrIleGlnPheThrAspGlu 379

Db 1270 AGCAAGACATGAGAGAAACAATCTTGGATGTGGGACAAATTCATGCTCATGATGA 1339  
Qy 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
Db 1330 ATGTGATGATACGCGACGCTTGTGTCTTACACCCATAGAGCTGCGCACATCTTTT 1389  
Qy 400 AlaValIleThrGluAAsPAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
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Qy 420 GluThrValAspGlyAlaGluHhIeGlyLeuProAspThrSerTrrPserProProAlaMet 439  
Db 1450 GAGACAGTGAACGAGACAGACATGCTTACCTCAACTTGTGTGCTCCACTGCAATG 1509  
Qy 440 AlaSerThrSerLeuSerGluAlaProProPhePheAlaSerIlePheSerLeu 459  
Db 1510 GCCTTACTCTCTGTCAGAGCTTCACCTTCTTTATGGATCAAGCATCTTCTCTTG 1569  
Qy 460 ThrAspGlnGlyThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
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Qy 480 ThrIleProThrSerAspTrrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHhIePro 499  
Db 1630 ACCATCCCAACAGATTAATTCGCAATCAGCAACTGGCTCGGGAATTTCAATCCA 1689  
Qy 500 ProAlaSerSerAAsPAsPserAArgSerAlaGlyGlyAlaAsPMetValArgHhIeLeu 519  
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Qy 520 AspGluMetAAsPLeuSerAspThrProAlaProSerGluValProGluLeuSerGluYr 539  
Db 1750 GATGAATGATCTGTCTGACACTCTGCCCCCATCTGAGTACAGAGCTCAGCAATAT 1809  
Qy 540 ValSerValProAspPhePheLeuGluAspThrThrProValSerAlaLeuGlnYrIle 559  
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Qy 560 ThrThrSerSerMetThrIleAlaProYsGlyArgGluLeuValIlePhePheSerLeu 579  
Db 1870 ACCACTATTTTATGACCATTTGCCCCCAAGGCGAGAGCTGTGTGTGTTCTTCAGTTG 1929  
Qy 580 ArgValAlaAAsPMetAlaPheSerAAsPLeuPheAAsPserSerLeuGluYrArg 599  
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Qy 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProYrYsLeuArgSerAAsPLeuThrGly 619  
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Qy 620 PheYsGlnLeuGluIleLeuAAsPheArgAAsPValIleValAAsPserYsMet 639  
Db 2050 TTTAAGCAACTTGAATTACTTAACAGAAACGGAAGTGAATGTGAATAGCAAAATG 2109  
Qy 640 LysPheAlaYsSerValProYrAAsPLeuThrYsAlaValHhIeGlyValLeuGluAAsP 659  
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Qy 660 PheArgSerAlaAlaIleGlnGlnLeuHhIeLeuGluIleAAsPserYrYsSerLeuAAsP 679  
Db 2170 TTTCTGTTCTGCTGACGCCCAACTCCATCTCGAAATAGACAGCTACTCTCTCAACAT 2229  
Qy 680 GluProAlaAspGlnAlaAsPProCysYsPheLeuAlaCysGluGluPheAlaGlnCys 699  
Db 2230 GAACCACTGATCAAGCAGATCTCTGCAAGTCTCGGAGTGGGAAATTTGGCCAAATGT 2289  
Qy 700 ValYsAAsGluArgThrGluGluAlaGluCysArgCysYsPProGlyYrYrAsPserGln 719  
Db 2230 GTAAAGAAACGAACGACATGAGGAAGCGAGTGTCTGCTCAACAGCAATATGACAGCCAG 2349  
Qy 720 GlySerLeuAAsPglyLeuGluProGlyLeuYsGlyYrProGlyYrThrYsGluCysGluVal 739  
Db 2350 GGAAGCTGGAACGGTCTGGAACAGGCTCTGTGCTCTGCGACAAAGAAATGCGAGGTC 2409



QY	740	LeuGInGlyLyvGIGlyAlaProCyvAvtgLeuProAspHisSerGluuAnGlnAlaTyLyS	779		
Db	2410	CTCCAGGGGAAAGGAGGCTCCATGCAGGTTGCCAGATCACTGTGAAATCAAGCATCAAA	246		
QY	760	ThrsSerValLyvLysPheGlnAnGlnGlnIaenAsnLyvValIleSerLyvSAAGvAnSer	779		
Db	2470	ACTAGTGTAAAAAGTTCCAAATCAACAAATPACAGGTAATCACTGTAAGAAATTC	2522		
QY	780	GluLeuLeuThrValGluTyrgIuGluIupheAsnHisGlnAspTrrpIuGluIyaen	797		
Db	2530	GAATTACTGACCGGTAGATATGAAAGATTTAACATCAAGATTGGAGAGAAAT	2583		
RESULT 3					
ID	AAA46205	standard; cDNA; 3263 BP.			
XX	AAA46205;				
XX	04-SEP-2000	(first entry)			
DT					
XX	cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).				
DE					
XX	Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;				
KW	chromosome 6q13-q15; ocular disease; retinal detachment;				
KW	chorioretinal degeneration; retinal degeneration; cone degeneration;				
KW	age related macular degeneration; photoreceptor degeneration;				
KW	retinal pigment epithelium degeneration; mucopolysaccharidosis;				
KW	rod-cone dystrophy; cone-rod dystrophy; ss.				
XX					
OS	Homo sapiens.				
XX					
FT	Key	Location/Qualifiers			
FT	CDS	128..244			
FT	/*tag= a				
FT	/transl_except= (pos: 2411..2414, aa: Lys)				
FT	/product= "interphotoreceptor matrix proteoglycan IPM150"				
XX					
PN	WO200026367-A2.				
XX					
PD	11-MAY-2000.				
XX					
XX	29-OCT-1999; 99WO-US025440.				
PF					
XX	29-OCT-1998; 98US-00183972.				
PR					
XX					
PA	(IOWA ) UNIV IOWA RES FOUND.				
XX					
PI	Hageman GS, Kuehn MH;				
XX					
DR	WPI; 2000-365616/31.				
XX					
DR	P-PsDB; AAY93336.				
XX					
PT	Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for				
PT	preventing, diagnosing and treating ocular disorders such as retinal				
PT	detachment and chorioretinal degeneration.				
XX					
PS	Claim 2; Fig 3; 183pp; English.				
XX					
CC	The present sequence encodes an interphotoreceptor matrix (IPM)				
CC	proteoglycan, designated IPM150. The protein is an IPM component (IPMC).				
CC	Two subfamilies of IPMC, IPM150 and IPM200, exist. The human IPM150 gene				
CC	is located on chromosome 6q13-q15, between markers CHLC.GAT11F10 and				
CC	D6S284. The IPM proteins may be used to supplement a patient's own				
CC	production of the protein or to rectify alterations in their nucleic				
CC	acids that result in expression of an inactive protein. The IPM nucleic				
CC	acids may be used in this way to treat ocular diseases such as retinal				
CC	detachment, chorioretinal degeneration, retinal degeneration, age related				
CC	macular degeneration, photoreceptor degeneration, RPS (retinal pigment				
CC	epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-				
CC	cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may				
CC	also be used to assay for other modulators of IPM proteoglycan expression				
CC	and activity that may be used to treat ocular diseases. The nucleic acids				

CC	and proteins may also be used as diagnostic reagents to detect the
CC	presence of 16 nucleic acids and their products in samples from patients
CC	according to standard methodologies
XX	
XX	Sequence 3263 BP; 1040 A; 721 C; 663 G; 838 T; 0 U; 1 Other;
Alignment Scores:	
Pred. No.:	4,92e-317 Length: 3263
Score:	4039.50 Matches: 794
Percent Similarity:	99.62% Conservative: 1
Best Local Similarity:	99.50% Mismatches: 2
Query Match:	98.12% Indels: 3
DB:	3 Gaps: 0
US-10-007-270-2 (1-797) x AAA46205 (1-3263)	
QY	1 MetTyrLeuGluGluThrArgArgAlaIlePheValIlePheTrpIlePheLeuGluValGlnGly 20
DB	128 ATGATATTTGGAAATCTAGAAAGACCTATTTTGTGATTTTCTCCAAAGTTCAAGGA 167
QY	21 ThrIysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
DB	188 ACTAAAGATATCTCCATTACATATACCTTTGTGAACCTAAAGACATACATATCCCCA 247
QY	41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60
DB	248 AGAAATGAACAACATGAAGTACTGAAAATATGTCAAAATATGTCAACTATAGACCAATA 307
QY	61 PheAspLeuAlaLysHisIleArgThrIysValSerAlaPhePheProThrGlyValLysVal 80
DB	308 TTCGATTTGGCAAAACATCGAACAATAAGATCCGATTTTCCCAACGGGGGTTAAAGTC 367
QY	81 CysPProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
DB	368 TGTCACACGAGANTCCATGAAACAGATTTTGAACGCTTCAAGCTTATATATAGATTGAGA 427
QY	101 ValCysGlnGluAlaValITrpGluAlaTyrArgGluIlePheLeuAspArgIleProAspThr 120
DB	428 GTGTGTCAAGAAAGCATATGGGAACATATATGGATCTTTCTGGATCGATCCCTGACACA 487
QY	121 GlyIuTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
DB	488 GGGGAATATCGAGACTGGGATCGAGATCTGCCGACGAGAACCTTCTGCTTTTGACATT 547
QY	141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgIleLysGln 160
DB	548 GGAATAAACTTCAGCAATTTCCACGAGGACCTCGGATCTTCTCAGACGAGAAATAAACAG 607
QY	161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
DB	608 AGAAGTTTCCCTGACAGAAAGATGAATATTTCTGCAGAGAAACATTTGGGAGAGCTGCT 667
QY	181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
DB	668 GAAACCATATTCATTTCAACAGATGTGCCAACGCTCACTTGAGGCTTTCCCTCCACT 727
QY	201 ProAspAspThrIleLeuAsnGluIleLeuAspAsnThrIleAsnAspThrLysMetPro 220
DB	728 CCTGATGACACCTCTCCATGAATATTTCTCGATTAATACCTACACACCAAGATGCCCT 787
QY	221 ThrThrArgLysArgLysThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerVal 240
DB	788 ACACACAGAAAGAAACAGAAATTCCTGTGTGGAGACACAGAGGTGAGCTCAACGCTC 847
QY	241 SerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGln 260
DB	848 TCTCTGGTAAACCAAGACTTCAAGCACAAGGCTCGCTGACTCCCAAGTCCCATATTAACAAG 907
QY	261 GluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPhe 280
DB	908 GAGCTACAGAGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAACTTCACAGATTC 967
QY	281 LysLysIleHisValLeuGluIlePheArgProLysGluLysAspGlySerSerSerThr 300

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Db      ||| 968 AAAAAATCCATGCTTAGATTAGACCAAGAAAAGAAAGATGCTCAAGCTCCACA 1027
Qy      ||| 301 GJumetGlnLeuThrAlaIlePheIysArgHisSerAlaGluAlaIysSerProAlaSer 320
Db      ||| 1028 GAGATGCAACTTAACGGCCATCTTTAAGACACAGGAGAGAGAAAAGCCCTCGCAAT 1087
Qy      ||| 321 AApLeuSerPheApeSerAenlysiIleGluSerGluValTyrHisGlyThrMet 340
Db      ||| 1088 GACCTCCTCTCTTTGATTCCAAAGAAATTTGAAAGAGAGAGAGTCTATATGGAACATG 1147
Qy      ||| 341 GJugLysPLeuGlnProGluIleTyrLeuThrAlaThrAspLeuIysArgLeuIleSer 360
Db      ||| 1148 GAGGAGACACAGCAACCAAAATCTATCTACAGCTACAGACTCAAAAGGCTGATCAGC 1207
Qy      ||| 361 LysAlaLeuGlnGlnGlnGlnSerLeuAapValGlyThrIleGlnPheThrAspGluIle 380
Db      ||| 1208 AAGGACCTAGAGAAACAAATCTTGGATGTGGGACAAATTCAGTTCACTATGAAAT 1267
Qy      ||| 381 AlaGlySerLeuProAlaPheGlyProAapThrGlnSerGluLeuProThrSerPheAla 400
Db      ||| 1268 GCTGGATCACTGCAAGCTTTGGTCTCTGACACCAATCAGAGTGGCCACATCTTTGCT 1327
Qy      ||| 401 ValIleThrGluAspAlaThrIleuSerProGluLeuProValGluProGlnLeuGlu 420
Db      ||| 1328 GTTATTAACAGAGATGCTACTTGTGAGTCCAGAACTTCTCTGTGAAACCCAGCTTGAG 1387
Qy      ||| 421 ThrValAspGlyAlaGluIleGlyLeuProAapThrSerThrSerProProAlaMetAla 440
Db      ||| 1388 ACGAGTGAAGAGACAGACAGATGTCTACCTGACACTTCTGTGCTCACCTGCTATAGGC 1447
Qy      ||| 441 SerThrSerLeuSerGluAlaProProphePheMetAlaSerSerIlePheSerLeuThr 460
Db      ||| 1448 TCTACTCTCCTGTCAAGACTCCACTTTCTTATGATCAAGCATCTTCTCTGAT 1507
Qy      ||| 461 AapGlnGlyThrThrAspThrMetAlaThrAapGlnThrMetLeuValProGlyLeuThr 480
Db      ||| 1508 GATCAAGGACACCAACATCAATGCGCAGTCAACAAACATGCTAGTACAGAGCTCACCC 1567
Qy      ||| 481 IleProThrSerAspThrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500
Db      ||| 1568 ATCCCAACAGATGATTAATCTGCAATCAGCACTGCTCTGGAAATTTCCATCCACT 1627
Qy      ||| 501 AlaSerSerAspApeSerAenlysiIleGlyGluAspMetAlaArgHisLeuAap 520
Db      ||| 1628 GCATCTTCAGATGACAGCCGATCAAGTCAAGTGGGAGAGATGTGTCAGACACCTAGAT 1687
Qy      ||| 521 GJumetAapLeuSerAapThrProAlaProSerGluValProGluLeuSerGluTyrVal 540
Db      ||| 1688 GAAATGATCTGTCTGACACTCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATGTT 1747
Qy      ||| 541 SerValProAapHisPheLeuGlnAapThrThrProValSerAlaLeuGlnTyrIleThr 560
Db      ||| 1748 TCTGTCCAGATATTTCTTGAGATACACCTCTGCTCAAGCTTTACAGTATATCACCC 1807
Qy      ||| 561 ThrSerSerMetThrIleAlaProLysGlyArgGluLeuValPhePheSerLeuAap 580
Db      ||| 1808 ACTAGTTCTATGACCAATGGCCCAAGGGCCGAGACTGGTAGTGTCTTCAGTCTGGCT 1867
Qy      ||| 581 ValAlaAsnMetAlaPheSerAenlysiIleGluLeuPheAsnLysSerLeuGluTyrAla 600
Db      ||| 1868 GTTGCTAACATGGCTCTTCCCAAGACCTGTTCAACAGAGCTCTGAGGTACCGAGCT 1927
Qy      ||| 601 LeuGlnGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAenlysiIleThr 620
Db      ||| 1928 CTGGAGCAACAATTCACAGCTGTGTGCTCAATCTAGATCCATCTTACAGGATTT 1987
Qy      ||| 621 LysGlnLeuGluIleLeuAenPheArgAenGlySerValIleValAsnSerLysMetLys 640
Db      ||| 1988 AAGCAACTTGAATATCTTAATCTCAGAAACGGAGGTGATTTGTGAATACAAAAGAAAG 2047
Qy      ||| 641 PheAlaLysSerValProTyrAenLeuThrLysAlaValHisGlyValLeuGluAapPhe 660

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Db      ||| 2048 TTTCCTAAGTCTGTGCTGCTATTAACCTCACCAAGGCTGTGACAGGGGCTTGGAGATTTT 2107
Qy      ||| 661 ArgSerAlaIleAlaGlnGlnLeuHisIleuGluIleAapSerTyrSerLeuAsnIleGlu 680
Db      ||| 2108 GCTTCTGCTGACGCCCAACAATCTCATCTGGAATAAGACGCTACTCTCTCAACATGAA 2167
Qy      ||| 681 ProAlaAapGlnAlaAapProCyseIysPheLeuAlaCyseGlyGluPheAlaGlnCyseVal 700
Db      ||| 2168 CCAAGTATCAAGCAGATCCCTGCAAGTTCTCTGGCTGGGGGAAATTTGGCCAAATGTGA 2227
Qy      ||| 701 LysAenGluAgtThrGlnGlnAlaGluCyseArgCyseIysProGlyTyrAspSerGlnGly 720
Db      ||| 2228 AAGAACGAACGACCTGAGAAAGCGAGGTGCTGCCAACCAAGATATGACAGCGAGG 2287
Qy      ||| 721 SerLeuAapGlyLeuGluProGlyLeuCyseGlyProGlyTyrThrIleGlyLeuValLeu 740
Db      ||| 2288 AGCTGAGCGGCTGGAACCAAGCCTCTGTGG-CTGGACCAAAAGAAATGCAAGGTCCTC 2346
Qy      ||| 741 GlnGlyLysGlyAlaProCyseArgLeuProAapHisSerGluAenGlnAlaTyrLysThr 760
Db      ||| 2347 CAGGAAAGGAGAGCTCCATGGG--GTTCCAGATCACTCGAAATCAAGCATACAAAAT 2404
Qy      ||| 761 SerValLysLysPheGlnAenGlnAenAenlysiValIleSerLysArgAenSerGlu 780
Db      ||| 2405 AGTGTAAAGAAATTCAAATCCAAATCAACAAATGAACAGTAACTCAAGAAATTTCTGAA 2464
Qy      ||| 781 Leu-LeuThrValGluTyrGlnGluPheAenHisGlnAapTyrGluGlyAen 797
Db      ||| 2465 TTATCTGACCGTAGAATATGAAGAAATTTAACATCAAGATTTGGAGAGAAAT 2516

RESULT 4
ACCS7960
ID      ACCS7960 standard; cDNA, 3261 BP.
XX
AC      ACCS7960;
XX
DT      11-AUG-2003 (first entry)
XX
DE      Human Interphotoreceptor matrix IPM 150, isoform A variant, cDNA.
XX
KW      Human; Interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX      receptor; ophthalmological; gene therapy; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      128..2443
FT      FT      /*tag= a
FT      FT      /product= "IPM 150"
XX
PN      MO2003039346-A2.
XX
PD      15-MAY-2003.
XX
PF      08-NOV-2002; 2002WO-US036090.
XX
PR      08-NOV-2001; 2001US-00077270.
XX
PA      (IOWA ) UNTIV IOWA RES FOUND.
XX
PI      Hageman GS, Kuehn MH;
XX
DR      MPI; 2003-441440/41.
XX
DR      P-PSDB; ABR42354.
XX
PT      New interphotoreceptor matrix proteins and polynucleotides, useful for
XX      treating or preventing photoreceptor death or retinal detachment, or for
XX      treating ocular disorders.
XX
PS      Claim 1; Page 91-94; 105pp; English.
XX
CC      The present sequence is that of cDNA encoding a variant of isoform A of
XX      novel human interphotoreceptor matrix 150 (IPM 150), a member of the

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CC newly identified interphotoreceptor matrix component (IPMC) gene family.  
 CC The cDNA was isolated from a human retinal cDNA library. The IMP 150 gene  
 CC is located on chromosome 6q13-q15, a region that also contains loci for  
 CC progressive bilateral choriorretinal atrophy, autosomal dominant Stargard's  
 CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
 CC disease. Members of the IPMC gene family have been identified in humans,  
 CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
 CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
 CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
 CC antibodies that specifically bind the polypeptides, and vectors  
 CC comprising the polynucleotides. A claimed method of treating or  
 CC preventing photoreceptor death or retinal detachment involves  
 CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
 CC claimed is a method for identifying a compound capable of modulating IPMC  
 CC gene expression

XX Sequence 3261 BP, 1039 A, 721 C, 663 G, 837 T, 0 U, 1 Other;

## Alignment Scores:

Pred. No.:	6,896-316	Length:	3261
Score:	4024.50	Matches:	793
Percent Similarity:	99.62%	Conservative:	1
Best Local Similarity:	99.50%	Mismatches:	3
Query Match:	97.75%	Indels:	3
DB:	9	Gaps:	0

US-10-007-270-2 (1-797) x ACCS7960 (1-3261)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValIlePheTrpIlePheLeuGluValGlnGly 20  
 DB 128 ATGTAATTCGAAACATAGAAAGACTATTTTGTGTTTGGATTTTTCCTCAATTCAGAGA 187  
 QY 21 ThrIleAspIleSerIleAsnIleTyrIleSerGluThrIleAspIleAspIleProPro 40  
 DB 188 ACTAAAGATATCTCATTAACATATACCATCTCGAAACTAAAGACATAGACATCCCCCA 247  
 QY 41 ArgAsnGluThrThrGluSerThrGluIleMetTyrIleMetSerThrMetArgArgIle 60  
 DB 248 AGAAATGAAACACTGAAAGTCTGAAAGAAATGTAACAAATCTCAACTATGAGAGAAATA 307  
 QY 61 PheAspLeuAlaIleAsnIleAsnIleTyrIleAspIleAspIleProProIleValIleVal 80  
 DB 308 TTGCAATTCGCAAGACATGAGCAAAAGATCCGATTTTCCCAACGGGGTTTAAAGTC 367  
 QY 81 CysPheGlnGluSerMetIleGlnIleLeuAspSerLeuGlnAlaIleTyrIleArgLeuArg 100  
 DB 368 TGTCCACAGGATCATGAAACAGATTTTACAGCTTCAAGCTTATATAGATTGAGA 427  
 QY 101 ValCysGlnGluAlaIleValIleTyrGluAlaIleTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 428 GTGTCTCAGGAAGCATGATGGAGACATATCGGATCTTTCGATCGCATCCCTGACACA 487  
 QY 121 GlyIleTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 488 GGGGAATTCAGGATCGGCTGCGATCTGCCACGAGAGACCTTCTGCTCTTTGACATT 547  
 QY 141 GlyIleAsnPheSerAsnSerGlnIleIleLeuAspLeuLeuGlnIleArgIleIleGln 160  
 DB 548 GGAATAAACTTCAGCAATTCCTCCAGAGACCTCGATCTTCTCCACAGAAATAAACAAG 607  
 QY 161 ArgSerPheProAspArgIleAspGluIleSerAlaGluIleValIleGluIleGluProGly 180  
 DB 608 AGAATCTTCCTCAGCAGAAAGATGAAATATCTGACAGAAAGACATGGAGAGGCTGAT 667  
 QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 DB 668 GAAACCATGTCATTTCAACAGATGTTGCCACGCTCACTGGGCTCTTCCCTCTCACT 727  
 QY 201 ProAspAspThrIleLeuAsnGluIleLeuAspAsnThrIleAsnAspThrIleMetPro 220  
 DB 728 CTTGATGACACCTCTCTCAATGAAATTTCTCGATTAATACCTCAACAGACCAAGATGCT 787  
 QY 221 ThrThrGluArgGluThrGluPheAlaValIleGluGluGlnArgValGluLeuSerVal 240

DB 768 ACAACGAAAGGAAACAGATTCCTGTTGGAGGACAGAGGTGAGCTCAGCGTC 847  
 QY 241 SerIleValIleGlnIlePheIleValIleGluAlaIleAspSerGlnSerProTyrIleGln 260  
 DB 848 TCTGTGTAAACCAAGAGATTCAAGGACAGAGCTCGCTGACTCCCACTTCCATATTAACAG 907  
 QY 261 GluLeuAlaGlyIleSerGlnIleGlnIleMetGlnIleIlePheIleValIleLeuProGlyPhe 280  
 DB 908 GAGCTAGAGAGAAATCTCCAACTTCAGATGCAAAAGATATTTAATAAACTTCACAGATTC 967  
 QY 281 LysIleIleIleIleValIleGluIlePheArgProIleValIleGluIleValIleSerSerThr 300  
 DB 968 AAAAAATCCATGTCTTGGATTTAGACCAAGAAAGAAAGAAAGATGCTCAAGCTCCACA 1027  
 QY 301 GluMetGlnLeuThrAlaIlePheIleValIleIleSerAlaGluAlaIleValIleSerProIleSer 320  
 DB 1028 GAGATGCAACTTACGGCCATCTTTAAAGAGACACAGTCAGAAAGCAAAAGCCCTGCAAGT 1087  
 QY 321 AspLeuLeuSerPheAspSerAsnIleIleGluSerGluGluValIleTyrIleGlyIleThrMet 340  
 DB 1088 GACCTCCGTCTTGTGATTCACAAATAAGTGAAGTGTATCATGGAACCAATG 1147  
 QY 341 GluGluAspIleGlnProGluIleIleTyrIleThrAlaIleThrAspLeuIleValIleSer 360  
 DB 1148 GAGAGGACAGACCAAGCAAGAAATCTATCTCACAGCTTACAGACCTCAAAAGGCTGATCAGC 1207  
 QY 361 LysAlaLeuGluGluGluGlnIleSerIleValIleGlyIleGlnIlePheThrAspGluIle 380  
 DB 1208 AAAGACATAGAGGAAGCAATCTTGTGATGGGGAACAATTCAGTTCACTGATGAATTT 1267  
 QY 381 AlaGlySerIleProAlaIlePheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
 DB 1268 GCTGATCATCTGCAAGCTTGTGCTTGCACACCAATCAGAGCTCCACATCTTTTCT 1327  
 QY 401 ValIleThrGluAspAlaIleThrLeuSerProGluLeuProProValGluProGluIleGlu 420  
 DB 1328 GTTATACAGAGATGCTACTTGTGATGCTCAAGACTTCTCTGTTAAACCCAGCTTAG 1387  
 QY 421 ThrValAspGlyAlaGluIleGlyLeuProAspThrSerTrpSerProProAlaIleMetAla 440  
 DB 1388 ACAGTGAGCGAGAGACAGACATGCTTACCTACCACTTCTGTCCACCTGCTATGAGC 1447  
 QY 441 SerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThr 460  
 DB 1448 TCTACTCTCCGTGAGAGAGCTCCACCTTCTTATGTCATAGCATCTTCTCTGACT 1507  
 QY 461 AspGlnGlyThrThrAspThrMetAlaThrAspGlnIleThrMetLeuValProGlyLeuThr 480  
 DB 1508 GATCAGGACACACAGATACAAATGAGCCACTGACAGACAAATGCTAGTACAGGGCTCAC 1567  
 QY 481 IleProThrSerAspIleValIleSerGlnIleValIleSerIleAspProPro 500  
 DB 1568 ATCCCACTCATGATATATCTGCAATCAGCCAACTGCTCTGGAAATTTCACTCACT 1627  
 QY 501 AlaSerSerAspAspSerArgSerSerAlaGlyIleGlyIleAspMetValIleArgIleLeuAsp 520  
 DB 1628 GCATCTTCAGATGACAGCGCATCAAGTCAGAGTGGCGAAATATATGTCAGACACCTAGAT 1687  
 QY 521 GluMetAspLeuSerAspThrProAlaProSerGluValIleProGluLeuSerGluTyrVal 540  
 DB 1688 GAAATGATCTGTCTGACACTCTGCCCATCTGAGTACAGAGCTCAGGAAATATTT 1747  
 QY 541 SerValProAspIlePheLeuGluIleAspThrThrProValSerAlaLeuGlnIleThr 560  
 DB 1748 TCTGTCCAGATCATTTCTTGGAGATACCACTCTGCTCAGCTTATACATATATCAAC 1807  
 QY 561 ThrSerSerMetThrIleAlaProIleGlyIleArgGluLeuValIlePhePheSerLeuArg 580  
 DB 1808 ACTAGTTCTATGACCATTTGCCCCCAAGGGCGAGAGCTGTGATGTTCTTCACTGCTGCT 1867  
 QY 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnIleValIleSerSerIleGluTyrArgAla 600

Db 1868 GTTGCTAACATGACCTCTCCACGACCTGTTCAACAAAGCTCTGAGTACCGAGCT 1927  
QY LeuGluGlnGlnPheThrGluLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 1928 CTGGAGCAACATTCACACAGCTGCTGGTTCATATCTCAATCCAACTTCATACAGATTT 1987  
QY LysGlnLeuGlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
Db 1988 AAGCAACTTGAAATCTTAATTCACTTACAGAAACGGGAGTGTGATGTGAATAGCAAAATGAAG 2047  
QY PheAlaLysSerValProTyrAsnLeuThrLysAlaValHleGlyValLeuGlnAspPhe 660  
Db 2048 TTTGCTAAGTCTGTCGCGTATACCTCACCAAGGCTGTGACGCGGCTTTGAGAGATTTT 2107  
QY ArgSerAlaAlaGlnGlnLeuHleuGlnIleAspSerTyrSerLeuAsnIleGln 680  
Db 2108 GATTCTGCTGACGCCCAACACTCCATCTGGAATAGACAGTACTCTCTCAACATTA 2167  
QY ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGlnPheAlaGlnCysVal 700  
Db 2168 CCAAGCTGATCAAGCAGATCCCTGCAAGTCTGCGCTGCGGCGAATTTGCCAATGTGTA 2227  
QY LysAsnGluArgThrGlnGlnAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720  
Db 2228 AAGAAGCAACGGAAGTGAAGGAGGAGTGTGCTGCAACAGATATGACAGCGAGGG 2287  
QY SerLeuAspGlyLeuGlnProGlyLeuCysGlyProGlyTyrThyGlnCysGlnValLeu 740  
Db 2288 AGCCGTGACGCTGTGAACAGGCTGTGTGG-CTGGGCAAAAGAAATGCGAGGTCTGC 2346  
QY GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGlnAsnGlnAlaTyrLysThr 760  
Db 2347 CAGGGAAGGAGGAGCTCCATGCG--GTTCAGATCACTCTGAAATACAGCAATACAAACT 2404  
QY SerValLysLysPheGlnAsnGlnGlnAsnValIleSerLysArgAsnSerGln 780  
Db 2405 AGTGTTTAA-AGTTCCAAAATCAACAAATTAACAAGTATCATGTAAGAAATCTGAA 2463  
QY LeuLeuThrValGluTyrGlnGlnPheAsnHleGlnAspTyrGlnGlyAsn 797  
Db 2464 TTACTGACCGTGAATATGAAATTTAACATCAAGATTGGGAAAGAAAT 2514  
RESULT 5  
ID ADA14866 standard; cDNA; 3261 BP.  
XX ADA14866;  
AC ADA14866;  
XX  
XX  
XX 06-NOV-2003 (first entry)  
XX  
XX Human cDNA encoding variant IPMC 150 isoform A.  
XX  
XX  
XX ss; gene; human; IPMC 150 isoform A; gene therapy;  
XX interphotoreceptor matrix component; IPMC; ocular disorder;  
XX macular degeneration; photoreceptor death; retinal detachment.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FH 128..2443  
XX FT /tag= a  
XX FT /product= "Variant IPMC 150 isoform A"  
XX  
XX US2002160954-A1.  
XX  
XX 31-OCT-2002.  
XX  
XX 08-NOV-2001; 2001US-00007270.  
XX  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;  
PI WPI: 2003-238235/23.  
DR P-PSDB; ADA14867.  
XX  
XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.  
XX  
XX Claim 3; Page 63-66; 76pp; English.  
XX  
XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding  
CC variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
XX  
SQ Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;  
Alignment Scores:  
Pred. No.: 6,896-316 Length: 3261  
Score: 4024.50 Matches: 793  
Percent Similarity: 99.62% Conservative: 1  
Best Local Similarity: 99.50% Mismatches: 3  
Query Match: 97.75% Indels: 3  
DB: 10 Gaps: 0  
US-10-007-270-2 (1-797) x ADA14866 (1-3261)  
QY 1 MetTyrLeuGlnThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
Db 128 ATGTATTTGGAAATCATGAAGAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGGA 187  
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
Db 188 ACTAAAGATATCTCATTAACATATACCATCTGAACTTAAGATGACATGACAAATCCCCCA 247  
QY 41 ArgAsnGluThrTrpGlnGlnSerThrGlnLysMetLysMetSerThrMetArgArgIle 60  
Db 248 AGAAATGAAACACTGAAAGTACTGAAAGAAATGTAACAATGTCATATAGACGAATTA 307  
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
Db 308 TTGCATTTGGCAAGAGCATCGAACAAGATCCGCAATTTTCCCAAGGGGTTTAAAGTC 367  
QY 81 CysProGlnGlnSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
Db 368 TGTCACAGAGATCATGAAACAGATTTTAAACAGTCTTCAAGCTTATATAGATTGAGA 427  
QY 101 ValCysGlnGlnAlaValTyrGlnAlaTyrArgIlePheLeuAspArgIleProAspPhe 120  
Db 428 GTGTGTCAAGAGCAAGTATGAGGAAAGCATATGAGATCTTTCGAGTCGATCCGACACA 487  
QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle 140  
Db 488 GGGGAATTCAGAGATGAGTGCATCTGCCAGCAGAGAGACCTTGTGCTCTTTGACATT 547  
QY 141 GlyLysAsnPheSerAsnSerGlnGlnIleLeuAspLeuLeuGlnGlnArgIleLysGln 160  
Db 548 GGAATAAACTTCAGCAATTCACAGAGACCTGATCTTCTCCAGCAAGATAAAGAG 607  
QY 161 ArgSerPheProAspArgLysAspGlnIleSerAlaGluTyrThrLeuGlnGluProGly 180  
Db 608 AGAAGTTTCCCTGACAGAAAGATGAATATCTGCAAGGAAGACATTTGGAGAGCTTGT 667  
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200





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Db      1211 GCAATCAGCCAACTGCGCTGGGAATTTCACATCCATCGATCTTCAGATGACAGCCGA 1270
QY      508 SerSerAlaGlyGlyGluAspMetValAlaGHisLeuAspGluMetCysLeuSerAspThr 527
Db      1271 TCAAGTGCAGGTGGCCAAAGATATGTGTGACAGCACCTGAAATGATATGCTGTGACACT 1330
QY      528 ProAlaProSerGluValProGluLeuSerGluTyValSerValProAspHisPheLeu 547
Db      1331 CCGCCCCCATCTGAGGTACCGAGGCTCAGCGAATAGCTTTCTGTCCAGATCAATTTCTTG 1390
QY      548 GluAspThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAla 567
Db      1391 GAGGATACCACTCTGCTGCTCAGCTTACAGTATATACCACTAGTCTTATGACATTGGCC 1450
QY      568 ProValGlyValArgIleuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db      1451 CCCAAGGCGGAGAGCTGTGATGTCTTCAGTCTCGTGTGCTTAACTAGGCTCTTCCG 1510
QY      588 AsnAspLeuPheAsnLysSerSerLeuGluTyTrArgAlaLeuGlnGlnPheThrGln 607
Db      1511 AACGACCTGTTCAACAAGAGCTCTTGAGATACCGAGCTCTGGAGCAACATTCACACAG 1570
QY      608 LeuLeuValProTyLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
Db      1571 CTGCTGCTTCCATATCTACGATCCATCTTACAGATTTAAGCACTTGAAATACTTAAC 1630
QY      628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTy 647
Db      1631 TTCAGAAACGGGAGTGTGATTGTGAATAGCAAAATAGATTGCTAAGCTGTGCGGTAT 1690
QY      648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667
Db      1691 AACCTACCAAGGCTGTGACGGGGCTTGAGAGATTTCGTTCTCTGAGAGCCCAACAA 1750
QY      668 LeuHisLeuGluIleAspSerTyTrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687
Db      1751 CTCGATCTGGAAATATACAGCTACTCTCTCAATTTGAACAGCACTGATCAAGAGATCCC 1810
QY      688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValIleAsnGluArgThrGlnGlu 707
Db      1811 TCGAAGTCTCGGCTGCGCGCGCAATTGCGCAATGTGTAAAGAACGACGACTGAGGAA 1870
QY      708 AlaGluCysArgCysLysProGlyTyTrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
Db      1871 GCGGAATGTGCTGCGCAACGAGATATGACAGCGAGGAGCTTGACGCTGGAACCA 1930
QY      728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db      1931 GGCCTCTGTGGCCCTGGCACAAAGAAATGCGAGTCTCTCAGGGAAGGAGGAGCTCCATGC 1990
QY      748 ArgLeuProAspHisSerGluAsnGlnAlaTyTrLysThrSerValLysLysPheGlnAsn 767
Db      1991 AGGTTCAGATCATCTGAAATATCAAGCATTAACAAACTAAGTGTAAAGTTCCAAAT 2050
QY      768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyGlu 787
Db      2051 CAACAAATAAACAAGGTAAATCACTAAAGAAATTCGAATTACTGACCGTAGAATATGAA 2110
QY      788 GluPheAsnHisGlnAspTrpGluGlyAsn 797
Db      2111 GAATTTAACATCAAGATTGGAGAGGAAT 2140

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RESULT 7
ADAl4842
ID      ADAl4842 standard; cDNA; 2887 BP.
XX
AC      ADAl4842;
XX
DT      06-NOV-2003 (first entry)
XX
DE      Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.
XX
KW      89; gene; human; IPMC 150 isoform B; gene therapy;

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KW      interphotoreceptor matrix component; IPMC; ocular disorder;
KW      macular degeneration; photoreceptor death; retinal detachment.
XX
OS      Homo sapiens.
XX
XX
FH      Key      Location/Qualifiers
FT      CDS      5..2143
FT              /tag=a
FT              /partial
FT              /product= "IPMC 150 isoform B"
FT              /note= "No start codon given. Encodes residues 8-719 of
FT              {seqid:4}"
PN      US2002160954-A1.
PD      31-OCT-2002.
XX
PF      08-NOV-2001; 2001US-00007270.
XX
PR      29-OCT-1998; 98US-00183972.
PR      29-OCT-1999; 99US-00430195.
XX
PA      (IOWA ) UNIV IOWA RES FOUND.
PI      Hageman GS, Kuehn MH;
XX
DR      WPI; 2003-238235/23.
DR      P-PSDB; ADAl4843.
XX
PT      New isolated or recombinant interphotoreceptor matrix component
PT      polynucleotide and polypeptide, useful for diagnosing, preventing,
PT      treating or prognosticating ocular disorders, e.g. macular degeneration
PT      or retinal detachment.
XX
PS      Claim 3; Page 33-34; 76pp; English.
XX
CC      The invention relates to an isolated or recombinant interphotoreceptor
CC      matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC      comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC      gene operatively linked to the IPMC polynucleotide. The IPMC
CC      polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC      preventing, treating or prognosticating ocular disorders, e.g. macular
CC      degeneration, photoreceptor death or retinal detachment. They are also
CC      useful for identifying a compound capable of modulating IPMC gene
CC      expression in a cell. The present sequence represents cDNA encoding human
CC      interphotoreceptor matrix component, IPMC, 150 isoform B.
XX
SQ      Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.:      4,22e-283      Length:      2887
Score:          3619.00      Matches:      711
Percent Similarity: 90.00%      Conservative: 0
Best Local Similarity: 90.00%      Mismatches: 1
Query Match:      87.90%      Indels:      78
DB:              10      Gaps:      1

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US-10-007-270-2 (1-797) x ADAl4842 (1-2887)
QY      8 AlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27
Db      5 GCTATTTTGTGATTTTGTGATTTTCTCCAAAGTTCAAGAACCAAA----- 49
QY      28 IleTyHisSerGluThrLysAspIleAspAsnProArgAsnGluThrThrGluSer 47
Db      49 ----- 49
QY      48 ThrGluLysMetTyTrLysMetSerThrMetArgAlaIlePheAspLeuAlaLysHisArg 67
Db      49 ----- 49
QY      68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysPProGlnGlnLysMetLys 87

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Db 49 ----- 49  
 QY 68 GlnIleuAspSerLeuGlnAlaIrrYrYrArgLeuArgValCyGlnGlnIuAlaValTrp 107  
 Db 50 ----- 70  
 QY 108 GlnAlaIrrYrArgIlePheLeuAspArgIleProAspThrGlyGluYrYrGlnAspTrpVal 127  
 Db 71 GAAGATATTCGATCTTTCTGATGCATCCCTGACACAGGGGAATATACAGACCTGGGTC 130  
 QY 128 SerIleCyGlnGlnGluThrPheCyLeuPheAspIleGlyLyAsnPheserAsnSer 147  
 Db 131 AGCATCTGCACAGACAGACTTCTGCTTGTGACATTGGAAGAAAACCTTCGACATTC 190  
 QY 148 GlnGluHleuAspLeuGlnGlnIuArgIleLyAsnIuArgSerPheProAspArgIys 167  
 Db 191 CAGGAGACCTGATCTCTCCAGCAGAGAAATPAAACAGAGAAATTTCCCTGACAGAAA 250  
 QY 168 AspGluIleSerAlaGlyIuYrThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
 Db 251 GATGAAATATCTGCAGAGAAAGACATTGGAGAGCCTGGGAAACCATTTCTCATTTCAACA 310  
 QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
 Db 311 GATGTTGCCAAGCTCTCACTGGGCTTTCCCTCTCACTCGATGACACCTCTCTCAAT 370  
 QY 208 GlnIleuAspAsnThrLeuAspAspThrIlyAsnMetProThrThrGluArgGluThrGlu 227  
 Db 371 GAAATTTCTGATTAATACACTCAACAGACCAAGATGCTTCAACAGAAAGAAACAGAA 430  
 QY 228 PheAlaValIleuGlnGluIuArgValGluLeuSerValSerLeuValAsnGlnIysPhe 247  
 Db 431 TTCGCTGTCTGAGAGAGAGAGAGGCTGAGCTCAAGCTCTCTCTGTTAAACAGAAAGTTC 490  
 QY 248 IyValIleGluLeuAlaAspSerGlnSerProYrYrYrGlnGluLeuAlaGlyIysSerGln 267  
 Db 491 AAGGCGAGAGCTCGTCACTCCAGCTCCCATTTACAGAGACTGACAGAAAGGCCCA 550  
 QY 268 LeuGlnMetGlnIyIlePheIyIyIyLeuProGlyPheIyIyIleIleIleValIleuGly 287  
 Db 551 CTTCGATGCAGAAAGATATTTAAGAACTTCCAGGATTCAGAAATTCATGTGTAGGA 610  
 QY 288 PheArgProLyLeuGlyIyIyAspGlySerSerSerThrGluMetGlnLeuThrAlaIle 307  
 Db 611 TTTAGCCAAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAATTACGGCCATC 670  
 QY 308 PheIyAspArgIleSerAlaGluAlaIySerProAlaSerAspLeuLeuSerPheAspSer 327  
 Db 671 TTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGTGAACCTCTCTTTGATTCC 730  
 QY 328 AsnIyValIleGluSerGlnIuValIyIleGlyIyThrMetGlnIuAspIyAsnProGlu 347  
 Db 731 AACAAATTTGAAAGAGAGAGAGCTATCATGAAACCATGAGAGAGACAAAGCAACAGAA 790  
 QY 348 IleYrLeuThrAlaIrrAspLeuIyAspGlyIleSerIyAlaLeuGlnIuGlnIuGln 367  
 Db 791 ATCTATCTCAAGCTACAGCTCTCAAAAGCTGATAGCAAAAGCACTAGAGAAAGAAACA 850  
 QY 368 SerLeuAspValIyIrrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
 Db 851 TCTTTGATGTGGGACAATTCACTGATGAAATGCTGATCACTGCACAGGCTTT 910  
 QY 388 GlyProAspThrGlnSerGluLeuPProThrSerPheAlaValIleThrGluAspAlaThr 407  
 Db 911 GGCTCCGAGACCCAAATCAGAGCTGCCACATCTTTGCTGTTATTAACAAGAGATGTCTACT 970  
 QY 408 LeuSerProGluLeuProProValIyGluProGlnLeuGluThrValAspGlyAlaGluHle 427  
 Db 971 TTGAGTCCAGAACTTCTCTCTGTTGAACCCAGCTTGAACAGTGAACGAGACAGAGCAT 1030  
 QY 428 GlyLeuProAspThrSerIrrPserProProAlaMetAlaSerThrSerLeuSerGluAla 447  
 Db 1031 GGCTCACTGACACTTCTTGCTCTCAACCTGCTATAGGCTCTACCTCCCTGTCAGAAAGCT 1090

QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467  
 Db 1091 CCACCTTTCTTTATGGCATCAAGCATCTTCTCTGACTGATTCAGAGCAACAGATATCA 1150  
 QY 468 MetAlaIrrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTrpSer 487  
 Db 1151 ATGGCACTGACAGACAAATCTAGTACAGAGGCTCACACATCCCAACAGAGATTAATCT 1210  
 QY 488 AlaIleSerGlnIuAlaLeuGlyIleSerIleProProAlaSerSerAspAspSerArg 507  
 Db 1211 GCAATCAGCCAACTGGCTCTGGGAATTCACATCACTGATCTTCAGATGACAGCCGA 1270  
 QY 508 SerSerAlaGlyIyGlyIyAspMetValArgIleIleuAspGluMetAspLeuSerAspThr 527  
 Db 1271 TCAGTGCAGGTGGCGAAGATATGTGTCAAGACCTAGATGAATATGATCTGTCAACCT 1330  
 QY 528 ProAlaProSerGluValProGluLeuSerGluYrYrValSerValProAspPhePheLeu 547  
 Db 1331 CTGCCCCATCTGAGGTATCCAGGGCTCAGCAATATAGTTTCTGTGCCAGATCATTTCTTG 1390  
 QY 548 GluAspThrThrProValSerAlaLeuGlnIyIrrIleThrThrSerSerMetThrIleAla 567  
 Db 1391 GAGGATACCACTCTCTGCTCAGCTTACAGTATACACACTAGTCTATAGACCAATGCC 1450  
 QY 568 ProIySGlyArgGluLeuValIlePhePheSerLeuArgValAlaAsnMetAlaPheSer 587  
 Db 1451 CCAGAGGCGCAAGACTGTATGTGTCTTCAAGTCTGCTGCTGCTGCTTCAATAGGCTTCC 1510  
 QY 588 AsnAspLeuPheAsnIySerSerLeuGluYrYrArgAlaLeuGlnGlnIuPheThrGln 607  
 Db 1511 AACGACCTGTTCAACAAGAGCTCTTGAGATACGAGCTCGAGACAACAATTCAACAG 1570  
 QY 608 LeuLeuValProYrIleuAspSerAsnLeuThrGlyPheIySGlnIleuGlnIleuAsn 627  
 Db 1571 CTGCTGTTCCATATCTACAGATCCAAATCTTACAGATTTAAGCACTTGAATATCTTAC 1630  
 QY 628 PheArgAsnGlySerValIleValAsnSerIyMetIyPheAlaIySerValProYr 647  
 Db 1631 TTCAGAAACGAGAGTGTATGTGATATGCAAAATGAAGTTTCTGAATCTGTGCCGAT 1690  
 QY 648 AsnLeuThrIyAlaValIleGlyValIleuGluAspPheArgSerAlaAlaGlnGln 667  
 Db 1691 AACCTCAACAAGGCTGTGCAAGGCTTGGAGATTTCTGTTCTGTCGAGCCCAACA 1750  
 QY 668 LeuHleuGlnIleAspSerTrpSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687  
 Db 1751 CTCCATCTGGAATATGACAGCTACTCTCTCAACATTGAACAGCTGATCAAGCAGATCC 1810  
 QY 688 CysIyPheLeuAlaCyGlyGluPheAlaGlnCyValIyAsnGluArgThrGlnGlu 707  
 Db 1811 TGCAGTTCTGGCTGGCGGAAATTTGCCAAATGTGAAGAAAGAAACGAGATGAGAA 1870  
 QY 708 AlaGluCyArgCyIyProGlyYrAspSerGlnIySerLeuAspGlyLeuGluPro 727  
 Db 1871 GCGAGTGTCCGTGAAACAGAGATATGACAGCCAGGGAAGCTGAGCTGGAACA 1930  
 QY 728 GlyLeuCyGlyIyProGlyThrIySGluCySGluValIleuGlnGlyIySGlyAlaProCyS 747  
 Db 1931 GGCTCTGTGGCCCTGGCAAAAGAAATGCAAGGCTCTCCAGGGAAGAGAGCTCAATGC 1990  
 QY 748 ArgLeuProAspPheSerGluAsnGlnAlaIrrYrYrThrSerValIyLeuPheGlnAsn 767  
 Db 1991 AGTTGCCAGATCACTGAAATATCAACATACAAACATGATTTAAAGTTCCAAAT 2050  
 QY 768 GlnGlnAsnAsnIyValIleSerIyAspArgAsnSerGluLeuLeuThrValGluYrGlu 787  
 Db 2051 CAACAATTAACAAGATATCACTAAAGAAATTTGAAATTAATGACCGTAGAATATGA 2110  
 QY 788 GluPheAsnHleuAspTrpGluIyAsn 797  
 Db 2111 GAATTTAACATCAAGATTTGGAGAGAAAT 2140



RESULT 8  
 ID AAA46328  
 AC AAA46328; standard; DNA; 2966 BP.  
 DT 04-SEP-2000 (first entry)  
 DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.  
 XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 KW chromosome 6q13-q15; ocular disease; retinal detachment;  
 KW choriorretinal degeneration; retinal degeneration; cone degeneration;  
 KW age related macular degeneration; photoreceptor degeneration;  
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KW rod-cone dystrophy; cone-rod dystrophy; ss.  
 OS Homo sapiens.  
 XX MO200026367-A2.  
 PN 11-MAY-2000.  
 PD 29-OCT-1999; 99WO-US025440.  
 PF 29-OCT-1999; 98US-00183972.  
 PR 29-OCT-1998; 98US-00183972.  
 PA (IOWA) UNIV IOWA RES FOUND.  
 XX Hageman GS, Kuehn MH,  
 PI MPI; 2000-365616/31.  
 DR Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 PT preventing, diagnosing and treating ocular disorders such as retinal  
 PT detachment and choriorretinal degeneration.  
 XX Claim 3; Fig 18; 183pp; English.  
 PS The present sequence represents a splice variant of an interphotoreceptor  
 CC matrix (IPM) proteoglycan, designated IPM150. The sequence is missing  
 CC exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs,  
 CC IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome  
 CC 6q13-q15, between markers CHC.GAT11F10 and D6S284. The IPM proteins may  
 CC be used to supplement a patient's own production of the protein or to  
 CC rectify alterations in their nucleic acids that result in expression of  
 CC an inactive protein. The IPM nucleic acids may be used in this way to  
 CC treat ocular diseases such as retinal detachment, choriorretinal  
 CC degeneration, retinal degeneration, age related macular degeneration,  
 CC photoreceptor degeneration, RPS (retinal pigment epithelium)  
 CC degeneration, cone degeneration, mucopolysaccharidosis, rod-cone  
 CC dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also  
 CC be used to assay for other modulators of IPM proteoglycan expression and  
 CC activity that may be used to treat ocular diseases. The nucleic acids and  
 CC proteins may also be used as diagnostic reagents to detect the presence  
 CC of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies  
 XX  
 SQ Sequence 2966 BP; 918 A; 687 C; 624 G; 737 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,38e-275 Length: 2966  
 Score: 3526.50 Matches: 707  
 Percent Similarity: 89.62% Conservatve: 1  
 Best Local Similarity: 89.49% Mismatches: 4  
 Query Match: 85.66% Indels: 81  
 DB: 3 Gaps: 1  
 US-10-007-270-2 (1-797) x AAA46328 (1-2966)  
 QY 8 AlailepheValIpheTrpIlePheLeuGlnValGlnGlyThrIleAspIleSerIleAsn 27  
 DB 5 GCTATTGTTGTTTGGATTTCCTCCAGTTCAAGAACCA----- 49

QY 28 IleTyrHisSerGluThrIleAspIleAspAsnProProAsnGluThrThrGluSer 47  
 DB 49 ----- 49  
 QY 48 ThrGluYMetTyrIleMetSerThrMetArgArgIlePheAspLeuAlaYSHISArg 67  
 DB 49 ----- 49  
 QY 68 ThrIleArgSerAlaPhePheProThrGlyValIleValCysProGlnGluSerMetIlys 87  
 DB 49 ----- 49  
 QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGlnAlaValTyr 107  
 DB 50 -----GTCGTCCAGAGAACGACTAATGG 70  
 QY 108 GlnAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127  
 DB 71 GAAGCATATCGAATCTTCTGATCGCATCCCTGACACAGGAGAAATATCAGACTGGGTC 130  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyIleAsnPheSerAsnSer 147  
 DB 131 AGCATCTCCAGCAGAGAACCTTCGCTCTTTGACATTGAAAAAATTCAGCAATTC 190  
 QY 148 GlnGluHisLeuAspLeuLeuGlnGlnArgIleIleYsglnArgSerPheProAspArgIlys 167  
 DB 191 CAGAGCACCTGGATCTTCTCCAGCAGAGAAATTAACAGAAAGTTTCCCTGACAGAAAA 250  
 QY 168 AspGluIleSerAlaGluIleThrLeuGlyGluIleProGlyGluThrIleValIleSerThr 187  
 DB 251 GATGAATAATCTGCAGAGAAACACATTGGAGAGCTGTGAAACCATTTGATTCATCAACA 310  
 QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
 DB 311 GATGTGCAACGTCTCACTTGGGCTTTCCCTCTCACTCTGATGACACCTCTCAT 370  
 QY 208 GluIleLeuAspAsnThrIleuAsnAspThrIlysMetProThrThrGluArgGluThrGlu 227  
 DB 371 GAAATTCCTCGATTAATATACCTACACACACCAAGATGCTTAACACAGAAAGAACAGAA 430  
 QY 228 PheAlaValIleGluGlnGlnArgValGluLeuSerValSerIleValAsnGlnIlePhe 247  
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 QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGlnIleuAlaGlyIleSerGln 267  
 DB 491 AAGCAGAGCTCGCTGACTCCCACTCCCATTTACCGAGGCTGACGAGAAAGTCCAA 550  
 QY 268 LeuGlnMetGlnIlePheIleValLeuProGlyPheIleYsIleHisValIleGly 287  
 DB 551 CTTAGATGCAAAAGATTTTAAGAACTTCAAGATTCAGAAAAATTCAGTGTTAAGA 610  
 QY 288 PheArgProIleYsGlnIleAspGlySerSerSerThrGlnMetGlnLeuThrAlaIle 307  
 DB 611 TTTAGACCAAAAGAAAGAAAGATGCTCAAGCTTCCACAGATGCAACTTAAGGCAATC 670  
 QY 308 PheIleArgHisSerAlaGlnAlaIleYsSerProIleAspLeuLeuSerPheAspSer 327  
 DB 671 TTTAAGAGACACAGTGCAGAGCAAAAGCCCTCAAGTCACTCTCTCTTTGATTCC 730  
 QY 328 AsnIleIleGluSerGlnIleValIleTyrHisGlyThrMetGlnIleAspLeuGlnProGlu 347  
 DB 731 AAACAAATTTGAAGTGAAGAGTCAATCAATGAGAACCTTGAGAGACCAACCAACAGAA 790  
 QY 348 IleTyrLeuThrAlaIleAspLeuIleArgIleIleSerIleYsAlaIleGlnGlnGln 367  
 DB 791 ATCTATCTCACAGCTACACCTCAAAAGCTGATGCAAGCACTAGAGAGAAAGAACAA 850  
 QY 368 SerLeuAspValIleGlyThrIleGlnPheThrAspGluIleIleGlySerLeuProAlaPhe 387  
 DB 851 TCTTTGATGTGGGAGCAATTCAGTTCATGATGAATGTGATGATCACTCCAGCCTTT 910

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QY 388 GYProAepThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407
DB 911 GGTCTGACACCCATCAGAGCTGCCACATCTTTTGGCTTATACAGAGAGATCTACT 970
QY 408 LeuSerProGluLeuProProValGluProGluLeuThrValAspGlyValIleGluHis 427
DB 971 TTGAATGCCAGAACTTCCTCTGTTGAACCCAGCTTGAGACAGTGGACGAGACAGACAT 1030
QY 428 GYLeuProAepThrSerThrSerProProAlaMetAlaSerThrSerLeuSerGlu 447
DB 1031 GGTCTACCTGACACATCTTGTGTCACCTGCTATGAGCTCTTACCTCCCTGTCAGAACCT 1090
QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467
DB 1091 CCACCTTCTTATGGCATCAAGCATCTTCTCTGACGATCAAGGACCCACATATCA 1150
QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487
DB 1151 ATGGCCACTGACAGACATGCTAGTACAGAGGCTCACCATCCACACAGATATTATCT 1210
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArg 507
DB 1211 GCAATCAGCAACTGGCTCTGGAAATTTCATCCACTGCACTTCAGATGACAGCCGA 1270
QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
DB 1271 TCAAGTGCAGGTGGGGAAGATATGGTCAGACACCTAGAGAAATGATGTGCTGACACT 1330
QY 528 ProAlaProSerGluValProGluLeuSerGlyTyrValSerValProAspHisPheLeu 547
DB 1331 CCTGCCCATCTGAGAGTACACAGGCTCAGCGAATCGTTTGTCTCCAGATCATTTCTTG 1390
QY 548 GluAspThrThrProValSerAlaLeuGlnIlyrIleThrThrSerSerMetThrIleAla 567
DB 1391 GAGGATACCACTCTGCTCAGCTTACAGTATATCACACATGTTCTATGACCATTGGC 1450
QY 568 ProGlyGlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
DB 1451 CCCAAGGGCCGAGAGCTGTGATGTTCTTCACTGCGGTGCTTAACATGGCCCTTCTCC 1510
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DB 1511 AACGACCTGTTCAACAAGAGCTCTCGAGTACCGGAGCTCGAGACCAATTCACACAG 1570
QY 608 LeuLeuValProThrLeuAspSerAsnLeuThrGlyPheGlyLeuGluIleLeuAsn 627
DB 1571 CTGCTGTTCCATATCTACGATCCATCTTACAGATTTAAACCACTTAATCTTAAC 1630
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647
DB 1631 TTCAGAAACGGAGTGTGATTTGTGAATACCAAAATGAATTTGCTTAAGTCTGTCCGAT 1690
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667
DB 1691 AACCTCACCAAGGCTGTGACACGGGCTCTGAGAGATTTTCGTTGCTCCACCAACAA 1750
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687
DB 1751 CTTCATCTGAAATATACAGCTACTCTTCAACATTGAACCAAGCTGATTAACAGATCCC 1810
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
DB 1811 TGCAGATCTGCGCCCTGGCGGCAATTTGCCAATGTGTAAAGACCAACGACTAGGAA 1870
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
DB 1871 GCGGAGTGTGCTGCAAAACAGGATATGACAGCCAGGAGGAGCTGGACGCTGGAACCA 1930
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGlyValLeuGlnGlyLysGlyLysProCys 747
DB 1931 GGCCTCTGTGG-CTTGCGCAAAAGGAATCGAGGTCTCTCAGGAAAGGAGACTCCATGC 1989
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysPheGlnAsn 767

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DB 1990 G--GTTCAGATCTCTGAAATACAGACATACAAATCTATGTTAA-AATTCCAAAT 2046
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
DB 2047 CAACAATAATACAGATATCAGTAAAGAAATCTGATTAATACCGTGAATATGAA 2106
QY 788 GluPheAsnHisGlnAspTyrGluGlyAsn 797
DB 2107 GAATTTAACATCAAGATTGGAGAAAT 2136

RESULT 9
AAA46329
ID AAA46329 standard; DNA; 2244 BP.
XX
AC AAA46329;
XX
DT 04-SEP-2000 (first entry)
XX
DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.
XX
KM Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KM Chromosome 6q13-q15; ocular disease; retinal detachment;
KM Choroidretinal degeneration; retinal degeneration; cone degeneration;
KM Age related macular degeneration; photoreceptor degeneration;
KM Retinal pigment epithelium degeneration; mucopolysaccharidosis;
KM rod-cone dystrophy; cone-rod dystrophy; ss.
XX
OS Homo sapiens.
XX
PN WO20026367-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025440.
XX
PR 29-OCT-1998; 98US-00183972.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2000-365616/31.
XX
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT preventing, diagnosing and treating ocular disorders such as retinal
PT detachment and choroidretinal degeneration.
XX
XX
XX Claim 3; Fig 19; 183p; English.
XX
XX The present sequence represents a splice variant of an interphotoreceptor
XX matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an
XX additional intron after exon 5. The protein is an IPM component (IPMC).
XX Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
XX is located on chromosome 6q13-q15, between markers CHDC.GATA11P10 and
XX D6S284. The IPM proteins may be used to supplement a patient's own
XX production of the protein or to rectify alterations in their nucleic
XX acids that result in expression of an inactive protein. The IPM nucleic
XX acids may be used in this way to treat ocular diseases such as retinal
XX detachment, choroidretinal degeneration, retinal degeneration, age related
XX macular degeneration, photoreceptor degeneration, RP (retinal pigment
XX epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
XX cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
XX also be used to assay for other modulators of IPM proteoglycan expression
XX and activity that may be used to treat ocular diseases. The nucleic acids
XX and proteins may also be used as diagnostic reagents to detect the
XX presence of IPM nucleic acids and their products in samples from patients
XX according to standard methodologies
XX
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
XX

Alignment Scores: 2,966-259 Length: 2244
Pred. No.:

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Score: 3323.00 Matches: 667  
 Percent Similarity: 95.564 Conservative: 0  
 Best Local Similarity: 95.564 Mismatches: 10  
 Query Match: 80.718 Indels: 23  
 DB: 3 Gaps: 1

US-10-007-270-2 (1-797) x AAA46329 (1-2244)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 DB 151 ATGTATTTGGAAACTGAAAGAGCTATTTGTTTGGATTTTCTCCAAAGTTCAAGA 210  
 QY 21 ThrTyrAspIleSerIleAsnIleTyrHisSerGluThrTyrAspIleAspAsnPro 40  
 DB 211 ACCAAAGATATCTCCATTACATATACATCTCGAAACTTAAGACATACATACATCCCA 270  
 QY 41 ArgAsnGluThrThrGluSerThrGluTyrMetTyrTyrMetSerThrMetArgArgIle 60  
 DB 271 AGAAATGAAACAACTGAAAGTACTGAAAAAATGTACAAATGTCACACTATGAGACGATA 330  
 QY 61 PheAspLeuAlaLysHisArgThrTyrAspSerAlaPhePheProThrGlyValLysVal 80  
 DB 331 TTTCGATTTGGCAAGAGATGAAACAAAGATCCGCAATTTTCCCAACGGGGGTTAAAGTC 390  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 391 TGTCCACAGGATCCATGAAACAGATTTTAGACAGCTTCAGACTTATATAGATTGAGA 450  
 QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 451 GTGTGCAGGAAGACAGCATGGGAGACATTCGGATCTTCTGGATCGCATCCCTGACACA 510  
 QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 511 GGGGAAATACAGACATCGGTGACATCTGCCAGCAGACACCTTCCCTCTTGGACAT 570  
 QY 141 GlyLysAsnPheSerAsnSerGlnGlnIleLeuAspLeuLeuGlnArgIleLysGln 160  
 DB 571 GGAHAAACTTCAGCAATTCCTCCAGAGACCTGGATCTTCTCCAGCAGAAATTAACACG 630  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
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 QY 181 GluThrIleValIleSerThr----- 187  
 DB 691 GAAACCATTTGTCATTTCAAC-AGCAATCTACATTTCAAAAGCTTGGGCGATTTCTAAGA 749  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 750 AAACCTCAGAAAGCAAAATTCAAGATGTGCGCAACGTCTCACTTGGGCTTTCCTCTC 809  
 QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
 DB 810 ACTCCGATGAGACACCTCTCTCAATGGAATTCGTGATATACATCAACACACCAAGATG 869  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnGlnArgValGluLeuSer 239  
 DB 870 CCTACAAACGAAAGGAAACAAATTCGTGTGTGGAGACAGAGGGGTGAGCTCAGC 929  
 QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
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 DB 990 CAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTTTAAGAAATTTCCAGCA 1049  
 QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
 DB 1050 TTCAAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCC 1109  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319

DB 1110 ACGAGATGCCAATCTTACGGCCATCTTTAAAGACACAGTGCAGAAAGAAAGCCCTGCA 1169  
 QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyTyr 339  
 DB 1170 AGTGACCTCTCTGTCTTTGATTCCAACAAATTTGAAGTGAAGAGTATATCATGGAACC 1229  
 QY 340 MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle 359  
 DB 1230 ATGAGAGAGGACAAACCAACCAAAATCTATCTCACAGCTACAGACTCAAAAGGCTGATC 1289  
 QY 360 SerLysAlaLeuGluGluGluGlnSerLeuAspValGlyTyrIleGlnPheThrAspGlu 379  
 DB 1290 AGCAAGACCTTAGAGAAAGAACATCTTTGATGTGGGACAAATTCAGTTCCTGATGAA 1349  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
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 DB 1410 GCTGTATTAACAGAGATGCTACTTGAATCCAGAACTTCTCTGTGAAACCCAGCTT 1469  
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 DB 1470 GAGACAGTGCAGGAGCAGAGCATGTCTTACTGACATTTCTTGGTCTTCCACTGCTATG 1529  
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 DB 1530 GCCCT-ACCTCCCTGTCAAGAGCTCACCTTTCTTATAGGATCAAGATCTTCTCTG 1588  
 QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
 DB 1589 ACTGATCAAGGACACACAGATACATGACCTGACACAGACAAATCTGATACAGGGCTC 1648  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
 DB 1649 ACCATCCCAACAGATTAATTTCTGCATACACCACAGCTGCTTGGAAATTCACATCCA 1708  
 QY 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519  
 DB 1709 CCTGCATCTTCAAGATGACAGCGCATCAAGTGAGGTGGCGAAGATATGAGACAGACCTTA 1768  
 QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
 DB 1769 GATGAAATGATCTGTCTGACACCTCTGCCCATCTGAGGTACACAGAGCTCGCAATAT 1828  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
 DB 1829 GTTCTGTCCAGATCAATTTCTTGAGAGATACCACTCTGCTCAGCTTTACAGTATATC 1888  
 QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValIlePhePheSerLeu 579  
 DB 1889 ACCACTAATTTCTATACCATTTGCCCAAGGGCGAGAGCTGTGATGTCTTCACTGCTG 1948  
 QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
 DB 1949 CGTGTGCTTAACATGCTCTTCCCAACGACCTGTCAACAGAGACTATTTGGAGATACGA 2008  
 QY 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuAspSerAsnLeuThrGly 619  
 DB 2009 GCTCTGAGCAACAATTTACACAGCTGTGTGCTCATATCTACAGTCCAACTTACAGCA 2068  
 QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
 DB 2069 TTTTAAGCAACTTGAATAATCTTACCTTCAGAAACGAGATGTGATTTGTAATGCAAAATG 2128  
 QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValIleHisGlyValLeuGluAsp 659  
 DB 2129 AAGTTTGTAAATGATGATGCTGATTAACCTCAACAGGCTGTGACAGGGGCTTGTGAGAT 2188  
 QY 660 PheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeu 677

DB 2189 TTTCGTTCTGTCGACGCCACAGACTCCATCTGGAATAGACGCTACTCTCTC 2242  
 RESULT 10  
 ACC57948  
 ID ACC57948 standard; cDNA; 2244 BP.  
 XX  
 AC ACC57948;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Human interphotoreceptor matrix IPM 150, isoform C, cDNA.  
 XX  
 KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
 XX receptor; ophthalmological; gene therapy; gene; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 151..747  
 FT /tag= a  
 FT /product= "IPM 150"  
 FT sig\_peptide 151..210  
 FT /tag= b  
 FT unsure 265..267  
 FT /tag= c  
 FT /note= "encodes Pro"  
 FT unsure 346..348  
 FT /tag= d  
 FT /note= "encodes His"  
 XX  
 PN WO2003039346-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-US036090.  
 XX  
 PR 08-NOV-2001; 2001US-00077270.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Hageman GS, Kuehn MH;  
 XX  
 DR MPI; 2003-441440/41.  
 DR P-PSDB; ABR42344.  
 XX  
 PT New interphotoreceptor matrix proteins and polynucleotides, useful for  
 PT creating or preventing photoreceptor death or retinal detachment, or for  
 PT treating ocular disorders.  
 XX  
 PS Claim 1; Page 79-80; 105pp; English.  
 XX  
 CC The present sequence is that of cDNA encoding isoform C of novel human  
 CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
 CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
 CC is located on chromosome 6q13-q15, a region that also contains loci for  
 CC progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's  
 CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
 CC disease. Members of the IPMC gene family have been identified in humans,  
 CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
 CC Subfamilies are designated IPM 150 (or IMPG1) and IPM 200 (or IMPG2). The  
 CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
 CC antibodies that specifically bind the polypeptides, and vectors  
 CC comprising the polynucleotides. A claimed method of treating or  
 CC preventing photoreceptor death or retinal detachment involves  
 CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
 CC claimed is a method for identifying a compound capable of modulating IPMC  
 CC gene expression  
 XX  
 SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other:  
 Alignment Scores: 2,966-259 Length: 2244  
 Pred. No.: 3323.00 Matches: 667  
 Score:

Percent Similarity: 95.56% Conservative: 0  
 Best Local Similarity: 95.56% Mismatches: 10  
 Query Match: 80.71% Indels: 23  
 DB: 9 Gaps: 1  
 US-10-007-270-2 (1-797) x ACC57948 (1-2244)  
 QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGluValGlnGly 20  
 DB 151 ATGATTTGGAAACTAGAGAGCTATTTTGGTTTGGATTTTCTCCAGGTTCAAGA 210  
 QY 21 ThrTyrAspIleSerIleAsnIleTyrHisSerGluThrTyrAspIleAspAsnProBro 40  
 DB 211 ACCAAGATATCTCATTAACATATACCATTTCTGAACTTAAGACATAGACATATCCCA 270  
 QY 41 ArgAsnGluThrThrGluSerThrGluTyrMetTyrTyrMetSerThrMetArgArgIle 60  
 DB 271 AGAATGAAACACTGAAAGTACGAAAAATGACAAAATGTCAACTATGACGAAATTA 330  
 QY 61 PheAspLeuAlaTyrHisArgThrTyrArgSerAlaPhePheProThrGlyValIleVal 80  
 DB 331 TTGGATTTGGCAAGATCGAACCAAAAAGATCCGATTTTCCACGGGGGTTTAAATGC 390  
 QY 81 CysProGlnGluSerMetTyrGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 391 TGTCACAGAAATCATGAAACAGATTTTACAGAGTCTTCAAGCTTATATAGATTGAGA 450  
 QY 101 ValCysGlnGluAlaValITrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 451 GTGTGTGCAAGACGACATGGGAAAGCATATCGATCTTCTGATCGCATCCCTGACACA 510  
 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 511 GGGGAATATCAGAGCTGGTGCATCTGCACGACGAGAGACTTCTGCTCTTGGACATT 570  
 QY 141 GlyTyrAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleTyrGln 160  
 DB 571 GGAATAAACTTCAGCAATTCACAGAGACCTCGATCTTCTCCAGCAGAGATAAACAAG 630  
 QY 161 ArgSerPheProAspArgTyrAspGluIleSerAlaGluTyrThrLeuGluGluProGly 180  
 DB 631 AGAAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGAAACAATTGGAGAGCTGGT 690  
 QY 181 GluThrIleValIleSerThr-----AspValAlaAsnValSerLeuGlyProPheProLeu 187  
 DB 691 GAAACATTTGCTATTTCAC-AGCAATCTACATTTCAAGAAGCTTGGGCAATATTTAAGA 749  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 750 AAACCTCAGAAAGACAATTCAGAGATGTTGCAACGCTCACTGGGCTTCCCTCTC 809  
 QY 200 ThrProAspArgThrLeuLeuAsnGluIleLeuAspAsnThrLeuAspThrTyrMet 219  
 DB 810 ACTCTGTATGACACCTCTCTCAATGGAATTTCTGATTAATACCTCAACAGACCAAGAATG 869  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGlnGluGlnArgValGluLeuSer 239  
 DB 870 CCTACAAAGAAAGAAAGAAACAGAAATTCCTGTGTGGAGAGACAGAGGCTGAGCTCAC 929  
 QY 240 ValSerLeuValAsnGlnTyrPheTyrAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
 DB 930 GTCTCTGTGTAACCAAGAGTTCAAGGACAGAGCTCGCTGACTCCCAATATTAAC 989  
 QY 260 GlnGluLeuAlaGlyTyrSerGlnLeuGlnMetGlnTyrIlePheTyrTyrLeuProGly 279  
 DB 990 CAGGAGCTAGACAGGAAATCTCCAACTTCAGATGCAAAAGAAATTTAAAGAAATCTCCAGA 1049  
 QY 280 PheTyrTyrIleHisValLeuGlyPheArgProTyrTyrGlyTyrAspGlySerSerSer 299  
 DB 1050 TTCAAAAAATTCATGTGTATGAGATTAGACCAAGAAAGAAAGATGGCTCAAGCTCC 1109  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheTyrArgHisSerAlaGluAlaTyrSerProAla 319

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Db      1110 ACAGAGATGCAACTTACGGCCATCTTAAAGACACAGTCAGAGCAAAAGCCCTGCA 1169
QY      320 SerApLeuLeuSerPheApSerAenlygllgluSerGluValIyrhlsqlythr 339
Db      1170 AGTGAACCTCCTGCTTTTATTCACAAATTTGAAAGAGAGAGTCTATCATGAGACC 1229
QY      340 MetGluGluAspLysGlnProGluIleYrleuThrAlaThrAspLeuYsArgLeuIle 359
Db      1230 ATGAGAGAGACACAGACACAGAAATCTATCTCACAGCTACAGACTCAAAAGGCTGATC 1289
QY      360 SerLyAlaLeuGluGluGlnInSerLeuAspValIglYThrIleGlnPheThrAspGlu 379
Db      1290 ACCAAAGCACTAGAGAGAAACAATCTTGATGTGGGACAATTCAGTTCATGATGA 1349
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Db      1350 ATTGCTGATCACTGCCACCTTTGGTCTTGACACCCAACTCAGAGTGCCTCCATCTTTT 1409
QY      400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419
Db      1410 GCTGTATACAGAGATGCTACTTGAATCCAGAACTTCTCTGTGTAACCCCAAGCTT 1469
QY      420 GluThrValAspGlyAlaGluIleGlyLeuProAspThrSerTrpSerProAlaMet 439
Db      1470 GAGACAGTGCAGAGACAGACATGCTTACTGACACTTCTTGCTCCACTGCTATG 1529
QY      440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459
Db      1530 GCCCT-ACCTCCCTGTCAGAGACTCCACTTTCTTATGAGCATCAAGCATCTTCTCTCG 1588
QY      460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479
Db      1589 ACTGATCAAGAGCAACCAATCAATGAGCTGACCAACAATGCTACTACAGAGGCTC 1648
QY      480 ThrIleProThrSerAspTyrsSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499
Db      1649 ACCATCCCAACAGATGATTTATCTGCAATCAGCCAACTGGCTCTGGAAATTTCAATCCA 1708
QY      500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519
Db      1709 CCTGCATCTTCAGATGACAGCCGATCAAGTCAGAGTGCGAAGATGACAGAGACTTA 1768
QY      520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlyTr 539
Db      1769 GATGAATGATCTGTCTGACACTCTGCTCCCATCTGAGTACCAAGAGTCAAGCAATAT 1828
QY      540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnIle 559
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QY      560 ThrThrSerSerMetThrIleAlaProLyGlyArgGluLeuValPhePheSerLeu 579
Db      1889 ACCACTAGTTCATATGACCATTCGCCCAAGGCCGAGAGCTGTGATGTTCTTCAGTCTG 1948
QY      580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGlyTrArg 599
Db      1949 CGTGTGCTCAATGCGCTTCTTCCAAAGCTGTTCAACAAAGCTATTTGAGATCCCA 2008
QY      600 AlaLeuGluGlnGluPheThrGlnLeuLeuValProTyLeuArgSerAsnLeuThrGly 619
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QY      620 PheLyGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerIysMet 639
Db      2069 TTTAAGCAACTTGAATATCTTAACCTTCAAGAAACGGAGGTGATGTAATGCAAAATG 2128
QY      640 LysPheAlaLysSerValProTyrsAsnLeuThrLyAlaValHisGlyValLeuGluAsp 659
Db      2129 AGTTTGTCAATGAGTGCCTGATACCTCAGCAAGGCTGTCAAGGGGCTTTGAGAGAT 2188
QY      660 PheArgSerAlaAlaIaGlnIleuHisLeuGluIleAspSerTyrsSerLeu 677
Db      2189 TTTGCTTCTGCTGACGCCCAACATCTCCATCTGGAATAGACAGTACTCTCTC 2242

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RESULT 11
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ID      ADAI4844 standard; cDNA; 2244 BP.
XX
AC      ADAI4844;
XX
DT      06-NOV-2003 (first entry)
XX
DE      Human Interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.
KW      ss; gene; human; IPMC 150 isoform C; gene therapy;
KW      interphotoreceptor matrix component; IPMC; ocular disorder;
KW      macular degeneration; photoreceptor death; retinal detachment.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      151..747
FT              /*tag= b
FT              /product= "IPMC 150 isoform C"
FT      sig_peptide 151..200
FT              /*tag= a
FT              /note= "Signal sequence"
FT      mat_peptide 201..744
FT              /*tag= c
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FT              /*tag= d
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FT      unsure     346..348
FT              /*tag= e
FT              /note= "Encodes His"
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PN      US2002160954-A1.
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PD      31-OCT-2002.
XX
PF      08-NOV-2001; 2001US-00007270.
XX
PR      29-OCT-1998; 98US-00183972.
PR      29-OCT-1999; 99US-00430195.
XX
PA      (IOWA ) UNITV IOWA RES FOUND.
XX
PI      Hageman GS, Kuehn MH;
XX
DR      MPI, 2003-238235/23.
DR      P-PSDB; ADAI4845.
XX
PT      New isolated or recombinant interphotoreceptor matrix component
PT      polynucleotide and polypeptide, useful for diagnosing, preventing,
PT      treating or prognosticating ocular disorders, e.g. macular degeneration
PT      or retinal detachment.
XX
PS      Claim 3; Page 36-37; 76pp; English.
XX
CC      The invention relates to an isolated or recombinant interphotoreceptor
CC      matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC      comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC      gene operatively linked to the IPMC polynucleotide. The IPMC
CC      polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC      preventing, treating or prognosticating ocular disorders, e.g. macular
CC      degeneration, photoreceptor death or retinal detachment. They are also
CC      useful for identifying a compound capable of modulating IPMC gene
CC      expression in a cell. The present sequence represents cDNA encoding human
CC      interphotoreceptor matrix component, IPMC, 150 isoform C.
XX
SQ      Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
XX
Alignment Scores:
Pred. No.:      2,966-259      Length:      2244
Score:          3323.00      Matches:      667

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Percent Similarity: 95.56%      Conservative: 0  
 Best Local Similarity: 95.56%      Mismatches: 10  
 Query Match: 80.71%      Indels: 23  
 DB: 10      Gaps: 1

US-10-007-270-2 (1-797) x ADA14844 (1-2244)

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 QY 21 ThrTyrAspIleSerIleAsnIleTyrHisSerGluThrTyrAspIleAspAsnProPro 40  
 Db 211 ACCAAAGATATCTCCATTAAACATATACATTCGAAACTAAAGACATAGACAAATCCCA 270  
 QY 41 ArgAsnGluThrThiGluSerThrGluTyrMetTyrTyrMetSerThrMetProArgIle 60  
 Db 271 AGAAATGAAACAACTGAAAGTACTGAAAAATGTACAAAATGTCAAAATGTGAGAGAAATA 330  
 QY 61 PheAspLeuAlaTyrHisArgThrTyrAspSerAlaPhePheProThrGlyValTyrVal 80  
 Db 331 TTGGATTTGGCAAAGATGAGAACAAATAATCCGCACTTTTCCCAAGGGGGTTAAAGTC 390  
 QY 81 CysProGluGluSerMetTyrGluIleLeuAspSerLeuGluAlaTyrTyrArgLeuArg 100  
 Db 391 TGTCCACAGGAATCCATGAAACAGATTTTAGACAGCTTCAAGCTTATATAGATTGAGA 450  
 QY 101 ValCysGluGluAlaValIleProGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 451 GGTGTCAAGAAAGACACATGGAGAGATATCGGATCTTCTGATCTGCATCCCTGACACA 510  
 QY 121 GlyGluTyrGluAspTyrValSerIleCysGluGluGluThrPheCysLeuPheAspIle 140  
 Db 511 GGGGAATATCAGAGATCGGCTCAGCATCTCCACAGAGAGACCTTCCTGCTTTGACATT 570  
 QY 141 GlyTyrAsnPheSerAsnSerGluGluHisLeuAspLeuLeuGluGluArgIleTyrGlu 160  
 Db 571 GGAATAAACTTCAGCAATTCCTCCAGAGACCTGGATCTTCCAGAGAGAAATTAACAG 630  
 QY 161 ArgSerPheProAspArgTyrAspArgIleSerAlaGluTyrThrLeuGlyGluProGly 180  
 Db 631 AGAAGTTTCCCTGACGAAAGATGAAATATCTGCAGAGAGACATTTGGAGAGCTGAT 690  
 QY 181 GluThrIleValIleSerThr----- 187  
 Db 691 GAAACCATTTGTCTATTCAAC-AGCATCTACATTTCAAAGACTGGGCAAGTATCTAAGA 749  
 QY 188 -----AapValAlaAsnValSerLeuGlyProPheProLeu 199  
 Db 750 AAACCTCAGAAAGACAAATTCAAGATGTTGCCAAGCTCTCACTTGAGCTTCCCTCTC 809  
 QY 200 ThrProAspAspThrIleuAsnGluIleLeuAspAsnThrIleuAsnAspThrIleuMet 219  
 Db 810 ACTCCGATGACACCTCTCTCATATGGAATCTCGAATAATACATCAACACCAAGAGAG 869  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGluGluArgValGluLeuSer 239  
 Db 870 CCTACACAGAAAGAGAAACAGAAATTCGCTGTGTGAGAGAGCAGGGGTGAGCTCAAC 929  
 QY 240 ValSerLeuValAsnGluTyrPheValGluLeuAlaAspSerGluSerProTyrTyr 259  
 Db 930 GTCTCTCTGGTAAACAGAAAGTTCAAGGACGAGCTGCTGACCTCCAGCTCCCAATATAC 989  
 QY 260 GlnGluLeuAlaGlyTyrSerGluLeuGluMetGluTyrIlePheTyrValLeuProGly 279  
 Db 990 CAGAGACTGACAGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAACTTCCAGAA 1049  
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 QY 340 MetGluGluAspTyrGluGluProGluIleTyrLeuThrAlaThrAspLeuTyrArgLeuIle 359  
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 QY 360 SerTyrAlaLeuGluGluGluGluSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
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 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGluSerGluLeuProThrSerPhe 399  
 Db 1350 ATTGCTGATCATCTGCCAGCTTGTGTGCTTGACACCAATCAGAGCTGCCACATCTTTT 1409  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGluLeu 419  
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 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrPheProAlaMet 439  
 Db 1470 GAGACAGTGGACGGAGCAGAGATGTCTACTGACATTTCTGTCTCCACCTGCTATG 1529  
 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
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 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGluLeuAlaLeuGlyTyrIleSerIlePro 499  
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 QY 500 ProAlaSerSerAspAspSerAspThrProAlaProSerGluValProGluLeuSerGly 519  
 Db 1709 CTTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCAAGATATGACAGAGACCTTA 1768  
 QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGly 539  
 Db 1769 GATGAATAGGATCTGTGACACTCTGCCCATCTGAGGTACCAAGACTCAGCAATAT 1828  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGluTyrIle 559  
 Db 1829 GTTTCGTGCCAGATCATTTCTTGGAGATACCACTCTGTCTCAGCTTTACAGATATATC 1888  
 QY 560 ThrThrSerSerMetThrIleAlaProTyrGluValArgGluLeuValIlePhePheSerLeu 579  
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 QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnTyrSerSerLeuGluTyrArg 599  
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 QY 600 AlaLeuGluGluGlnPheThrGluLeuLeuValProTyrLeuArgSerAsnLeuThrGly 619  
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 Db 2129 AAGTTTGTAAATCATGCTGCATTAACCTCAACCAAGGCTGTCAAGGGGTCTTGGAGAT 2188  
 QY 660 PheArgSerAlaAlaAlaGluGluLeuHisLeuGluIleAspSerTyrSerLeu 677  
 Db 2189 TTTGTTTGTGTCAGCCCAACACTCCATCTGAAATATGACAGCTACTCTCTC 2242





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Db 1324 CCATTGGGTGATGAATTACTGGGACACTC-----TTGACAGCTGTCACTGAACCATGAT 1377
Qy 395 LeupProthrsrPha1aVal1lePhrg1uaAp1a1aThrlrLeuSerProGluLeuProPro 414
Db 1378 CTGGCCAAAGCCCTTGTGATGTACAGAGATGACCTTGAATTCAGAACTTCCTTTC 1437
Qy 415 ValGluProGluLeuGluThrValAspGlyAlaGluH1sGlyLeuPro----- 430
Db 1438 GTTGAAGCCTGAGCTTGAAGCAGTGAAGAGATGTGAGCTCCCTGGATATGCTCC 1497
Qy 431 ---AspThrsrTyrSerProProAlaMetAlaSerThrsrLeuSerGluAlaProPro 449
Db 1498 AAGAGACAGTTCTTGGTCTCCACCTGTATCAAGCTCAATTTCCGATCAAGAAATCTACCT 1557
Qy 450 PhePheMetAlaSerSer1lePheSerLeuThrsrAspGlnGlyThrThrsrAspThrsrAla 469
Db 1558 TCGTTT---ACACCTGACATCTTCTCTGATAGTCTCAAGGCCCTCCCTGATGACC 1614
Qy 470 ThrAspGlnThrsrMetLeuValProGlyLeuThrlleProThrsrAspTyrSerAla1le 489
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Qy 490 SerGlnLeuAlaLeuGly1leSerH1sProProAlaSerSerAspAspSerArgSerSer 509
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Qy 510 AlaGlyGlyGluAspMetValArgH1sLeuAspGlyLumeAspLeuSerAspThrsrProAla 529
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Qy 530 ProSerGluVal1ProGlyLeuSerGlyTyrVal1SerVal1ProAspH1sPheLeuGluAsp 549
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Qy 550 ThrThrsrProVal1SerAlaLeuGlnTyr1leThrsrSerSerMetThrlleAlaProlys 569
Db 1855 ACCACACCCATCCCAACAGATACGATTCATCACACAGCTCCGAAACCATTCACCAAG 1914
Qy 570 GlyArgGlyLeuVal1PhePheSerLeuArgVal1AlaAspMetAlaPheSerAsp 589
Db 1915 GGCCAGAGAGTATGATTTCTTCAAGCTGCGTGTGTAACATCCGTTCTCTATGAC 1974
Qy 590 LeuPheAsn1ysSerSerLeuGlyTyrArgAlaLeuGlnGlnPheThrsrGlnLeu 609
Db 1975 CTGTTCAACAAAGATTCTCTGAGATATCAAGCCCTGGAACAACGATTCACAACTGCTG 2034
Qy 610 ValProTyrLeuArgSerAsnLeuThrglyPhe1ysGlnLeuGlu1leLeuAsnPheArg 629
Db 2035 GTTCCCTATCTACGATCGAATCTTACGGGATTTAAGCAACTGAAATACTCAGCTTCAGA 2094
Qy 630 Aang1ysrVal1leValAsnSer1ysMet1ysPheAla1ysSerVal1ProTyrAsnLeu 649
Db 2095 AACGGAAAGTATCTGTAACAGCAAGTGGGTTGCAAGCGGTACCTCAACACTC 2154
Qy 650 Thr1ysAlaVal1H1sGlyVal1leuGluAspPheArgSerAla1AlaGlnGlnLeuH1s 669
Db 2155 ACCCAAGCCGCTGGCGGGCTTTCGAGATCTTCGGTCCACCGAGCTCAAGGGCTCAT 2214
Qy 670 LeuGlu1leAspSerTyrSerLeuAsn1leGluProAlaAspGlnAlaAspProCy1ys 689
Db 2215 CTGGAAATCGAAAGCTACTCCCTCGCATTTGAACCAAGCGATTCAGCGGATCCCTGAAA 2274
Qy 690 Phe1ysAla1ysGly1leGluPhe1ysVal1ysAsnGlyArgThrglnGlu1leGlu 709
Db 2275 CTCTTACAGCTGTGGCAAAATTTGGCCAGTGTGAAGAAATGAATGAGCAAGAGAGAGAG 2334
Qy 710 CyAsrGlyProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729
Db 2335 TGTCTGTGACAGAGGACATATGAGCCACGGGACCTGATCAACAGACCTCAAGCTC 2394
Qy 730 CyGlyProGlyThrlsGlyGlyGluVal1leuGlnGly1ysGlyAlaProCyAsrGlyLeu 749
Db 2395 TGTCCCTCTGGA---AAGACTTGTGTGGCGCGGCGAGAACAAAGCAACTCTCATGCAAGCCA 2451

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Qy 750 ProAspH1sSerGluAsnGlnAlaTyr1ysThrsrVal1ys1ysPheGlnAsnGln 769
Db 2452 CCAAGTACCTTACAAACCAAGCTCAGAACCTGTGTAAAGCTA-----CGTCA 2505
Qy 770 AsnAsn1ysVal1leSer1ysArgAsnSerGlyLeuLeuThrsrVal1GlyTyrGlu1lePhe 789
Db 2506 CAATATAGATAGTCAAGAAAGAAATTTCTTAAGTATCAGCTATATGAGATTTGAAGAAATT 2565
Qy 790 AsnH1sGlnAspTyrGluGlyAsn 797
Db 2566 GAAACACAGACTGGAGAGGAAAT 2589

RESULT 13
ADA14847
ID ADA14847 standard; cDNA; 3668 BP.
AC ADA14847;
XX
DT 06-NOV-2003 (first entry)
XX
DB Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX
KM ss; gene; mouse; IPMC 150 isoform A; gene therapy;
XX interphotoreceptor matrix component; IPMC; ocular disorder;
XX macular degeneration; photoreceptor death; retinal detachment.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 196..2592
FT /tag=a
FT /product="IPMC 150 isoform A"

XX
PN US2002160954-A1.
XX
PD 31-OCT-2002.
XX
PF 08-NOV-2001; 2001US-00007270.
XX
PR 29-OCT-1998; 98US-00183972.
PR 29-OCT-1999; 99US-00430195.
XX
PA (IOWA ) UNIV IOWA RBS FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2003-238235/23.
DR P-Psdb; ADA14848.
XX
PT New isolated or recombinant interphotoreceptor matrix component
PT polynucleotide and polypeptide, useful for diagnosing, preventing,
PT treating or prognosticating ocular disorders, e.g. macular degeneration
PT or retinal detachment.
XX
PS Claim 3; Page 39-41; 76pp; English.
XX
CC The invention relates to an isolated or recombinant interphotoreceptor
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC gene operatively linked to the IPMC polynucleotide. The IPMC
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC preventing, treating or prognosticating ocular disorders, e.g. macular
CC degeneration, photoreceptor death or retinal detachment. They are also
CC useful for identifying a compound capable of modulating IPMC gene
CC expression in a cell. The present sequence represents cDNA encoding mouse
CC interphotoreceptor matrix component, IPMC, 150 isoform A.
XX
SQ Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;

Alignment Scores: 3.57e-196 Length: 3668
Pred. No.: 2548.50 Matches: 528
Score:

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Percent Similarity:	75.12%	Conservative:	79
Best Local Similarity:	65.35%	Mismatches:	180
Query Match:	61.90%	Indels:	21
DB:	10	Gaps:	9

US-10-007-270-2 (1-797) X ADA14847 (1-3668)

[illegible]

Dh	1147	GCAGAAAAGCCCTGATCTACTGATCTACTGCTCTTGAATTCGCAACAAATATTGAAAGTGAAGA	1208
Qy	335	ValTyrThiValGlyThrMetGluGluIuAerLysGlnProGluIuIleTyrLeuThrAlaThrAsp	354
Dh	1207	ATCCATCATGAGGAGTCAATA---GAAGACAAACCAACCAAGAAACCTTACAGCTTACAGAC	1263
Qy	355	LeuIuAerGluLeuIleSerLysValAlaLeuGluGluGluGlnSerLeuAspValGlyThrIle	374
Dh	1264	CTCAAAAAACATCATCAATCAACAACTATGATGAGGAACCTGCTCTTGTAAGAAAGGAAAAATT	1323
Qy	375	GlnPheThrArgGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu	394
Dh	1324	CCATTCGCGTATGAAAGTTACTGGGACACTC-----TTCAAGCTTGCATCGAAACCGAT	1377
Qy	395	LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro	414
Dh	1378	CTGCCCAAGCCCTTGCTGATGTGCAGAGAGATGCACTTGTGATGTCAGAACTTCCTTTC	1437
Qy	415	ValGluProGlnLeuGluThrValAlaArgGlyAlaGlnHisGlyLeuPro-----	430
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Qy	431	---AspThrSerThrSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro	449
Dh	1498	AAAGACAGTTCTTGATGTCTCAACCTGATCAAGCTCAATTTCCCGATAGAAATCTACT	1557
Qy	450	PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla	469
Dh	1558	TCGGTT---ACACCTAGCATCTTCTCTGTAGATGCTAAAGCCCTCCCTCTTATGACC	1614
Qy	470	ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle	489
Dh	1615	ACTGGCCCAACAGACATCATGCCCAACGCCAATCTCCCACTATGATGATTTATTCACATC	1674
Qy	490	SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerAspSerSer	509
Dh	1675	CGCCAAATTCGCTCTGGAATGTCATCATTCGCTGCACTCTCCAGTCAACAGACAGTATC	1734
Qy	510	AlaGlyIuGlyIuAerMetValArgHisLeuAspGluMetAspLysSerAspThrProAla	529
Dh	1735	ACAAGCAAGCATGACACAACTCCAGACACTAGATGCGATGATGTGTGACACGCCAGCC	1794
Qy	530	ProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAsp	549
Dh	1795	TTCGCAAGAAATATCAGAACTGAGTGATGATGATTCGCTCCGCGGTGAGTCTTGAGATG	1854
Qy	550	ThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAspGlu	569
Dh	1855	ACCAACACCCATCCCAACAGTACGGTTCATCAACACCGCTCCGAGACATTTGCCACCAAG	1914
Qy	570	GlyArgGluLeuValAlaPhePheSerLeuArgValAlaAspMetAlaPheSerAspAsp	589
Dh	1915	GGCCAGAGGCTAGTGATTCCTCAAGCTCCGAGTGCTAACACAGCCGTTCTCTTATGAC	1974
Qy	590	LeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu	609
Dh	1975	CTGTTCACAAAGATTCCTCGAGGTATCAAGCCCTGGAAACAAGATTCAACAGACTGCTG	2034
Qy	610	ValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg	629
Dh	2035	GTTCCCTCATCTAGCATGATCTTACCGGATTTTAAGCAATCGAAATAATCATCGATTCAGA	2094
Qy	630	AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu	649
Dh	2095	AACGGAAGTGTGATCGGAACACAAAGTCCGGTTGGCAAAAGCGGATACCTTCACACTC	2154
Qy	650	ThrLysValAlaHisGlyValLeuGluAspPheArgSerAlaAlaIleGlnGlnLeuHis	669
Dh	2155	ACCAGAGCCGTGGCGGGGCTCTTGAGAGATCTTCGGTCCACCCGACTCAAGGGCTCAAT	2214
Qy	670	LeuGluIuIleAspSerTyrSerLeuAsnIleGlnProAlaAspGlnAlaAspProCysLys	689
Dh	2215	CTGGAATTCGAAGGCTACTCCCTCCGATCGAATTCGAACACAGCTGATACAGCGGATTCCTCGAA	2274

Accession	Gene	Protein	Location/Qualifiers		
QY	690	Pheleum1aCy8gylgyluphealagincysvallysaangluar9ThrglUGL1aGLU	1..2130		
Db	2275	CTCCTAGACTGTGGCAAAATTTGGCCAGTGTGTAAAGAAATGATGTGAACAGAGAACGACAG	/*tag= a		
QY	710	Cysa9Cy8y8PrcgLytrAaspsergInglYserLeuAepgLyLeugluPrcgLyLeu	/transl_except= (pos: 16..18, aa: Val)		
Db	2335	TGTGCTGTCAACAGGACATGAGAGCCACGGACCTGTGACTACCAACCTGAACTCTC	/transl_except= (pos: 55..57, aa: Ala)		
QY	730	CysgLyPrcgLytrHyLyggluCysggluValLeugInglYLygLyAlaProCysa9rLeu	/transl_except= (pos: 58..60, aa: Tyr)		
Db	2395	TGTCCCTCTGGA---AGACTTGTGTGGCCGGCCGAGAAACAAAGCAACTCAGTACGAGCCA	/transl_except= (pos: 73, aa: Asp)		
QY	750	Proa9P8y8sergLuAanglu1a1aYrly8r8tr8serValy8y8y8PheglAaangluIn	/transl_except= (pos: 234..236, aa: Xaa)		
Db	2452	CCAGATCACTCTACAAACCAAGCTCAGAAACCTGTGTGTAAAAAGCTA-----CGTCAG	/transl_except= (pos: 271..273, aa: Xaa)		
QY	770	Aa9a9y8Val11eSerly8a9r8a9sergIuLeu1eulThrVa1gluTyrgluIuphe	/transl_except= (pos: 403..405, aa: Xaa)		
Db	2506	CAAAATTAAGTATGATCAAGAAAAAATTTCTTAACATATCACTATAGATTGAAGAAATTT	/transl_except= (pos: 2107..2109, aa: Xaa)		
QY	790	Aa9h1a91a9pTyrgluIyAa9n 797	/product= "interphotoreceptor matrix proteoglycan IPM150"		
Db	2566	GAAGACAGACTGTGGAGGAAAT 2569	/note= "Xaa is an unspecified amino acid"		
RESULT 14					
AAAA6309	AAAA6309 standard; cDNA, 3206 BP.				
XX	AAAA6309;				
XX	04-SEP-2000	(first entry)			
XX	cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).				
XX	Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;				
KW	chromosome 6q13-q15; ocular disease; retinal detachment;				
KW	chorioretinal degeneration; retinal degeneration; cone degeneration;				
KW	age related macular degeneration; photoreceptor degeneration;				
KW	retinal pigment epithelium degeneration; mucopolysaccharidosis;				
XX	rod- cone dystrophy; cone-rod dystrophy; ss.				
XX	Mus sp.				
XX	Key	Location/Qualifiers			
XX	Key	1..2130			
XX	CDs	/*tag= a			
XX	FT	/transl_except= (pos: 16..18, aa: Val)			
XX	FT	/transl_except= (pos: 55..57, aa: Ala)			
XX	FT	/transl_except= (pos: 58..60, aa: Tyr)			
XX	FT	/transl_except= (pos: 73, aa: Asp)			
XX	FT	/transl_except= (pos: 234..236, aa: Xaa)			
XX	FT	/transl_except= (pos: 271..273, aa: Xaa)			
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XX	FT	/product= "interphotoreceptor matrix proteoglycan IPM150"			
XX	FT	/note= "Xaa is an unspecified amino acid"			
XX	PN	WO20026367-A2.			
XX	PD	11-MAY-2000.			
XX	PF	29-OCT-1999; 99WO-US025440.			
XX	PR	29-OCT-1998; 98US-00183972.			
XX	PA	(IOWA ) UNIV IOWA RES FOUND.			
XX	PI	Hageman GS, Kuehn MH;			
XX	WI	WPI, 2000-365616/31.			
XX	DR	P-PSDB; AAY93338.			
XX	XX				

[illegible]

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Db      ||||| 559 ATATTAAAGAACTTCAGAGATTCCGAGAAATCCGTTATTAGATTAGACCAAGAA 618
Qy      ||||| 293 GLULysAspGlySerSerSerThrGluMetGluLeuThrAlaLeuPheLysArgHisSer 312
Db      ||||| 619 GAAGAAGATGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAAGAGGACAT 678
Qy      ||||| 313 AlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSer 332
Db      ||||| 679 GCGAAGCAAAAAGCCCTGATAGTCACTACGTCTCTTGAATTCACAAATAATGAAAGT 738
Qy      ||||| 333 GLUGluValIleLysIleGlyThrMetGluGluAspLysGluProGluIleTyrLeuThrAla 352
Db      ||||| 739 GAAGAATTCATCATGAGTCACTA---GAAGACAAACCAACCAACCACTTACCTCAAGCT 795
Qy      ||||| 353 ThrAspLeuLysArgLeuLysSerLysAlaLeuGluGluGluGlnSerLeuAspValGly 372
Db      ||||| 796 ACAGACCTCAAAAACCTCATCATCACTACAGTACAGAGACCTGCTTGGTAGAAGG 855
Qy      ||||| 373 ThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGln 392
Db      ||||| 856 AAAATTCATCGGTATGATAGTACTGGACACTC-----TTCAAGACCTGTCACTGAA 909
Qy      ||||| 393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412
Db      ||||| 910 CCAAGATCTGCCCAAGCCCTTGCTGATGTCAACAGAGATGCCACTTGGAGTCCAGAACTT 969
Qy      ||||| 413 ProProValGluProGluLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430
Db      ||||| 970 CTTTCGTGAGCGCTGAGCTTGAGGACAGTGAAGAGATCTGAGCTGCTGGATG 1029
Qy      ||||| 431 -----AspThrSerTyrSerProProAlaMetAlaSerThrSerLeuSerGluAla 447
Db      ||||| 1030 TCCCTCAAAAGACAGTCTTGCTGCTCCACTGATCACTCAATTCCTCCAGATCAAGAAAT 1089
Qy      ||||| 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnIleThrAspThr 467
Db      ||||| 1090 CTACCTCTGTT---ACACTAGCATCTTCTCTGATAGCTCAAAAGCCCTCCCTTG 1146
Qy      ||||| 468 MetAlaThrAspGlnIleThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487
Db      ||||| 1147 ATGACCACTGGCCCAACAGACTCATCCCAAGCCCACTCCCACTTCAGTTATTTCT 1206
Qy      ||||| 488 AlaIleSerGluLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArg 507
Db      ||||| 1207 ACCATCCCGCAATGCTGCAATGCTGCACTGGCTGCACTCCCTCAGTCAAGAGAG 1266
Qy      ||||| 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
Db      ||||| 1267 CTGATCAACAAGCCCATGACATCCAGACCTAGATGGCATGATGTCTGACAGC 1326
Qy      ||||| 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547
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Qy      ||||| 548 GluAspThrThrProValSerAlaLeuGluTyrIleThrThrSerSerMetThrIleAla 567
Db      ||||| 1387 GAGATGACACACCCATCCCAACAGTACGTTCAATCACACCAAGCTCCGAGACCAATTGCC 1446
Qy      ||||| 568 ProLysGlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db      ||||| 1447 ACCAAGGCGCAGAGCTAGTATCTTCAAGCTCAGCTGCTGCTAACAAGCCGTTCTCC 1506
Qy      ||||| 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnIlePheThrGln 607
Db      ||||| 1507 TATGACCTGTTCAACAAGAGTTCTCTGAGTATCAAGCCCTGGAACAAGATTCAAGAC 1566
Qy      ||||| 608 LeuLeuValProTyrLeuLysSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
Db      ||||| 1567 CTGCTGGTTCCTATCTACGATCGAATCTTACGGGATTTAAGCAACTGGAATACTCAAC 1626
Qy      ||||| 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647

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Db      ||||| 1627 TTCAGAAACGAAAGTGTGATCTGTGAACAGCAAGTCCGTTTTCAGAAAGCCGTAACCTTAC 1686
Qy      ||||| 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaIleGlnGln 667
Db      ||||| 1687 AACCTCACCAAGCCGTTGCGGGGCTTGAGAGATCTTCGGTCCACCCGAGCTCAAGG 1746
Qy      ||||| 668 LeuHisIleGluGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnIleAspPro 687
Db      ||||| 1747 CTCATCTCGAAATCGAAAGCTACCTCCCTCGACATTGAACACAGCTGATCAGCGGATCCC 1806
Qy      ||||| 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
Db      ||||| 1807 TCGAAACTCTAGACTGTGGCAAAATTTGCCAGTGTGTAAAGATGAGTGCACAGAGAA 1866
Qy      ||||| 708 AlaGluCysArgCysLysPheProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
Db      ||||| 1867 GCAGAGTGCCTGCAGACAGGACATGAGAGCCACCGGAGACCTGGACTACACAGACCTTG 1926
Qy      ||||| 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db      ||||| 1927 AACCTCTGCTCCCTGGA---AAGACTTGTGTGGCCCGCCGAGAACCAACTCCATGC 1983
Qy      ||||| 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767
Db      ||||| 1984 AGGCCACCAAGATCACTCTACAAACCAAGCTCAGAACTCGTGTAAAAGCTA----- 2037
Qy      ||||| 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
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RESULT 15
ACCS7951
ID ACCS7951 standard, cDNA; 1726 BP.
XX
AC ACS7951;
XX
AC
XX
DT 11-AUG-2003 (first entry)
XX
DE Mouse Interphotoreceptor matrix IPM 150, isoform D, cDNA.
XX
KW Mouse; interphotoreceptor matrix; IPM 150; chromosome 9; IPMC; receptor;
KW opthalmological; gene therapy; gene; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 140..1540
FT FT /*tag= a
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FT FT 140..199
FT FT /*tag= b
XX
PN WO2003039346-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036090.
XX
PR 08-NOV-2001; 2001US-00077270.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2003-441440/41.
XX
DR P-PSDB; ABR42346.
XX
PT New interphotoreceptor matrix proteins and polymucleotides, useful for
PT treating or preventing photoreceptor death or retinal detachment, or for

```

PT creating ocular disorders.

XX Claim 1; Page 82-83; 105bp; English.

XX The present sequence is that of cDNA encoding isoform D of novel mouse  
CC Interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
CC Interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 9. Members of the IPMC gene family have been  
CC identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and  
CC rat. IPM 2 subfamilies are designated IPM 150 (or IPMq1) and IPM 200 (or  
CC IPMq2). The invention provides IPM 150 and IPM 200 polynucleotides and  
CC polypeptides, antibodies that specifically bind the polypeptides, and  
CC vectors comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression

XX Sequence 1726 BP; 541 A; 383 C; 388 G; 414 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,38e-99 Length: 1726  
Score: 1342.50 Matches: 310  
Percent Similarity: 44.96% Conservative: 51  
Best Local Similarity: 38.61% Mismatches: 99  
Query Match: 32.61% Indels: 343  
DB: 9 Gaps: 9

US-10-007-270-2 (1-797) x ACC57951 (1-1726)

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DB 140 ATGAATTTTCAATTAACATCTATCTTGTGTTTGGATTTTCTCCAAAGTTCAAGCA 199  
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
DB 199 ----- 199  
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
DB 199 ----- 199  
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
DB 199 ----- 199  
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
DB 200 -----ATCAA 205  
QY 101 ValCysGlnGluAlaValIleTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
DB 206 GATATGTCAGAAAGTCGTGTGGAGACATATCGATCTTCTGACCAATTCCTACACA 265  
QY 121 GlyLysTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
DB 266 GAGGAATATCAAGACTCGGCTCAGCTCTGCCAGAAAGAACTTCGCTCTTTGACATT 325  
QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
DB 326 GGGAAAACTTCAGCAACTCCAGAGGACACTAGATCTTCTTCACAGAGAAATTAACG 385  
QY 161 ArgSerPheProAspArgLysArgLysIleSerAlaGluLysThrLeuGlnGluProGly 180  
DB 386 AAGAGCTTCCTGGAGGAAAGATGAGACAGCTTCATGAGACACTGAGACACCTACT 445  
QY 181 GlnThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
DB 446 GAAAGCCCTGTGTGATCCACAGATGTTTCCAGAGATGTCCTGGGCGCATTTCCACTTCT 505  
QY 201 ProAspAspThrLeuLeuAsnGluLysIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
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QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln 234  
DB 566 ACAACAGAAATATTAACAGAACTATTCACTGTCTGATTTCTCA-----TCAGAGGAG 619  
QY 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
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QY 255 GlnSerProTyrTyrGlnGlnLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
DB 680 GGGTCACCATCTACCGAGAACTGTGGAGACAGTCCCAACTGACAGTTGCAAAAGATATT 739  
QY 275 LysLysLeuProGlyPheLysValIleHisValLeuGlyPheAspProLysValGluLys 294  
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DB 800 GATGGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGACCATGCAAGAA 859  
QY 315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
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QY 335 ValTyrHisGlyThrMetGluGluAspLysGlnProGluLysTyrLeuThrAlaThrAsp 354  
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QY 375 GlnPheThrAspGluLysIleGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
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QY 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474  
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DB 1177 ----- 1177  
QY 515 MetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGluValPro 534  
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DB 1177 ----- 1177

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QY 575 ValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSer 594
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Db 1177 ----- 1177
QY 615 SerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIle 634
Db 1178 -----AGAAAGATCTGAGCTG 1195
QY 635 ValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHis 654
Db 1195 ----- 1195
QY 655 GlyValLeuGluAspPheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSer 674
Db 1195 ----- 1195
QY 675 TyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGly 694
Db 1196 -----CCTGCTGATCAGGCGGATCCCTGCAGAACTTCTAGACTGTGGC 1237
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Db 1298 GGACATGAGAGCGACGGAACCTGACATCCAGACCCCTGAACCTGTCTGCCCTGGA--- 1354
QY 735 LysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGlu 754
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 Job time : 1304 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 22:38:30 ; Search time 354 Seconds

(without alignments)  
4002.024 Million cell updates/sec

Title: US-10-007-270-2

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Searched: 1303057 seqs, 888780828 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	188.5	4.6	1721	3	US-10-029-517-3
2	183.5	4.5	1804	3	US-10-029-517-17
3	162	3.9	4935	3	US-09-949-016-1019
4	162	3.9	4935	3	US-09-949-016-5054
5	158	3.8	13815	3	US-10-149-736-2
6	157	3.8	19307	3	US-08-836-022A-10
7	157	3.8	19307	3	US-09-427-048A-10
8	146	3.5	8982	3	US-08-976-255-5
9	145.5	3.5	6192	2	US-08-479-537A-1

10	145.5	3.5	6192	3	US-09-083-116-1	Sequence 1, Appl1
11	145.5	3.5	6192	3	US-09-134-916A-1	Sequence 1, Appl1
12	145	3.5	8224	9	5160808-1	Patent No. 5160808
13	144.5	3.5	2472	3	US-09-248-796A-2596	Sequence 2596, Ap
14	144.5	3.5	3104	3	US-09-418-780A-2	Sequence 2, Appl1
15	144.5	3.5	3106	3	US-09-392-714-4	Sequence 4, Appl1
16	142.5	3.5	2610	3	US-09-949-016-1832	Sequence 1832, Ap
17	141.5	3.4	6407	2	US-08-616-844-7	Sequence 7, Appl1
18	141.5	3.4	6407	2	US-08-599-654-7	Sequence 7, Appl1
19	141.5	3.4	6407	3	US-08-944-868A-7	Sequence 7, Appl1
20	141.5	3.4	6407	3	US-08-944-423A-7	Sequence 7, Appl1
21	141.5	3.4	6407	3	US-08-944-496-7	Sequence 7, Appl1
22	141	3.4	1230230	3	US-09-438-165A-1	Sequence 1, Appl1
23	139.5	3.4	6852	3	US-10-172-502-3	Sequence 1, Appl1
24	138	3.4	580073	3	US-08-545-528D-31	Sequence 1, Appl1
25	137.5	3.3	2156	2	US-08-178-477B-31	Sequence 31, Appl1
26	137.5	3.3	2156	3	US-09-304-121-1	Sequence 1, Appl1
27	137.5	3.3	2156	3	US-09-023-655-1111	Sequence 1111, Ap
28	137.5	3.3	2230	3	US-09-949-016-2043	Sequence 2043, Ap
29	137.5	3.3	2458	3	US-09-513-783A-175	Sequence 175, App
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31	135.5	3.3	2835	3	US-09-134-001C-1515	Sequence 1515, Ap
32	135.5	3.3	3561	3	US-09-134-001C-1685	Sequence 1685, Ap
33	135.5	3.3	4828	3	US-09-620-312D-329	Sequence 329, App
34	135.5	3.3	6414	3	US-09-134-001C-1626	Sequence 1626, Ap
35	135.5	3.3	12057	3	US-10-149-736-47	Sequence 47, Appl1
36	135.5	3.3	13957	3	US-09-782-378A-22	Sequence 22, Appl1
37	135.5	3.3	13957	3	US-10-149-736-1	Sequence 1, Appl1
38	135.5	3.3	13977	3	US-09-484-970B-60	Sequence 60, Appl1
39	135.5	3.3	32392	3	US-09-662-254B-27	Sequence 27, Appl1
40	135.5	3.3	50000	3	US-09-662-254B-23	Sequence 23, Appl1
41	134.5	3.3	7888	3	US-09-919-497-48	Sequence 48, Appl1
42	134.5	3.3	8312	3	US-09-620-312D-1048	Sequence 1048, Ap
43	134.5	3.3	11443	3	US-10-149-736-44	Sequence 44, Appl1
44	134	3.3	13473	3	US-09-993-777-1	Sequence 1, Appl1
45	134	3.3	13473	6	PCI-US96-03916-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-10-029-517-3  
; Sequence 3, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 3  
; LENGTH: 1721  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (58)...(1605)  
US-10-029-517-3

## Alignment Scores:

Pred. No.: 1,276-09  
Score: 188.50  
Percent Similarity: 40.06%  
Best Local Similarity: 23.53%  
Query Match: 4,588  
DB: 3  
Gaps: 15

US-10-007-270-2 (1-797) x US-10-029-517-3 (1-1721)

QY 367 GlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAla 386  
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Db      277 CAGGACAGAGATGTCACTGGCCCCGCGCACGGAACCAAGTTCAAGTTCAGCTGCACC 336
Qy      387 PheGlyProAspThrLeuIleuProThrsPheAlaValIle----- 402
Db      337 TGGGACAGAGATGTCACTGG--GTCACAGTCAACAGGCGAGCCCTGGGCTCCACACC 393
Qy      403 -----ThGluAspAlaThrLeuSerProGluLeuProPro-----ValGlu 416
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Qy      433 ---SerTyrSerProAlaMetAlaSerThrsLeuSerGluAla-----ProPro 449
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Qy      450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
Db      562 GGGTTCACGCGCGCCCGACGCCACCGGTGTCACT-----TGC 597
Qy      470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrs-----AspTyr 486
Db      598 GCGCCGACACACAGCGCGCGCGGTGTCACTCGGCCCGCCCGACGATGGTGTCACTCG 657
Qy      487 SerAlaIleSerGlnIleuAlaLeuGlyIleSerHisProPro-----AlaSerSer 503
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Qy      504 AspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAsp 523
Db      718 GCGTCAAGGCTGTGCATTCAGGCTCAGCTTCACTGTGTGTGACACAGCAGCCTGTGCAG 777
Qy      524 LeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSerValPro 543
Db      778 GCTACACCAACACCCGACGACCAAGACATCTCA-----TTCACAAATTC 822
Qy      544 AspHisPheLeuGluAspThrThrProVal----- 553
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Db      1003 TCTCTCTGGAAATATCCACAGCAGCACTACTACCAAGACTGTGACAGACATTTCTGA 1062
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Qy      648 AsnLeuThrLysAlaValHisGlyVal-----LeuGluAspPheAspSerAlaAla 664
Db      1168 -----ACCATCATATGTCCACGACGTGAGACACAGTTCAATCATATAAAGGAAGA 1221
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Db      1222 GCTCTGTGATTAACCTGACGATCTCAGACGTCAAGCTGAGTGTATGTGCA 1272

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; Patent No. 671627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO: 17
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(1500)
US-10-029-517-17

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Pred. No.: 4,8e-09 Length: 1804
Score: 183.50 Matches: 78
Percent Similarity: 38.82% Conservative: 54
Best Local Similarity: 22.94% Mismatches: 135
Query Match: 4,46% Indels: 73
DB: 3 Gaps: 12

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US-10-007-270-2 (1-797) x US-10-029-517-17 (1-1804)

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Qy      367 GlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAla 386
Db      292 CAGGACAGAGATGTCACTGGCCCCGCGCACGGAACCAAGTTCAAGTTCAGCTGCACC 351
Qy      387 PheGlyProAspThrGlnSerGluLeuProThrsPheAlaValIleThrGluAspAla 406
Db      352 TGGGACAGAGATGTCACTGG----- 372
Qy      407 ThrLeuSerProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlu 426
Db      373 -----GTCCACATCAACAGCCAGCGCTGGGTGTCCACCAACCCCGCAGCC 417
Qy      427 HisGlyLeuProAspThrSerTyrSerProAlaMetAlaSerThrsLeuSerGlu 446
Db      418 CACGATGTCACTTACGCCCCGACAAACAGCCCGCGGCTCCAC----- 465
Qy      447 AlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAsp 466
Db      466 GCGCCCGCA-----GCCACGATGTCACTGGCGCCGAC----- 501
Qy      467 ThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrs----- 484
Db      502 -----ACAGAGCGCGCGCGGTGTCCACCGCCCGCCATGTGT 543
Qy      485 ---AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro----- 500
Db      544 GTCACTCGGCGCCGACAAACAGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 603
Qy      501 AlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAsp 520
Db      604 GTCACTCGGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 663
Qy      521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540
Db      664 TCTGCCAGGCTTACCAACACCCAGCGACCAAGACATCTCA-----TTC 708
Qy      541 SerValProAspHisPheLeuGluAspThrThrProVal----- 553
Db      709 TCAATTCACAGACACATCTGTATCTCTACACCCCTTGCAGCAGCATAGACCAAGACT 768
Qy      554 -----SerAlaLeuGlnTyrIleThrThrsSerMetThrIle 566
Db      769 GATGCCAGTAGCACTCACCATGACAGCGTAACCTCTGTCACTCTCCATATACAGCACT 828
Qy      567 AlaProLysGlyArgGluLeuValValPhePhe-----SerLeuArgValAlaAspMet 584

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Db      829  TCTCCCACTGCTCTAATCGGGGCTCTCTTTCTCTTTCTCTCTTTCTCTTTCTCAATTTCAACCTC 888
Qy      585  AAlaPheSerAsnAspLeuPheAsnIlySerValIleValAsnSerIlyMetIlyArgAlaLeuGluGln 604
Db      889  CAGTTTAATCTCTCTGTGAAGATCCACACCGACTACTACCAAGAGCTGCAGAGAC 948
Qy      605  PheArgIleLeuValProTyrLeuArgSerAsnLeuThrGlyPheIlyGlnLeuGln 624
Db      949  ATTTCGAATATGTTTTTTCAGATTTATATTAACAAGG-----GTTTTCTGGGCTCTCC 1002
Qy      625  IleLeuAsnPheArgAsnIlySerValIleValAsnSerIlyMetIlyPheAlaIlySer 644
Db      1003  AATATTAACTTACGCGACGATCTGTGGTGTAACAATTGACTCTGGCTTCGAGAGAGT 1062
Qy      645  ValProTyrAsnLeuThrIlyAsnIleValHisGlyVal-----LeuGluAspPheArg 661
Db      1063  -----ACCATCAATGTCCACGACGTGAAGACACAGTTCAATCAGTATTA 1107
Qy      662  SerAlaAlaIleGlnIleuHisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681
Db      1108  ACGGAAGCAGCCTCTCGATATATACTGACGAGCTCAGACGTACGCTGAGTATGCCA 1167

RESULT 3
US-09-949-016-1019
; Sequence 1019, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001037
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1019
; LENGTH: 4935
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1019

Alignment Scores:
Pred. No.: 6,16e-06 Length: 4935
Score: 162.00 Matches: 155
Best Local Similarity: 32.90% Conservative: 101
Percent Similarity: 19.92% Mismatches: 304
Query Match: 3.93% Indels: 218
DB: Gaps: 32

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Qy      62  AspleuAlaIlyHisIleArgThrIlySerSerAlaPheProThr-----GlyVal 78
Db      655  AATTAAACGAAACACTCAACCCCATCGATTCGATTCACCAATTCACGATTTGGTGAG 714
Qy      79  LysValCysProGlnIleuSerMetIlyGlnIleLeuAspSerLeuGlnAlaIlyTyrArg 98
Db      715  GAAATGAGCGAAGACAGTTTCATTAACACGATTCGGAAGAACAGACGAGCTTAAG 774
Qy      99  LeuArgValCysGlnGlnIleValIleTrrGlnAlaTyrArgIlePheLeuAspArgIlePro 118
Db      775  CAGCGCTCGAAGCGTGAAGCT-----CGA 798
Qy      119  AspThrIleGlyIleTyrGlnAspTrrPheValSerIleCysGlnGlnIleuThrPheCysLeuPhe 138
Db      799  GAGAGTCGAGAACTTGAAAGAA-----GCTTCAGCTCAGTCGAGAGACGAGATGATCCAT 852

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QY	139	Asp11IegI	-----LysanPheSerAenSerGlnIuH1VleuAer	152
Db	853	CCTAGGAGAGTGGCTTCCCTGCTGCTCTCACTTTCAGACAGCTGAGAGCAACAG		912
QY	153	LeuIeuGInGInAtrG	-----I1eYsgInAtrSerPheProAspArgIyAerGlu	169
Db	913	CTGAGAGCTCAGACAGCATTCGCCAGAAAAGCTCTCTCAATTTCTGAAAGAAAGCTGAC		972
QY	170	I1eSerA1aGluYs	---ThreUGlYGluproGluYgluThrI1eValI1eSerThraP	188
Db	973	TCTGTATGATGAAACCAAGAAAGAAAGACATCATCTAGGTCAGACAGCAAGA		1032
QY	189	ValI1aenValSerLeuG1YProPheProIeu	-----ThrPro	201
Db	1033	GCAGTTAACTGTCTGAGGGCAGCCACCTCTGTGAGGAGAAAGATCAAGAAACACT		1099
QY	202	AspAerPThrLeuAenGluI1eIeuAerAenThrLeuAenAerPThrLysMetProTh		221
Db	1093	TCCAGAAACCTA	-----AGGGTCAGAGCAGATCGAAATTTGAAACCA	1133
QY	222	ThrGluAagG1uThrGluPheAlaValLeuGluGlnAtrGValGluIleuSerValSer		241
Db	1135	GAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAAAGATGATGAAGAGAGAAAGTAT		1194
QY	242	LeuValAenGInIlyPheIyAgluIleuAlaAerSerGInSerProTyTrGInGlu		261
Db	1135	GATGAGGAGCAAAAATCTAGG	-----GAGGCACCAATCTGTAAAGAG	1233
QY	262	LeuAlaGluYsSerGInLeuGInMetGInIlyI1ePheIyAluYleuProGluPheIy		281
Db	1237	TTTAAAGAAAGAGGGGAA	-----GAGATCTCTAGAGTAA	1272
QY	282	LysI1eH1sVleUGlYPhaXArgProIyYs	-----Glu	293
Db	1273	CCAGAGAGATGATGATGATGAGAGCCCAACAAAGATCCAGAAACAGAGGTGTTAAG		1333
QY	294	LysAerG1Y	-----SerSerSerThrGluMetGInLeuThrAlaI1ePheIyAerH1s	311
Db	1333	AGAGAGGAGGATTTACAAAGATCCAGAGAAAGGCTAGAAAAGTCATCTGGCAGACAG		1392
QY	312	SerAlaGluAlaYSerProAlaSerAerLeuLeuSerPheAerSerAerIyA1leGlu		331
Db	1393	CAGCAGAGAAAGAAATGAAACAAACATCTCCCTTGAGAGAGAAAGAAATAA		1452
QY	332	SerGluGInuValTYrH1aG1YThMetGInGluAerIySgInProGluI1eTYrIleuTh		351
Db	1453	TCTTCACAA	-----GCCTTAAAGAAAAATCGAAGTCTCTTCCCTCTCGACTG	1502
QY	352	AlaThraPleuIyAerGluI1eSerIyAlaIleuGluGInGInSerIeuAerVal		371
Db	1504	ACTGAAAGATCGAAAGAG	-----	1521
QY	372	GlyHrI1IeGInPheThAerGluI1eAlaIleGlySerIeuProAlaPheGluProAerPh		391
Db	1522	-----	-----GCCTCACTTGAAGGCTGCCAGACCAACT	1551
QY	392	GInSerGluIeuProThSerPheAlaValI1eThrGluAerAlaThraPleuSerProGlu		411
Db	1552	GCCAGCGAGAGAGAGACTCTCCACCTTTACTAACAAGAAAGCTCT	-----	1592
QY	412	LeuProProValGluProGInIleuGluThrValAerGluYAlaGluH1aGlyIleuProAer		431
Db	1600	TCTCCACACCTCATCCACAGCTCCATGCGCAAAAGAAATAGAG	-----CCCAATG	1650
QY	432	ThreIerPserProProAlaMetAlaSerThreIeuSerGluAlaProProPhePhe		451
Db	1651	GAAAGCCAGGCCCTCTGCTCTCATTCAGTATCT	-----CTCTCT	1692
QY	452	MetAlaSerI1ePheSerLeuThraPInGluYThrThraPThrMetAlaThraP		471
Db	1693	-----AATACAGATCTCTACACAGAGAGCTAATTTAGTATCTCAG		1731

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QY 472 GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491
DB 1732 CATACCTGTC-----CAG 1743
QY 492 LeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGly 511
DB 1744 TTGGTAGAGAGGCTGCTCT-----CCTTTGTCAAGTCTCTTCAGACACCAAGACAAATCTCCA 1800
QY 512 GlyGlu-----Asp 514
DB 1801 GCAGAGAAAGTCCAGAGAGAGTGTCTGCTCTGCTTCACAAAAACCACTGAGCTGAC 1860
QY 515 MetValArgHisLeuAsp-----GluMetAspLeuSerAspThrProAlaProSer 531
DB 1861 TACTAGACCCAGAGAGATCTTGAACCTGAGTCAGACAGATCTGTCAGAGCCCTCCTCTGA 1920
QY 532 GluValProGluLeu----- 536
DB 1921 AAAAATTGAGAAATTAGCACTGCGCCAAAGGAATCACTGAAGAAATGTCGAAACAGCATCT 1980
QY 537 -----SerGluTyrValSerValProAspHisPheLeuGlu 548
DB 1981 TTGGACAGAGAGAGAGAGAGAGTCTCTACCTCTCTCCAAACCCAGATTGAA 2040
QY 549 AspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaPro 568
DB 2041 CAGTCAGCTGATTCATCTCTAGCGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGATCA 2100
QY 569 LysGlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerGln 588
DB 2101 AATCTCTGC-----TCTCTCT 2115
QY 589 AspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThrGlnLeu 608
DB 2116 GAC-----AGTTCAGGTTCTCGGTCTCTACCCCTAGATCCAAAGACAGAGATGTA 2169
QY 609 LeuValProTyrLeuArgSerAsnLeuThrGlyPheGlyGlnLeuGluIleLeuAsnPhe 628
DB 2170 GCCCAGGACGTAATCATGATCCAAACCTCGTGTAGACCAAG-----ATGGGCTCC 2220
QY 629 ArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsn 648
DB 2221 AATATCAATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAGATCAG 2280
QY 649 LeuThrIleValIleHis-----GlyValLeuGluAspPheArgSerAlaIleAlaGlnGln 667
DB 2281 AACCAAAAATCTCTGAGCCCTGAGTCTCCAGGACAGACAC----- 2325
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAla-----AspGln 684
DB 2326 -----AGTATATCTGAAACCAAAAGATCCCTCTCTGTCAGAGAGTT 2367
QY 685 AlaAspProCysAlaPheLeuAlaCysGlyGlnPheAlaGlnCysValIleAsnGlnArg 704
DB 2368 GCAACTCCA-----CCAGTGCACAACTGACAGTCTGTAGCCAAAGAGAGAG 2415
QY 705 ThrGlu-----GluAlaGluCysArgCysLeuProGlyTyrAspSer 718
DB 2416 ACTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2475
QY 719 GlnGlySerLeuAspGlyLeuGluProGlyLeuGlyGlyProGlyThrIleGlyGlnCysGlu 738
DB 2476 AAGCATGTGACCAAGAGTTACAGCTTACAGCTGAGCGGAGGAGCCCA-----AAGAAAGTGTGA 2529
QY 739 ValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGln 756
DB 2530 GCTGAAGAGCAGAGCCACAGCTGCACACAGCCCAAACTCAGAGACTCAG 2583

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RESULT 4  
 US-09-949-016-5054  
 / Sequence 5054, Application US/09949016  
 / Patent No. 6812339  
 / GENERAL INFORMATION:

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/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USRS THEROF
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO: 5054
/ LENGTH: 4935
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-5054

Alignment Scores:
Pred. No.: 6,16e-06 Length: 4935
Score: 162.00 Matches: 155
Percent Similarity: 32.90% Conservative: 101
Best Local Similarity: 19.92% Mismatches: 304
Query Match: 3,93% Indels: 218
DB: 3 Gaps: 32

US-10-007-270-2 (1-797) x US-09-949-016-5054 (1-4935)
QY 62 AspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThr-----GlyVal 78
DB 656 AATTACAGAAACCTCAACACCCAGATGCTGATTCAGCCAAATTCACAGATTGCTGAG 715
QY 79 LysValCysProGlnGlnSerMetLysGlnIleLeuAspSerLeuAlaIleTyrTrArg 98
DB 716 GAAATGACCCAGAACAGTTTATTAACAGTATCGAAAAAGCAGACAGAGCTACTTAGG 775
QY 99 LeuArgValCysGlnGluAlaValIleProIleAlaTyrArgIlePheLeuAspArgIlePro 118
DB 776 CAGCCTCTGAAACGTAAGCT-----CGA 799
QY 119 AspThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPhe 138
DB 800 GAGCTGCAAACTTGAAGAA-----GCTTCAGCTGAGTGGAGAGCAAGATGATCCAT 853
QY 139 AspIleGly-----LysAsnPheSerAsnSerGlnGluHisLeuAsp 152
DB 854 CCTGAGGAGAGTGGCTTCCCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913
QY 153 LeuLeuGlnGlnArg-----IleLysGlnArgSerPheProAspArgLysAspGlu 169
DB 914 CTGAGAGCTCAGACAGATCTCCGCCAGAAAAGCTCTCTCAATTTCTGAAAGAGAAAGTGAAC 973
QY 170 IleSerAlaGluLys-----ThrLeuGlyGluProGlyGlnIleValIleSerThrAsp 188
DB 974 TCTGATGATGAAACCAAGAGAAAGAGAAAGACATCATCTAGAGGTGACAGACAGCAAGA 1033
QY 189 ValAlaAsnValSerLeuGlyProPheProLeu-----ThrPro 201
DB 1034 GCAGCTAAACTGTCTGAGGGCAGCCCACTGCTGAGAGAGAGAGAGATCAAGAAACACCT 1093
QY 202 AspAspThrIleLeuAsnGluIleLeuAsnAsnThrLeuAsnAspThrLysMetProThr 221
DB 1094 TCCAGAAACCTA-----AGGCTCAAGACAGATCGAAATTTGAAACCA 1135
QY 222 ThrGluArgGluThrGluPheAlaValLeuGlnGlnGlnArgValGluLeuSerValSer 241
DB 1136 GAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1195
QY 242 LeuValaGlnGlyPheLysLeuAlaGluLeuAlaAspSerGlnSerProTyrTrGlnGlu 261
DB 1196 GATGAGGAGCAAAATCTAG-----GAGGACACCAATCTCTGAAAGAG 1237

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Db      8102 ATAAAGTGTAGACGTGGCAAAATGATTTGGCACTGAAACTTCTCGGAGTATTCTGCTGAT 8161
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Db      8162 GATACCAAGAAAGTACATCATTAACAGAGAAATATCAATCTTGGGAAACATTCAT 8221
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Qy      661 -----ArgSerAlaAlaHlsglnGlnLeuHlLeuGluIleAaspSerTyr 675
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Db      8222 AAAAGAGTAAGTACAGCAAGAGCTGTTGGAAAGAACTATGATTAATTCAGCAGCATTC 8281
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Qy      724 -----GlyLeuGluProGlyLeuCyseGlyProGlyThrlGlyGluCyseGluValLeu 740
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Qy      779 SerGluLeuLeuThrlValGluTyrGluGlu 788
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RESULT 6
US-08-836-022A-10/c
/ Sequence 10, Application US/08836022A
/ Patent No. 6001557
/
/ GENERAL INFORMATION:
/ APPLICANT: Trustees of the University of Pennsylvania
/ APPLICANT: Wilson, James M.
/ APPLICANT: Fisher, Krishna J.
/ APPLICANT: Chen, Shu-Jen
/ APPLICANT: Weitzman, Matthew
/ TITLE OF INVENTION: Improved Adenovirus Virus and
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Howson and Howson
/ STREET: Spring House Corporate Cntr, P O Box 457
/ CITY: Spring House
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19477
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/836,022A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/331,381
/ FILING DATE: 28-OCT-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bak, Mary E.
/ REGISTRATION NUMBER: 31,215
/ REFERENCE/DOCKET NUMBER: GNP/PN.008PCT

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/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: 215-540-9200
/
/ TELEFAX: 215-540-5818
/
/ INFORMATION FOR SEQ ID NO: 10:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 19307 base pairs
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/ TYPE: nucleic acid
/
/ STRANDEDNESS: double
/
/ TOPOLOGY: unknown
/
/ MOLECULE TYPE: cDNA
/
/ US-08-836-022A-10
/
Alignment Scores:
Pred. No.: 0.000252 Length: 19307
Score: 157.00 Matches: 173
Percent Similarity: 35.60% Conservative: 151
Best Local Similarity: 19.01% Mismatches: 318
Query Match: 3.81% Indels: 268
Gaps: 44
DB:
US-10-007-270-2 (1-797) x US-08-836-022A-10 (1-19307)
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Qy      120 ThrGlyGluTyrGlnAaspTrpValSerIleCyseGlnGlnGluThrlPheCyseLeuAasp 139
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Qy      140 IleGlyLysAenPheSerAenSerGlnGlnIleLeuAplLeuGlnHlArgIleLys 159
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Qy      160 Gln-----ArgSerPheProAaspArgLysAaspGluIle 170
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Db      7900 AGCTTGAAGTCCGCGTGGCAGACATCTGCAAAAGAGCTGGCAGAAAGAGAAAGAGAT 7841
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Qy      171 SerAlaGluLysThrLeu-----GlyLysProGlyGluThrlLeuValIle 185
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Qy      186 SerThrAaspValAlaAenValSerLeuGlyProPheProLeuThrlProAaspThrLeu 205
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Qy      206 LeuAenGluIleLeuAaspAenThrlLeuAasnAplThrlYsMetProThrlThrlGluArgGlu 225
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Db      7729 CTAAGAAAG-----CAACTGACAAAGTCAAGTACTGCGCAGAAAGATTGCC 7682

```



```

CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-427-048A-10

Alignment Scores:
Pred. No.: 0.000252 Length: 19307
Score: 157.00 Matches: 173
Percent Similarity: 35.60% Conservative: 151
Best Local Similarity: 19.01% Mismatches: 318
Query Match: 3.81% Indels: 268
Gaps: 44
DB: 3

US-10-007-270-2 (1-797) x US-09-427-048A-10 (1-19307)
QY 14 Ilepheleuglnvalgln glyThrlysaaplleaserlleasnlelyrhis---sergln 32
DB 8368 CTTTAAAGCAAGAGAGAGCTCTTAAGATTAATAAGACAAATTGCAACAAATCTCAGGT 8309
QY 33 ThrlysaaplleaspaenProParganngluThrthrglnuSerThrglnuMetTyr 52
DB 8308 CGGATGATATTATTTACAAAGAAAGACAGACGCTTGCAAAAGTGCCACCTCCATGGA 8249
QY 53 LysMetSerThr-----MetargArg 59
DB 8248 AAGGTGAAGATGACAGAAAGCCGTGCACACAGATGATTTCCAGGGGAAATACTTATGAT 8189
QY 60 llepheaplleualalyehlsarThrlyrsargserala-----phephepro 75
DB 8188 ATGTCAAGAAAGACAGACAGGCGATTCACACAGATCGTTGAAAAAATGGCGACATTTCT 8129
QY 76 ThrlyvallyvalCyseProglnglnuSerMetlysglnlleleuaspserleuglnala 95
DB 8128 TATGATATGAAAGTA-----TTAATCAATGCGTGAATGAAAGTTGAACG 8084
QY 96 TyrTrpArgleuargvalCyseglnglnuAlavalTPGlu-----AlatyrArgllephe 113
DB 8083 TTTTCAAA---AAGACACAAAATCTGTAAGAACTGGAAACATGTAAATACAAATGCTAT 8027
QY 114 leuasparglleProasp----- 119
DB 8026 CTTAAGAACTCGAAGATGCGATTTGGGACGCTCAAGCTGTGTTGCAAGAACTGAATGCA 7967

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QY 120 ThrlygluTyrglnaspTrpvalserlleCyseglnglnuThrphCysleuPheasp 139
DB 7966 ACTGGGGA-----GAAATTAATTCACAG----- 7943
QY 140 lleglysaenPheaserAsnserClnghlnlsleuaplleuglnArgllelys 159
DB 7942 -----TCTTCAAAAACAGATGTCATATTTCTACAGAAATAATTAGCA 7901
QY 160 gln-----ArgserPheProaspArglyaspGlnlle 170
DB 7900 AGCTGAGCTTCGGGTGGACAGACATCTCAAGAGCTGGCAAGAAAGAAAGAGATT 7841
QY 171 SerlagluTyrrhLeu-----GlyluProglnglnThrillevalle 185
DB 7840 GAAGAACAAAAGATGCTGTCTGCATTAATTCAAAGAGATTTAAAGAAATTTGTTGTGG 7781
QY 186 SerThraspValAlaasnValserleuglyPropheroleuThrProaspaspThrleu 205
DB 7780 CTGGAAGAGCAGATACATGCTATTTACTCCTCATT-----GGAGATGAGCAGCAG 7730
QY 206 leuasnghlnlleleuaspasnThrleuasnaspThrlysmetProThrThrglnuArgln 225
DB 7729 CTAAAGAA-----CACTTGAACAGTCAGTACTGCGAAGAGATTGGCC 7682
QY 226 ThrghluhealavalleyuglnuGlnArgvalGluLeuSerValserleuvalangln 245
DB 7681 CTGCGCCAGGAAATTTCAAAACAATTAATGAACAGAGAGCAGTCTTGTATAGTCT 7622
QY 246 LysPheylsAlagluLeuAlaaspserlnserProTyrrglnuLeuAlaelyls 265
DB 7621 CCCATTAAGCCAGAAAGACAAAGATAA-----CTTGAAGAAAGCTCAAAACG 7574
QY 266 serglnleuglnmetGlnlyeillepheylslyseuPro-----GlyPheylslys 282
DB 7573 ACAATCTCCAGTGAATTAAGGTCTCCAGAGCTTACTGAGAAACAGAGAGCTTGAG 7514
QY 283 llehlsvalleyuglyPheArgProlyslsGlnlysaapglyserSerSerThrglnuMet 302
DB 7513 GTTCACTTAAAGATTTTACGACGCTTGACAGAGC-----CTGATCACTCG 7466
QY 303 GlnleuThrAlailepheylsArgHisserlAglnuAlalyserProAlaseraspLeu 322
DB 7465 CTTGTGGGTCTCTCTATTAGAAACCGTTGGAAATTTATACCAACAAAGTCAGGCA 7406
QY 323 leuSerPheaspserAsnlyeillegluserGlnuValTyrrhAglyThrmecGlnu 342
DB 7405 GAGCGCTTGAATTAAGAGATT-----GAGTAAACAGTTCCAGGT----- 7364
QY 343 AsplysglnProgluileTyrrleuThrAlaThrAspleuLyrsargleuileserlysa 362
DB 7363 ---AAACA-----GCGATGTGAAAGGCTTTTTCGAAAGGG 7328
QY 363 -----leuglnuGlnuGlnSerleuaspValglyThrilleglnPheThrAspGlnlle 380
DB 7327 CAGCATTTGTATAGGAAAA----- 7307
QY 381 AlaglySerleuProAlaPheGlyProaspThrglnuSerGlnuLeuProThrsPheAla 400
DB 7306 -----CCAGACTCAG----- 7295
QY 401 ValIleThrglnuaspAlaThrleuSerProgluLeuProProvalGlnProglnglnu 420
DB 7294 -----CCAGTCMAAGAGAAAGTTAGAA 7274
QY 421 Thrval-----AspGlyAlagluHlglyleu----- 429
DB 7273 GATCTGAGCTTGAGTGGAGGCTGTAAACATTTACTTCGGAGCTGAGACAAAGCAG 7214
QY 430 ProaspThrsertPserProProAlaMerAlaserThrsertleuSerGlnuAlaProPro 449
DB 7213 CTTGACCGTGCC-----CTGAGCTGAGCACTATGAGGCTCT----- 7175

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Qy 450 PhepMetAlaSerSerIlePheSerLeuThrApgIngluThrThrApgThrMetAla 469
Db 7174 -----GCCAGTCAGACTGTACTCTA-----GTGACACATCTGTGTGTT 7136
Qy 470 ThrApgIngluThrMetLeuValProGlyLeuThrIleProThrSerApgTyrSerAlaIle 489
Db 7135 ACTAAGGAACCT--GTCATCTCCAAACTAGAAATGACATCTCTCT-- 7094
Qy 490 SerGluLeuAlaLeuGlyIleSerHisProProAlaSerSerApgApgSerArgSerSer 509
Db 7093 -----TTGCTGTGGAGTA-----CTGCACTGGCAGACTTCAACCGAGCTTGG 7049
Qy 510 AlaGlyGlyGluApgMetValArgHisLeuApgGluMetApgLeuSerApgThrProAla 529
Db 7048 ACAGAACTTACAGACTGCTGTCTGTCTGTAGTAAATCAACAGAGTAGTG 6989
Qy 530 ProSerGluValProGluLeuSerGluTyrVal-----SerValProApg 544
Db 6988 GTGGGTGATCTGAGAACATCAATGAATGATCATCAACAGAAAGCAACGCACTGCAAGAT 6929
Qy 545 HisPheLeuGluApgThrThrProValSerAlaLeuGluTyrIleThrThrSerSerMet 564
Db 6928 -----TTGSAACAGAGACGCCCC-----CAATTGAGAAGACTTACTGTGCTGCCAG 6881
Qy 565 ThrIleAlaProLys-----GlyArgGluLeuValValPhePheSerLeuArgValAla 582
Db 6880 AATTGAAACAAACAAACAGCAATCAGAAAGCTAGAACATCATTCATGATCGAATTGAA 6821
Qy 583 AsnMetAlaPheSer----- 587
Db 6820 AGAATTCAAGATTCAGTGGATGAGTTCAGAAACAGCTGCAAAACAGAGACAAACAGTTG 6761
Qy 588 AsnApgLeuPheAsnLeuThrGlyPheLysGluLeu--GluIleLeuAsnPheArgAsn 607
Db 6760 AATGAAATGTTA--AAGGATTCACACAAATGCTGGAAGCTAGAGAAAGACCGAAG 6704
Qy 608 LeuLeu-----ValPro 611
Db 6703 GTCAATAGACAGGTGAGAGGCAAGCTTACTCATGGAAGAAGGCTCTCACAGTAGTAT 6644
Qy 612 TyrLeuApgSerAsnLeuThrGlyPheLysGluLeu--GluIleLeuAsnPheArgAsn 630
Db 6643 GCAATCCCAAAAGAAAGATCAGAAACCAAGCAAGTGGCCAAAGCCTCCGCAACGCGAG 6584
Qy 631 GlySerValIleVal-----AsnSerLysMetLysPheAlaLysSerValProTyrAsn 648
Db 6583 ATTAAGTGAAGCGTGGCAAAATGATTTGGCACTGAATCTTGGGACTATTCGCTGAT 6524
Qy 649 LeuThrLysAlaValHisGlyValLeuGluApgPhe----- 660
Db 6523 GATACCAAGAAAGTACATGATTAACAGAAATATCATATCTCTGGGGAACATTCAT 6464
Qy 661 -----ArgSerAlaAlaAlaGluLeuHisLeuGluIleApgSerTyr 675
Db 6463 AAAAGAGTAACTGAGCAAGAGCTGCTTTGGAAGAACTCATATGATTCGACAGCTTC 6404
Qy 676 SerLeuAsnIleGluProAlaApgIleApgProCysLysPheLeuAlaCysGlu 695
Db 6403 CCTCTGGACCTGGAG-----AAGTTCTTCTTCTGGAATTACG 6368
Qy 696 PheAlaGlnCysValLysAsn-----Glu 703
Db 6367 GAAGCAAGAAACAACCTGCCAATGTCTACAGACGCTTCCCGTAAGAGAAAGCTCCTA 6308
Qy 704 ArgThrGluGluAlaGluCysArgCysLysProGlyTyrApgSerGlnGlySerLeuApg 723
Db 6307 GACTCCAGGGAGTCAAGAGCTGATGAACCATGCAAGATCTCCCAAGAGAAATGAA 6248
Qy 724 -----GlyLeuGluProGlyLysGlyProGlyThrLysGluCysGluValLeu 740
Db 6247 ACTCAACAAGATATCTATCAACATCTTATGATGAAATGAGCCAAATATCTGAGATCCTG 6188
Qy 741 GlnGlyLysGlyAlaProCysArgLeuProApgHisSerGluApgIleAlaTyrIleThr 760

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Db 6187 GAAGTTCCGATGAGACCCCTGTACAAAGCGTTTGATTAACATGAATTCAGATGCG 6128
Qy 761 Ser-----ValLysLysPheGlnApgGlnApgAsnLysValIleSerLysArgAsn 778
Db 6127 AGTGAACCTGAGAAAGAGTCTCTCAACATTAGAGGCCATTTGGAAAGCAAGTTGACCA 6068
Qy 779 SerGluLeuThrValGluTyrGluGlu 788
Db 6067 TGAAGCGTTGATCTTCTCTTCAGAA 6038

RESULT 8
US-08-976-255-5
; Sequence 5, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plozman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-976-255-5

Alignment Scores:
Pred. No.: 0.000966 Length: 8982
Score: 146.00 Matches: 175
Percent Similarity: 32.72% Conservative: 109
Best local Similarity: 20.16% Mismatches: 302
Query Match: 3.55% Indels: 283
Gaps: 38

US-10-007-270-2 (1-797) x US-08-976-255-5 (1-8982)
Qy 40 ProArgAsnGluThrThrGluSerThrGluLysMetLysSerThrMetArgArg 59
Db 2203 CTTTCAACAATATATTAAATGATGTGACAAATCGAAGATTTGGCCAGTCACCAAAA 2262
Qy 60 IlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLys 79

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Db      2263 ATATGCACTTAATGAATTAAACGAGTTCAACGCACTTAAACCTGCACCTTAAGT 2322
Qy      80 ValCys-----ProGlnGluSerMetLeuGlnIleLeuAspSerLeuGlnIleIleTyr 96
Db      2323 TCACGTTTGATTAACCCCAAGAGTCAGT----- 2352
Qy      97 TyrArgLeuArgValCysGlnGluAlaValIleProGluIleValIlePheLeuAspArg 116
Db      2352 ----- 2352
Qy      117 IleProAspThrGlyGluTyrGlnAspTyrVal-----SerIleCysGlnGlnIleThr 134
Db      2353 -----ATAACAGGCCACTTTGAGAAAGAAAGCCCGTAAGATTTTGAACAGTGAGCCT 2406
Qy      135 PheCysLeuPheAsp----- 139
Db      2407 CTCGTGCTATCAATTAATCTTATGACCAAGATTAATTGATTCATTGAATGTTCAAGAA 2466
Qy      140 IleGlyLeuAspPhe-----SerAsnSer 147
Db      2467 TTGTCAAGAAACCTTTTATTTCTTCAAGAGAAAACTTACTAAAGGCTCATTTGTCAGC 2526
Qy      148 GlnGluHisLeuAspLeuLeuGlnGlnIleArgIleLeuGlnIleArgSerPheProAspArgLys 167
Db      2527 AAAGAACACATAATATGATCTTCAGACAGAACTTAAGATGCTGTTTACTGAAGCTATG 2586
Qy      168 AspGluIleSerAlaGluIleValIle-----GlyGluPro 179
Db      2587 TTAGAAGCTCAGTGAAGAACTCTTATAGATACAGCTCAGCTTCTGAAATAAGACCA 2646
Qy      180 GlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeu 199
Db      2647 GGC-----TTGTCTTTGTCAGAGAAAGTAGAC-----ACA 2679
Qy      200 ThrProAspAspThr-----LeuLeuAsnGluIleLeuAspAsnThrLeuAsn--- 215
Db      2680 AAGGAGGACGATACAGATGCTCATGACAGTGACACTTTGAGCACTCATTTGCAAGTCT 2739
Qy      216 -----AspThrIleMetProThrThrGluArgGluIleThrGluPheAlaValLeuGlnGlu 233
Db      2740 TCCCCCGAAGTGCAGTACTCTCTACTCTCTCGAAACAGAAAGAACGCCCGCTGGGATG 2799
Qy      234 GlnArgValGluLeuSerValSerLeuValAsnGlnIlePheValIleGluValIleAsp 253
Db      2800 CCCCAGACTCACTCCCAACACAGGAGAAACCCAGCCCACTGTTAAGATGTTATGTC 2859
Qy      254 SerGlnSerProTyrTyrGlnGlnIleValIleGlySerGlnLeuGlnMetGlnIleVal 273
Db      2860 CCGAGAGACTGTCTCCACAGGACATCACTGTCAGAGCTGTGCTCCCGGTGAATTT 2919
Qy      274 PheValIleLeuProGlyPheValIleValIleValIleValIlePheArgProLysValGlu 293
Db      2920 -----CTCTCACTGATGCCAGAACCCAGAGCTGATTAACAGS---TCCAGAGAC 2967
Qy      294 LysAspGlySerSerSerThrGlnMetGlnLeuThrAlaIlePheValIleValIleSerAla 313
Db      2968 TCTCTGGGAGAGTAGAGAGACCTGCACTCAC-----GAAAGTGACTCTGTT 3018
Qy      314 GlnAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGlu---Ser 332
Db      3019 CTTCGTGATGATCACTCTTCGACAGGAGTGAGTGAGGAGTATCTCCCGAAGCTGGGA 3078
Qy      333 GlnGluValIleTyrHisGlyThrMetGlnGluAspLysGlnProGluIleTyrLeuThrAla 352
Db      3079 CAGGAATTGCACAAATAACCATTTTCGGAAGACCATCACAGTCAT----- 3123
Qy      353 ThrAspLeuLysArgLeuIleSerLysAlaLeuGlnGlnIleGlnIleSerLeuAspValGly 372
Db      3124 -----CGCGGCTAGAGAAAACTTAGAGGCTGTGGAGCTTTAATAATGACCTC 3171
Qy      373 ThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGln 392
Db      3172 AATTCAAAAGACGACCAAAAGAAAGACAGGCTTGCTGCTCTCTCCGACCTCA--- 3228

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Qy      393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412
Db      3229 -----ACCACTAGAGACAGACCTCTCGAGAGAC---AGCTTTCAGACACCTTCC 3273
Qy      413 ProProValGluProGlnLeuGluThrValIleAspGlyAlaGlu----- 426
Db      3274 CCAAGCTTGAGGCTGCTCCCTGGAAACCCCGGACTCTCTGAGTCAATGATGTCACGAA 3333
Qy      426 ----- 426
Db      3334 GCGCTACTGAGACTTTAGATCTCAGCTCCCAAGAACTAGTCCCGCATTAAGCCG 3393
Qy      427 -----HisGlyLeuProAspThrSerTyrSer---ProProAla 438
Db      3394 GAGACAGTGGCTACGAAACAGAGAACTTGAAGTCTCCGAGTGAACCTTGATCCCGCT 3453
Qy      439 MetAlaSerThrSerLeuSerGlu-AlaProPhePheMetAlaSerSerIlePheSer 458
Db      3454 CCGAGAGGACCCGCACTCAAGAACAGCCACCAAGGCGATGAGCGGACACAGCGGTCTG 3513
Qy      458 rLeuThrAspGlnGlyThr----- 464
Db      3514 CCTCCCAACCGGATCATTTGTCATCTCAGATGCCGGATGTCACAGAGCACAGAAAGT 3573
Qy      465 -----ThrAspThrMetAlaThrAspGlu 472
Db      3574 ACCCTGACAGCTTCAACAGCTGCTCCAGGCTTCAATACCGAGACTCTCGTATCTTCA 3633
Qy      472 nThrMet---LeuValIleProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlu 491
Db      3634 GACATGACTCTGAGCCCGAAGAAAGCTGTGAGAGAGTCCCGGAA-ACCTCCCACTCCG 3692
Qy      491 nLeuAlaLeuGlyIleSerHisPro-----ProAla 501
Db      3693 CTTCGTGTTGTTGATACAGAGACAGCCCTTACCGAGCCAGTCTCCCGAGCAAAAGTCTCG 3752
Qy      501 AspSerAsp-----AspSerArgSerSerAlaGlyGluAspMetValIleArgHis 518
Db      3753 TCCCAAGATTAAGCTGCTCGGAAAGCCAGAAAGAGCCAGCCAGATTAAGATGTTGTCCTG 3812
Qy      518 nLeu-----AspGluMetAspLeuSerAspThrProAlaProSerGlu-----Val 533
Db      3813 TTTCGACAACTCCAGTACCTGAAATTAAGCCACGCGGAGCCAGCACAGACTGCTGT 3872
Qy      533 lProGlu-----LeuSerGlu 538
Db      3873 TCCCAAGCAGGTGATCCACGGAAGACAGGCGCAGAGTCCCTGAGTGTGCTGAATGC 3932
Qy      538 nTyrValSerValIleProAspHisPhe---LeuGluAspThrThrProValSer----- 554
Db      3933 AGAACTTAGCAGCGGCGATGACTCGAGACACAGACAGATCGCCCTCGACCTCGCTTC 3992
Qy      555 -----AlaLeuGlnIleThrIleThr----- 561
Db      3993 CACGGGAGCAACAGAACGAACTCTTGCTTACCACTTGTGCGCTGAGACAAGTCCCT 4052
Qy      562 -SerSerMetThrIleAlaProLysGlyArgGlnLeuValIle-----PheAsp 577
Db      4053 GTCCAGCACTCCGAGGCGCGAAGTTGAAGAGCCGAGACATCGAAAGGAATTAATCTGGG 4112
Qy      577 eSerLeuArgValAlaAsnMetAla---PheSerAsnAsp----- 589
Db      4113 GAAACTCGGAGTGTGAGGATGTCGAACTTCAAGAGACGAGATGATGTCAGACAGAGA 4172
Qy      590 -----LeuPheAsnLysSerSerLeuGlu 597
Db      4173 GAGCAAAACAGCGACGACTCGAGACGAGACCTGCGGCGCTTCAACTGCAATAGCCTCAG 4232
Qy      597 nTyrArgAlaLeuGlnGlnIlePheThrGlnLeuLeuValIleProTyrLeuArgSerAsnLe 617
Db      4233 CTCGAGTCTGAGAGACAGS-----ACGAGACACCCCGTGGCCATCATCTCGACACGA 4286

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OY      617   UTHGJLYHelySGINleuAGUllleLeuAAnPhetrgAnSlySerValIleVaIAenSe    637
Db      4287   GGACGGAAAGCACCTCGCGAGTCTTTAAAG-----                     4317
OY      637   rLyseWellyrPheAlalyrSerValProTYrAsnleuthrybAlaVAlHgIyVAlle    657
Db      4318   -----CCCAcAGGGCCATgCCCCGACCATTGCC-----                     4356
OY      657   uGIuApHe--ArgserAlaAlAgInleuHtSleuglullleapSerTyRse    676
Db      4351   -GAGACTCGGAAGAAGAAAAGAACGACGTCACTTTTTGCATGTCACAGTCACT    4409
OY      676   rLeuanntlegU---ProAlaepGlAlalaSProCYslyrPheleuAlCyAGlyGI    695
Db      4410   GTTGACCAAGAGACCCCAACCAAGAGCTGGGGCCCTGTGGAGAGAGCGTGGGCC    4465
OY      695   u-----PheAlagInCySAlylsAB    702
Db      4470   GGAACCTGAGCGGCCGACGCCCAAGCTCAGCTCTCCCTTAACCTGACAGCAAGTGCATCACT    4529
OY      702   ngIUArThrgIUgluaIgIU    709
Db      4530   CGAAAGCTCCACCGACGAAGAA    4551

RESULT 9
US-08-479-537A-1
Sequence 1, Application US/08479537A
Patent No. 5861381
GENERAL INFORMATION:
APPLICANT: CHAMON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
APPLICANT: HAREUVENT, Maira
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITL OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATTHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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1 LENGTH: 615192 base pairs
2 TYPE: nucleic acid
3 STRANDEDNESS: single
4 TOPOLOGY: linear
5 MOLECULE TYPE: DNA (genomic)
6 FEATURE:
7 NAME/KEY: s1g_peptide
8 LOCATION: 58..120
9 FEATURE:
10 NAME/KEY: repeat_region
11 LOCATION: 439..5239
12 OTHER INFORMATION: /note="The nucleotides spanning
13 OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
14 OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
15 OTHER INFORMATION: The number of such repeats varies from 1 to 80."
16 FEATURE:
17 NAME/KEY: mat_peptide
18 LOCATION: 121..6166
19 FEATURE:
20 NAME/KEY: repeat_region
21 LOCATION: 457
22 OTHER INFORMATION: /note="Nucleotide 457 is X1 = NNN
23 OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
24 OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
25 FEATURE:
26 NAME/KEY: repeat_region
27 LOCATION: 487
28 OTHER INFORMATION: /note="Nucleotide 487 is Y = NNN
29 OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
30 OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
31 FEATURE:
32 NAME/KEY: repeat_region
33 LOCATION: 496
34 OTHER INFORMATION: /note="Nucleotide 496 is X2 = NNN
35 OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
36 OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
37 US-08-479-537A-1
38
39 Alignment Scores:
40 Pred. No.: 0.000558 Length: 6192
41 Score: 145.50 Matches: 74
42 Percent Similarity: 38.11% Conservative: 51
43 Best Local Similarity: 22.56% Mismatches: 144
44 Query Match: 3.53% Indels: 59
45 DB: 2 Gaps: 13
46
47 US-10-007-270-2 (1-797) x US-08-479-537A-1 (1-6192)
48
49 Oy 389 ProAepThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeu 408
50 Db 4921 CCGGACNNNAGG---CCGNNCCGGGCTCCACCGCCCCNNNGCCACGGTGTCACTCG 4977
51 Oy 409 SerProGluLeuProPro-----ValGluProGlnLeuGluThrValAspGly 424
52 Db 4978 GCCCGGACNNNAGGCGCGNNCCGGGCTCCACCGCCCCNNNGCCACGGTGTCACTCG 5037
53 Oy 425 AlaGluIleGlyLeuProAepThr---SerTyrSerProAlaMetAlaSerThrSer 443
54 Db 5038 GCCCGGACNNNAGGCGCGNNCCGGGCTCCACCGCCCCNNNGCCACGGTGTCACTCG 5097
55 Oy 444 LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGly 463
56 Db 5098 GCCCGGACNNNAGCGCG-----NNNCCGGGC 5124
57 Oy 464 ThrThrAspThrMetAlaThrAspGlnThrMetLeu-----ValProGly 478
58 Db 5125 TCACACGCGCCCGCCNNNGCCACAGGTGTCACTCGGCCCGGACNNNAGCGCGNNCCGGGC 5184
59 Oy 479 LeuThrIleProThrSer-----AspTyrSerAlaIleSerGlnLeuAlaLeuGly 495
60 Db 5185 TCACACGCGCCCGCCNNNGCCACAGGTGTCACTCGGCCCGGACNNNAGCGCGNNNTTGGC 5244
61 Oy 496 IleSerHisProPro-----AlaSerSerAspAspSerArgSerSerAlaGlyGly 512

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[illegible]

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1 FILING DATE:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: WO PCT/FR91/00835
4 FILING DATE: 23-OCT-1991
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 08/039,320
7 FILING DATE: 04-APR-1993
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 08/403,576
10 FILING DATE: 14-MAR-1995
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Teskin, Robin L.
13 REGISTRATION NUMBER: 35,030
14 REFERENCE/DOCKET NUMBER: 017753-025
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (703) 836-2021
17 TELEFAX: (703) 836-6620
18 INFORMATION FOR SEQ ID NO: 1:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 6192 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: DNA (genomic)
25 FEATURE:
26 NAME/KEY: sig_peptide
27 LOCATION: 58..120
28 FEATURE:
29 NAME/KEY: repeat_region
30 LOCATION: 439..5239
31 OTHER INFORMATION: /note="The nucleotides spanning
32 OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
33 OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
34 OTHER INFORMATION: The number of such repeats varies from 1 to 80."
35 FEATURE:
36 NAME/KEY: mat_peptide
37 LOCATION: 121..6166
38 FEATURE:
39 NAME/KEY: repeat_region
40 LOCATION: 457
41 OTHER INFORMATION: /note="Nucleotide 457 is X1 = NNN
42 OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
43 OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
44 FEATURE:
45 NAME/KEY: repeat_region
46 LOCATION: 487
47 OTHER INFORMATION: /note="Nucleotide 487 is Y = NNN
48 OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
49 OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
50 FEATURE:
51 NAME/KEY: repeat_region
52 LOCATION: 496
53 OTHER INFORMATION: /note="Nucleotide 496 is X2 = NNN
54 OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
55 OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
56 US-09-083-116-1
57
58 Alignment Scores:
59 Pred. No.: 0.000558 Length: 6192
60 Score: 145.50 Matches: 74
61 Percent Similarity: 38.11% Conservative: 51
62 Best Local Similarity: 22.56% Mismatches: 144
63 Query Match: 3.53% Indels: 59
64 DB: 3 Gaps: 13
65
66 US-10-007-270-2 (1-797) x US-09-083-116-1 (1-6192)
67
68 Oy ProAePrHrgInSeScIuLeuProThrSerPheAlaValIleThrgIuAspAlaThrIeu 408
69 |||||:::|||||
70 Db 4921 CCGGACNNAGG---CCGNNNCCGGGCTCCACGCCGCCNNNGCCACGGGTGACCTCG 4977
71 ::|||:::|||||
72 Oy SerProGluLeuProPro-----ValGluProGluLeuGluThrValAspGly 424
73 ::|||:::|||||

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; OTHER INFORMATION: /note="Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-134-916A-1

Alignment Scores:
Pred. No.: 0.000558 Length: 6192
Score: 145.50 Matches: 74
Percent Similarity: 38.11% Conservative: 51
Best Local Similarity: 22.56% Mismatches: 144
Query Match: 3.53% Indels: 59
DB: 3 Gaps: 13

US-10-007-270-2 (1-797) x US-09-134-916A-1 (1-6192)
QY 389 ProaPthrGlnSerGluLeuProThrSerPheAlaValIleThrGluApaIaThrLeu 408
DB 4921 CCGGACNNNAGG---CCGNNCCGGGCTCCACCGCCCGCCNNNGCCACAGGTGTCACTCG 4977
QY 409 SerProGluLeuProPro-----ValGluProGluLeuGluThrValaPgly 424
DB 4978 GCCCGCGACNNNAGGCGGNNCCGGGCTCCACCGCCCGCCNNNGCCACAGGTGTCACTCG 5037
QY 425 AlaGluHieGlyLeuProaPthr---SerTrpSerProAlaMetAlaSerTrpSer 443
DB 5038 GCCCGCGACNNNAGGCGGNNCCGGGCTCCACCGCCCGCCNNNGCCACAGGTGTCACTCG 5097
QY 444 LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAapGlnGly 463
DB 5098 GCCCGCGACNNNAGGCGG-----NNNCCGGGCG 5124
QY 464 ThrThrAapThrMetAlaThrAapGlnThrMetLeu-----ValProGly 478
DB 5125 TCCACCGCGCCCGCCNNNGCCACAGGTGTCACTCGCGCCCGACNNNAGCGCCGNNCCGGGCG 5184
QY 479 LeuThrIleProThrSer-----AapTrpSerIleAlaSerGlnLeuAlaGlnGly 495
DB 5185 TCCACCGCGCCCGCCNNNGCCACAGGTGTCACTCGCGCCCGACNNNAGCGCCGNNNTTGGGCG 5244
QY 496 IleSerHisProPro-----AlaSerSerAapAapSerAapSerAapSerAapGly 512
DB 5245 TCCACCGCGCCCGCCNNNGCCACAGGTGTCACTCGCGCCCGACNNNAGCGCCGNNNTTGGGCG 5304
QY 513 GluAapMetValArgHisLeuAapGluMetAapLeuSerAapThrProAlaProSerGlu 532
DB 5305 TCTACTCTGTGTACACACGACCTTGTCCAGGGCTACCAACACCCACGACGACGACGACG 5364
QY 533 ValProGluLeuSerGluTrpValSerValProAapHisPheLeuGluAapThrTrpPro 552
DB 5365 ACTCCACCC-----AGCATTTCCAGCCACCTGTGATCTCTCTACGACC 5409
QY 553 Val-----SerAlaLeuGlnTrp 558
DB 5410 CTTGCCAGGCATAGACCAAGACTGACAGTAGACACTCACCATAGCACGCTACTCTCT 5469
QY 559 IleThrTrpSerSerMetThrIleAlaProGlyArgGluLeuValIlePhePhe--- 577
DB 5470 CTCACCTCTCTCAATACAGACACTTCTCCCGCAGTTGTCTACTGGGGGTCTCTTCTTTTC 5529
QY 578 ---SerLeuArgValAlaAapMetAlaPheSerAapAapLeuPheAapLeuSerSerLeu 596
DB 5530 CTGTCTTTTCACTTCAAACTCCACGTTTAATCTCTCTGTGAAATCTCCAGACGACGAC 5589
QY 597 GluTrpArgAlaLeuGluGlnIlePheThrGlnLeuLeuValProTrpLeuArgSerAap 616
DB 5590 TACTACCAAGAGCTGCAGAGAGACATTTCTGAAATTTTTTGAGATTAATAACAAGG 5649
QY 617 LeuThrGlyPheLeuGlnLeuGluIleLeuAapPheArgAapGlySerValIleValAap 636
DB 5650 -----GGTTTCTGGGCTCTCCAAATATTAAGTTACAGGCAAGAACTGTGGGTGACAA 5703
QY 637 SerTrpMetLeuPheAlaLeuSerValProTrpAapLeuThrLeuAlaValHieGlyVal 656

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DB 5704 TTGACTGTGGCTTCCGAAAGT-----ACCATCAATGTCCACGACGNG 5748
QY 657 -----LeuGluAapPheArgSerAlaAlaGlnGlnLeuHieLeuGluIleAap 673
DB 5749 GAGACACAGTTCAATCATCATATTAACAGGACGACCTCGATATTAACCTGACATCTCA 5808
QY 674 SerTrpSerLeuAapIleGluPro 681
DB 5809 GACGTACAGGTGATCATGTGTGCCA 5832

RESULT 12
5180808-1
; Patent No. 5180808
; APPLICANT: RUOSLAHTI, ERKKI I.
; TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
; SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
; ANTIBODIES, AND METHODS OF DETECTING THE SAME
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/441,179
; FILING DATE: 27-NOV-1989
; SEQ ID NO:1:
; LENGTH: 8224
5180808-1

Alignment Scores:
Pred. No.: 0.00106 Length: 8224
Score: 145.00 Matches: 185
Percent Similarity: 31.30% Conservative: 128
Best Local Similarity: 18.50% Mismatches: 342
Query Match: 3.52% Indels: 346
DB: 9 Gaps: 43

US-10-007-270-2 (1-797) x 5180808-1 (1-8224)
QY 40 ProaGangGluThrThrGluSerHisGlyMetCysTrpMetSerThrMetArgArg 59
DB 4377 CCTCAAAATCAGACTGTACAGGTGGCAGAGAAATC---CAGACTGTATGACCAACAACC 4433
QY 60 IlePheAapLeuAlaLeuHisArgThrIleArgSerAlaPhePheProThrGlyValIys 79
DB 4434 ATTAATGAAACAAGACTTACAGAAATCTTCAACAGCAAGAAAT----- 4478
QY 80 ValCysProGlnGluSerMetCysGlnIleLeuAapSerLeuGlnAlaTrpTrpArgLeu 99
DB 4479 -----AACGAAACAACAACCTCATCTGATTTTCTGGCTAGACCTTATGGTTT 4529
QY 100 ArgValCysGlnGluAlaValIlePheGluAlaTrpArgIlePheLeuAapArgIleProAap 119
DB 4530 GAAATGGCCAAAGAAATTTGTATCATCAGCAACCAACCATCTGACTTGTATTATGAACCT 4589
QY 120 ThrGluGluTrpGlnAapTrpValSerIleCysGlnGlnIleThrPheCysLeuPheAap 139
DB 4590 TCTGAGAAAGATCTCGAAGAACTG-----GAT 4616
QY 140 IleGlyIysAapPheSerAapSerGlnGluHieLeuAapLeuGlnGlnArgIleIys 159
DB 4617 ATTTGTTGATTCATTT-----CACACTTCTGCAACTACTGACGCAACACAGA 4661
QY 160 GlnAapSerPheProAapArgIysAapGluIleSerAlaGluIysThrLeuGluIysPro 179
DB 4662 CAAGAAAGACAGACACATTTGTTTCTGATGGGTCCCTGGAAAAACATCTTGAAGTGCAC 4721
QY 180 GlyIleThrIleValIleSerThrAapValAlaAapValSerLeuGlyProPheProLeu 199
DB 4722 AGCGTAAAGCTTACTACTGTATGATGATTTCCACAGATTTTCAAGTGTG---ATGCTGCTCT 4778
QY 200 -----ThrProAapAapThrLeuLeuAap----- 207
DB 4779 CATTCAGACAGACAAAGAACTCCCTGATTCACACTAGACACATCTGCAATATCAAGTGTCA 4838
QY 208 -----GluIleLeuAapAapThr 213

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Db 4839 TATGAGAGCTCCACAGACGATGTTCCAGACCGCTTTCAGGGAATTCAGAGATTCCACC 4898  
 Qy LeuAenAepThrLyMetProthrThrglu----- 223  
 Db 4899 TTTAAACCTACACGAAAAAACCCCTGAAAAATTTATTCATGACCTGGACAAAGAGAC 4958  
 Qy 224 ArgGluThrgluPheAlaValIleuGluGluGlnArgValGluLeuSerValSerIleuVal 243  
 Db 4959 AAGATTTAATATTGATGACATTTACAGAGATGACCATCTTGAAATTTCTACCTGAGCTGACA 5018  
 Qy 244 AenGluYsPheIleuValIleGluLeuAlaAepSerGlnSerProTyrTyrGlnIleuAla 263  
 Db 5019 TCGGATTAATAATATCATATGATATGATATGATCTAAACCTGCTGATGAAACATTTCTT 5078  
 Qy 264 GlyYsSerGlnIleuGlnIleuGlnIleuYsIlePheYsYsIleuProGlyPheYsYsIle 283  
 Db 5079 GGA-----ATGCAAAACAGATTTAGTATACAGAGTTCATCA----- 5114  
 Qy 284 HisValIleuGlyPheArgProYsYsGlyYsAepGlySerSerSerThrGluMetGln 303  
 Db 5115 -----GAACCATGACAGATATGATGAAAGTAAATGATGACAGACACTCA 5159  
 Qy 304 LeuThrAlaIlePheYsAepThrHisSerAlaGluAlaYsSerProAlaSerAepIleu 323  
 Db 5160 GTTCAAGAGATCTATGAG-----GCAGCTGTCAACTT 5192  
 Qy 324 SerPheAepSerAenIleIleGluSerGluGluValTyrHisGlyThrMetGluGluAep 343  
 Db 5193 TCTTTA-----ACTAGGAAACATTTGAGGGCTCT----- 5222  
 Qy 344 LysGlnProGluIleTyrIleuThrAlaThrAepIleuYsArgIleuIleSerYsAlaIleu 363  
 Db 5223 -----GCGATGTTCTGGCTAGCTACACTCAGCAACACATGATGATCAATGACTTAT 5276  
 Qy 364 GluGluGluGlnIleuSerIleuAepValGlyThrIleGlnPheThrAepGluIleAlaGlySer 383  
 Db 5277 GAAAGTAAAGCCCATGATCATGAGCTTGAGCTTTCACCTTCCACAACT-----GAG 5324  
 Qy 384 LeuProAlaPheGlyProAepThrGlnSerGluLeu-----ProThr 397  
 Db 5325 ATCCCTGCT-----CTTAGCACAAAGAAAGAAATTTAGACGTTTACTTCCACGGCAACA 5378  
 Qy 398 SerPheAlaValIleThrGluAepAlaThrIleuSerProGluLeuProProValGluPro 417  
 Db 5379 TCCCTGCCAATTCCTCGTAAGTGTGCGACAGTTATTCCAGAGATTGAAGAAATAAAGCT 5438  
 Qy 418 GlnIleuGluThrValAep----- 423  
 Db 5439 GAAAGCAAAAGCCCTGATGACATGTTGAAATCAAGCACTTGTCTGATGTCAGACTAT 5498  
 Qy 423 ----- 423  
 Db 5499 GCAGACCAAAAGTAAATAATACCAACATTTGGCCATTTGAAAAGACTCAGAGAGATAT 5558  
 Qy 424 -----GlyAlaGluHis 427  
 Db 5559 GAAAGCAAAAAACATGCTGCTCTTTTTCAGCCAGAAATCTCTTCAGAGACTAGAGAG 5618  
 Qy 428 GlyIleu-----ProAepThrSerTTPSerProProAlaMetAlaSerThrSer 443  
 Db 5619 GCATATGATGACCATACTCTTATCTAAGTATTTGCTATCCTACCACTTATGATCAGAGT 5678  
 Qy 444 LeuSerGluAla-----ProProPhePhe----- 451  
 Db 5679 GTTAACAGAGGTCCTCGATGTTGATGGAAGATCCAAATCCCAATATTTACCTGATTCACACA 5738  
 Qy 452 MetAlaSerSerIlePheSerIleuThrAepGlnGlyThrThrAepThrMetAlaThr--- 470  
 Db 5739 TTAGAGAGTTTCAACATTTGCGAAAGTTGCTCTTCAGACACACATCATCTCCCTCACTATC 5798  
 Qy 471 -----AepGlnThrMetIleuValProGly 478  
 Db 5799 TACTGAGGAGTGAAGCTCTGAGACACAGAGATCCCGACCGACAGTGTCTGTCCAGAGA 5858

Qy 479 LeuThrIleProThrSer----- 484  
 Db 5859 ATAGACGTGGCTCATCTGTATGTCCCCACAGATTTCTTTAAGAAATTCATGTAAAT 5918  
 Qy 485 -----AepTyrSerAlaIleSerGlnIleuAlaIleuGlyIleSerHisProProAla 501  
 Db 5919 ATTGAAGCACTTCAAAACCATCAAGTGAAGATATCTTCAATPACATGAGCCCTCCCT 5978  
 Qy 502 SerSerAepAepSerAepSerSerAlaGlyValGluAep---MetValArgHisIleuAep 520  
 Db 5979 TTATCTCTGACACAAATTTAGAACTTTCAGAGATGATGTGTAACCTGAGTTATTAGAA 6038  
 Qy 521 GluMetAepIleuSerAepThrProAla----- 529  
 Db 6039 GAAATGAGAGCTTCTCCACAGAACTTATGCTGTGGAAGGAATCTGAGATTCTCCAGAT 6098  
 Qy 530 -----ProSer--- 531  
 Db 6099 TTCCAAACCAAAACCGATGTCAAGTTCTGGAAGACATCAAGATGTTTCCACACTT 6158  
 Qy 532 GluValProGluIleuSerGluTyrValSerValProAepHisAep---LeuGluAepThr 550  
 Db 6159 AAAACACCTGAGGCTGGAACCTGTATTACAACTGCCGATGAATTAATGAAAGTGCT 6218  
 Qy 551 Thr----- 551  
 Db 6219 ACAAGTGGCCACACTCTTCTGCTTCTGACCACTATGGAGTGGAGGAGCTGTGCTG 6278  
 Qy 552 -----ProValSerAlaIleuGlnTyrIleThrThrSerSerMetThrIleAla 567  
 Db 6279 CTTGGCTAAGTCCACAGACTTGTGAGAGGCCACGCTTCTTCTTCTCCAGAAATTAAC 6338  
 Qy 568 Pro-----LysGlyArgGluIleuValIlePhePheSerIleuArg 580  
 Db 6339 CTTGAACCTCAAGCATTTATATCAAGAGGAGGAGATTCACAGATGACGACATCAAAACG 6398  
 Qy 581 -----ValAlaAenMetAlaPheSerAepAepIleuPheAenYsSerSerIleuGluTyr 598  
 Db 6399 CAAGTGGACGAGAGATTTCTGTATTTCCATGATATGACGCAACGTAACCCGTGGAATTT 6458  
 Qy 599 ArgAlaIleuGluGlnIlePheThrGlnIleuIleuValProTyrYsIleArgSerAenIleThr 618  
 Db 6459 AAT-----ACTGAGGTTGCAACACCACTATTTCCCTTCTGAGACT 6500  
 Qy 619 Gly-PheIleGlnIleuGluIleIleuAenPheArgAenIleSerValIleValAenSerIle 638  
 Db 6501 TCTAATGAACAAGATTTCTGATTG-----GCATTAATGAAGATCA 6542  
 Qy 638 AMetYsPheAlaYsSerValProTyrAenIleu-----ThrYsAlaIle 653  
 Db 6543 GTGAAAGCACGCGCATTTATTTACAGAGACTGATGCTGCAAAATGAAACCCGTGCTT 6602  
 Qy 653 HisGlyValIleuGluAepPheArgSerAlaAlaIleGlnIleuHisIleuGluIleAe 673  
 Db 6603 A-----ACGAGAGCACCTGTATCTCTAAGAACTTCC 6635  
 Qy 673 PserTyrSerIleuAenIleGlu-----ProAlaAepGlnAla-----AepThr 687  
 Db 6636 TACGTATACACC-TGTGACAGATACAGCGGAGACAGTGTGAACCTGATTTTGAAGA 6694  
 Qy 667 OcyYsYsPheIleuAlaCysGlyGluPheAlaGlnCysValIysAenGluArgThrGluGlu 707  
 Db 6695 ATGTCACTTAATCCCTCTGTAATGAGGCCACTTGTGTGATGAGTTTAAACACA----- 6749  
 Qy 707 ValaGluCysArgCysYsProGlyTyrAepSerGlnYsIleuAepGlyIleuGluPur 727  
 Db 6750 -TTCAAGGTGCTGTGCTTCCAGATTATGTTGCT----- 6782  
 Qy 727 OcyIleuYsGlyProGlyThrThrGluCysGluVal-----LeuGlnGly 743  
 Db 6783 -GCACCTTGTGAGCAAGATACCGAGACATGTGACTATGAGCTGGACAAATTCGAAGGCA 6841



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Db      1486 AATATGACGACGACGCAACAAAGCTAGTCTTCACTAAATATATCAGTTTGTGCA 1545
Qy      579 LeuArgValAlaAsn-----MetAlaPheSerAsnAspLeuPhe 591
Db      1546 GATACAGTAGTAAATTCATTTCAATTCGAAACGTCAACCTTATCATCTGAT----- 1599
Qy      592 AsnLysSerSer-LeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609
Db      1600 ---GACACTACTCTCTTCGGATATCCAGCATTTAGCTCAACAACTCATGATACTG 1651

RESULT 14
US-09-418-780A-2
; Sequence 2, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(2346)
US-09-418-780A-2

Alignment Scores:
Pred. No.: 0.000205 Length: 3104
Score: 144.50 Matches: 150
Percent Similarity: 34.23% Conservative: 116
Best Local Similarity: 19.31% Mismatches: 321
Query Match: 3.51% Indels: 191
DB: Gaps: 32

US-10-007-270-2 (1-797) x US-09-418-780A-2 (1-3104)
Qy      16 LeuGlnValGlnGlyThrLysAspLysSerLysLeuLysLysSerGluThrLysAsp 35
Db      764 CTGCAACTTCAGCAGCTTAAAGCAAGTAGTGAATTTCTCAACATTCACAGAA-AAATCA 822
Qy      36 Ile-----AspAsnProPheArgAsn----- 42
Db      823 GTGGCAGCTGCCACCTATAAAGAAATATGCCAAAGATGTTTGGCAGATTTCTCAGCA 882
Qy      43 -----GluThrThrGlnSerThrGluLysMetTyrLysMetSerThrMet 57
Db      883 CAATATATATGTTGTGAGACTGTATAAGTAACTGAACAATTAAAGCAGCTGTAGTGAAT 942
Qy      58 ArgArgLysPheAspLeuAlaLysHisArgThrLysArgSerAlaPhePhe---ProThr 76
Db      943 CTTAAAGAAATGCTTGAAGAAAGAAACATTTTTCATATGATGAGCCCTTTTATATCTGTT 1002
Qy      77 GlyValLysValLysProGlnGlnLysMetLysGlnLysLeuAspSerLeuGlnAlaTyr 96
Db      1003 GACCTTATGCTTTG-----GACTCCATTACTACTATGAGCTTGTCAAAATCCG 1053
Qy      97 TyrArgLysArgValLysGlnGlnLysAlaValTyrGlnAlaTyrArgLysPheLeuAspArg 116
Db      1054 ATGATCTTGAACATTAATAAGAGAAATG----- 1083
Qy      117 IleProAspThrGlnGlyLysGlnLysPhePheValSerLysCysGlnGlnGluThrPheCys 136
Db      1084 -----GATAACCAAGAAATATATAGATGATCATCTATTCGCGCA----- 1122

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Qy      137 LeuPheAspLysGlyLysAsnPheSerAsnSerGlnGlnLysLeuAspLeuLeuGln 156
Db      1123 -----GATGTAGATTATATGTTCTGATATGCTTCAAGATAC----- 1158
Qy      157 ArgLysGlnArgSerPheProAspArgLysAspGlnLysSerLysGlnLysThrLeu 176
Db      1159 -----AATCTCCAGATCAGCAAGGTGTGACAAATGGCAAGATGCTT 1200
Qy      177 GlyLysProGlnGlnThrLysAlaLysThrAspValAlaAsnValSerLeuGlyPro 196
Db      1201 CAGAT-----GTTTTCGAAACGCAATTTTCAAGATCCGATTTCAACCT 1245
Qy      197 PheProLeuThrProAspAspThrLeuLeuAsnGlnLysLeuAspAsnThrLeuAsp 216
Db      1246 GTTAGAGTAGTCCCTTATATGTTACATCAAAACAGATATCACAGAAACCATGCTAGAGAG 1305
Qy      217 ThrLysMetProThrThrGlnArgGluThrGluPheAlaValLeuGluGlnAlaArgVal 236
Db      1306 AACACTAATGAAGCCTCTGAAAGGAACTCTTGATGATTCGAAGATGAGCGAGTT 1365
Qy      237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerLys 256
Db      1366 -----AAGGCTTTCGAAAGCTTCAGAGCACCTTAAA 1398
Qy      257 ProTyrTyrGlnGlnLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLys 276
Db      1399 GCTGACATCAACAGCTCCAGGTTTGTCCCAAGTACTTCCGTAAGCTTAATTAATTAAG 1458
Qy      277 LeuProGlyPheLysLysLysIleValLeuGlyPheArgProLysLysGlnLysAspGly 296
Db      1459 AAGAGAAAGCTTAATAAG-----GAAAGAAAGAAAGAAAGGTTAAT 1500
Qy      297 SerSerSer-----ThrGlnMetGlnLeuThrAlaIlePheLys 309
Db      1501 AACAGCAATGAATAATCCAGAAATAATGTGAGCAAAATGAGGCTTAAGCAAAAGTCCAAAG 1560
Qy      310 ArgHisSerAlaGlnAlaLysSerProAlaSerAspLeuLysSerPheAspSerAsnLys 329
Db      1561 AGAAAT-----CAGCCAAAGAAAGAAACACAGTTCAATGGT----- 1599
Qy      330 IleGluSerGlnGlnValTyrHisGlyThrMetGlnGluAspLysGlnProGlnLysLysTyr 349
Db      1600 CTAATATCTGAAGAT-----GAAATATATGCTTAACCTATGAACATAT 1641
Qy      350 LeuThrAlaThrAspLeuLysArgLysLysSerLysAlaLeuGluGlnGlnSerLeu 369
Db      1642 -----GATGAGAAAGGACGTTAAGTGAATATGAACAACTCCCTGAGAT 1689
Qy      370 AspValGlyThrIleGlnPheThrAspGlnLysIleAlaGlySerLeuProAlaPheGlyPro 389
Db      1690 AAACCTGGCGAGTA-----GTTCCACATATATCAATCAAGAGACCTTCTGAGCAAT 1743
Qy      390 AspThrGlnSerGlnLeuProThrSerPheAlaValIleThrGlnAspAlaThrLeuSer 409
Db      1744 TCCATCTCGATGATGATGAGATAGACTTGAACACATG---AAAGCATCAACATAAGA 1800
Qy      410 ProGluLeuProProValGlnProGlnLeuGlnThrValaAspGlyAlaGlnHisGlyLeu 429
Db      1801 -----GAATTTAGAAATAATATGTTTCGCA-----TGCTTA 1830
Qy      430 ProAspThrSerTyrSerProProAla-----MetAlaSerThrSerLeuSer 445
Db      1831 AGAAGAGACCATTAATAACCTCTGCTAAGAAATATATGATGTCCAAAGAAAGAACTTCAAC 1890
Qy      446 GluAlaProProPhePheMetAlaSerSerLysPheSerLeuThrAspGlnGlyThrThr 465
Db      1891 TCACAGAAAAAACAAGATGGAAGAGCGTTACTGATGTTAATATACATTAATTAATCT 1950
Qy      466 AspThrMetAlaThrAspGlnThrMetLeuValProGlyLysLeuThrIlePro---ThrSer 484
Db      1951 AGAAGACGTCACAAATATGATTAACGCAACCATCCAAAGCGTTGAAATATGTTTCC 2010
Qy      485 AspTyrSerAlaIleSerGlnLeuAlaLeuGlyLysSerHisProProAlaSerSerSer 504

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277 LeuProGluPheIleValLeuGlyPheArgProGlyValAspGly 296  
1461 AAAGGAAGCTCTAAAAAG-----GAAAAGAAAAAGAAAGCTTAAT 1502

297 SerSerSer-----ThrGluMetGluLeuThrAlaIlePheIys 309  
1503 AACACCAATGAAATCCAAAGAAATGTGTGAGCAAAATGAGCTTAAAGAAATGTCGAAG 1562

310 ArgHisSerAlaGluAlaIleSerProAlaSerAlaLeuSerPheAspSerAsnIys 329  
1563 AGAAAT-----CACCCAAAGAAAAAGAAACACAGCTTCATTGCT- 1601

330 IleGluSerGluGluValTyrHisGlyThrMetGluGluAspIysGlnProGluIleTyr 349  
1602 CTAAATCTCGAAGAT-----GAAAGATAATGTCTAAACCTATGAAACAT 1643

350 LeuThrAlaThrAspLeuIysArgLeuIleSerIysAlaIleGluGluGlnGlnSerLeu 369  
1644 -----GATGAGAAAGGACGTTAACTCTGAAATATTAACAAATCCCTCGAGAT 1691

370 AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro 389  
1692 AAACCTGGCGGAGTA-----GTCCACATAATACATCAAGAGAGCCTTCTGTGAGCAT 1745

390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409  
1746 TCCAACTCTGATGATAGATAGATAGACCTTGAACACGTG---AAAGCATCAACCTAGA 1802

410 ProGluLeuProProValGluProGlnIleGluThrValAspGlyAlaGluHisGlyLeu 429  
1803 -----GAATTGAAAAATATGTTGGCA-----TGCTTA 1832

430 ProAspThrSerTyrSerProProAla-----MetAlaSerThrSerLeuSer 445  
1833 AGAAAGAGACATTAACCTCTCTCTAAGAAATATGATAGATGTCAAAGAAAGAACTTCAC 1892

446 GluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThr 465  
1893 TCACAGAAAAACAGAAATGTGAAAAAGCGGTATCTGATGTTAATATCAAGTTAAATCT 1952

466 AspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro---ThrSer 484  
1953 AGAAACGTCGAACAAATCTGATTAACAGCAACATCCAAAGCTGTGAAATGTTTCC 2012

485 AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAsp 504  
2013 GCACGTAGTGAAGACGACGACGACGACGACGACGCTCATGAGTCTGAAGTAGACGACGT 2072

505 Asp-----SerArgSerSerAlaGlyGluAspMetValArgHisLeuAspGlu 521  
2073 GACTTAAGCTCTTCAGACGACGAGTATCTGATCATCAAAATGTTCCCTCAAGTTTACGAA 2132

522 MetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSer 541  
2133 GTAAACCAAAATGATTTCTCTTAAAGACATGTAAGAAATATAGAAATGAATGATCA 2192

542 ValProAsp-----HisPheLeuGluAspThrThrPro 552  
2193 CTGCTGAAGAAAGAAAGACGCTCACACAGATAGATATGTGTGCAAGACAAACCTCT 2253

553 Val---SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProIysGlyArg 571  
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572 GluLeuValValPhePheSerLeuArgValAlaIleMetAlaPheSerAsnAspLeuPhe 591  
2313 CAATTAGCA-----TTT 2324

592 AsnIysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThr-----GlnLeuLeu 609  
2325 AATTATCAAGATTAGAACATTTCAGACGTGTGAAAAACATTTACACCTTACAAATTTCTG 2388

610 ValPro-----TyrLeuArgSerAsnLeuThrGlyPhe----- 620

Db 2385 CCTCCCTCAGGTGATTCTGAAACAGCTCTCAAAATGGCATTAAGTGCATCCATCTGGT 2444A  
QY 621 -----LysGlnLeuGlu 624  
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QY 625 ILeuLeuAmpheArgaenGlySerValIleValAmpSerLysSmeLysPheAlaLysSer 644  
Db 2505 ATTAAGAAAT-----GCAGATCTATCGAAAAAGTTTAGGCCAAACCA 2543A  
QY 645 Val--ProTyrAenLeuThrLysAlaValHisGlyValLeuGluAapPheArgSerAla 663  
Db 2544 GTGAACAACCATCAGGCTAATGAAATCCCTCAGATGAGCTCTTCAACCAATTTTAGAAAAGCA 2603A  
QY 664 Ala-----AlaGlnGlnLeu-----HisLeuGluIle 672  
Db 2604 GCCATAGAAAAAGAAAGTAAAAAGCTCGGACACACAGGAACCATACGGAAGCAATTTGGAAACAA 2663A  
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Search completed: January 15, 2006, 04:15:47  
Job time : 524 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 21:46:50 ; Search time 10253 Seconds  
(without alignments)  
4418.632 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLETRRAIFWVIFLQVQ.....NSELTVEYEFHNDMEGN 797

Scoring table:

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	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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Database :

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3: gb.env:\*  
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5: gb.ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
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14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4117	100.0	3268	8 AF047492	Homo sapi
2	3370	81.9	2009	6 C0725539	Sequence
3	2759	67.0	3552	4 AB047844	Bos tauru

Result No.	Score	Query Match	Length	DB ID	Description
4	2548.5	61.9	3668	9 AF266478	
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6	2543.5	61.8	2850	9 AB047843	
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18	885	21.5	555	8 AF047491	
19	876	21.3	6961	9 BC048863	
20	776.5	18.9	3326	6 C0728190	
21	565	13.7	259413	14 AC161554	
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23	483.5	11.7	157596	9 AC120388	
24	434	10.5	214606	14 AC161819	
25	408.5	9.9	537	8 H51MPG02	
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27	408.5	9.9	186301	8 AL356662	
28	406.5	9.9	444	8 H51MPG10	
29	384	9.3	477	8 H51MPG15	
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#### ALIGNMENTS

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LOCUS  
DEFINITION  
AF047492  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE

AF047492 3268 bp mRNA linear PRI 26-OCT-1999  
Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMP1)  
mRNA, complete cds.  
AF047492  
AF047492.2 GI:6118565  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 3268)  
Kuehn,M.H. and Hageman,G.S.  
Expression and Characterization of the IPM 150 gene (IMP1)  
product, a novel human photoreceptor cell-associated  
chondroitin-sulfate proteoglycan  
Matrix Biol. 18 (5), 509-518 (1999)  
10601738  
2 (bases 1 to 3268)  
Kuehn,M.H. and Hageman,G.S.  
Direct Submision  
Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,  
University of Iowa, 200 Hawkins Drive, 1190B FFP, Iowa City, IA  
52240, USA  
3 (bases 1 to 3268)  
REFERENCE



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Qy 481 ILeProThSerAspTySerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500
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LOCUS CQ725539 2009 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 11473 from Patent WO02068579.
ACCESSION CQ725539
VERSION CQ725539.1 GI:42286477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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```

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kite, such as nucleic acid arrays, comprising a majority of humeones or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 11473 06-SEP-2002;
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity: 86.05% Mismatches: 1
Query Match: 81.86% Indels: 106
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Db 3 ATCTCATTAACATATACATTCATCTGAACTAAAGCATATAGACATCCCCCAAGAAATGAA 62
Qy 44 ThrThrGlnSerThrGlnLysMetTyIleSerSerThrMetArgArgIlePheAspLeu 63
Db 63 ACAACTGAAGATGACGAAATAATGTAACAAATGTCACTATGAGACGAATATTCATATTTG 122
Qy 64 AlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysValCysProGln 83
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Qy 144 PheSerAsnSerGlnGlnIleLeuAspLeuLeuGlnGlnAlaGlyIleLysGlnArgSerPhe 163
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Db 402 -----GAA 404
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Db	542	-----	542
Oy	304	LEUTHRALALEPHELYARGHISSESLAGUALALYSSERPROLSSERASPLEUEN	323
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Db	585	TCTTTGATTCCAACAAATTGAAGTAGGAAAGCTCATGGAACCATGGAGGAGAC	644
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DEFINITION			MM 30-AUG-2000
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Bos taurus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;			
Pecora; Bovidae; Bovinae; Bos.			
1 (sites)			
Uehara, F., Ohba, N. and Ozawa, M.			
Isolation and characterization of mucinlike glycoprotein associated			
with photoreceptor cells			
Invest. Ophthalmol. Vis. Sci. 41 (9), 2759-2765 (2000)			
2 (bases 1 to 3552)			
Uehara, F., Ohba, N. and Ozawa, M.			
Direct Submission			
Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University			
Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,			
Kagoshima 890-8520, Japan			
(E-mail: f.uehara@meds.kufm.kagoshima-u.ac.jp, Tel:81-99-275-402,			
Fax:81-99-265-4894)			
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REFERENCE
AUTHORS Kuehn,M.H., Wietzecki,D.T. and Hageman,G.S.
TITLE Molecular characterization of the murine orthologue of the human
retinal proteoglycan IPM 150
Mol. Vis. 6 (2000) In press
JOURNAL 2 (bases 1 to 3668)
REFERENCE Kuehn,M.H., Wietzecki,D.T. and Hageman,G.S.
AUTHORS Direct Submission
TITLE Submitted (10-MAY-2000) Ophthalmology, University of Iowa, 2501
JOURNAL Crosspark Rd., Coralville, IA 52241, USA
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Abrahamson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butcherfield, Y.S., Krzywinski, M.I., Skalska, U., Smallue, D.E.,  
Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Strausberg, R.  
Direct Submission  
Submitted (04-FEB-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulèsed, H.,  
Kovats, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

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 REFERENCES  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Core Protein of rat Mucinlike Glycoprotein Associated with  
 Photoreceptor Cells  
 Published Only in Database (2000)  
 2 (bases 1 to 2850)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Direct Submision  
 Submitted (28-AUG-2000) FumiYuki Uehara, Kagoshima University  
 Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,  
 Kagoshima 890-8520, Japan  
 (E-mail: fuhara@meds.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,  
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## ORIGIN

## Alignment Scores:

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Pred. No.: 5,86e-155 Length: 2850
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Percent Similarity: 75.15% Conserv: 92
Best Local Similarity: 63.78% Mismatches: 178
Query Match: 61.78% Indels: 23
DB: 9 Gaps: 10

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US-10-007-270-2 (1-797) x AB047643 (1-2850)

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DB 127 ATGAATTTGGAGATTAAACATGCTATCTTGTTGTGGATTTTCTCCAGATTCAAGCA 186
QY 21 ThrIlyAspIleSerIleAsnIleTyrHisSerGluThrIlyAspIleAspAsnProPro 40
DB 187 ATCAAGATACCTCTACTAAACACACAGCTTGGAACTTAAACAAATGAGCAAAACCCCA 246
QY 41 ArgAsnGluThrThrgIuSerThrgIuIyMetTYrIyMetSerThrMetArgArgIle 60
DB 247 AGAATTGAACAACCTGAAAGCACTTCAGAGTGCACAAAGCCTCAACATGAAAGACATG 306
QY 61 PheAspLeuAlaIlyHisArgThryIyAspSerAlaPhePheProThrgIyAlaIlyVal 80
DB 307 TTCGCTGTGGCAAAAGCTTCGAAACAAAGATCGGACATGTTCCCA---GCTGTGAACATC 363
QY 81 CysProGlnGluSerMetIyGlnIleLeuAspSerIleGlnAlaIleTyrTYrArgLeuArg 100
DB 364 TGTCCGCGGGAATCCTTAGGCGAGATTTTGAAGATCTTCAAGAAATATTATTCGACTGGA 423
QY 101 ValCYSGInGluAlaIValTTrGluAlaIyArgIlePheLeuAspArgIleProAspThr 120
DB 424 GATATTCAGAAATAGTGTGGGAGACATTCGATCTTTCGATCGCGTTCCTGACACA 483
QY 121 GlnIyIyTrGlnAspTTrpValSerIleCysGlnGlnIyThrPheCysLeuPheAspIle 140
DB 484 GAGGAATATCAAGATCGGCTCAGCTTCGCCAGAGAGACCTTCGCTCTTTGACATT 543
QY 141 GlnIyAsnPheSerAsnSerGlnIyHisIleuAspIleuGlnIyArgIleIyGln 160
DB 544 GGGAAAAAATCTGACAACTCCAGAGACCTCGAGATCTTTCACACAGAAATTTTTCAG 603
QY 161 ArgSerPheProAspArgIyAspGluIleSerAlaGluIyThrLeuGlyIyGluProGly 180
DB 604 AGAAGCTTCTCGGAGAGAAAGATGATATGTCCTCCCATAGAGATATCTGGAGATGCTTAC 663
QY 181 GlnThrIleValIleSerThraspValAlaAsnValSerIleGlyIyProPheProLeuThr 200
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 664 AAGACCCCTGTGTTACCATAGATGTTTCCAGTATGTCATGAGACCCCTTCCACTCCCT 723
QY 201 ProAspAspThrLeuLeuAsnGluIleIleuAspAsnThrIleAsnAspThrIyMetPro 220
DB 724 CTTATGACACAGACTCTCAAGAGATC-----ACCATCAAAAGACATCAACAGGCC 774
QY 221 ThrThrgIuArgIuThrGluPhe-----AlaValI 230
DB 775 ATAGCAATTAAGAGAGAGCTGAGTTGGAAGTAACACAGAGCTTACTACGTGATGTAATTC 834
QY 231 LeuGluGluGlnAlaIyValIyGluLeuSerValSerIleuValaGlnIyIyPheIyAlaGlu 250
DB 835 TCATCCAGAGGAGAAAGTGAAGTTCAAGATCTCTGCGAAACCAAGAGTTCAAGCAGAG 894
QY 251 LeuAlaAspSerGlnSerProTYrTYrGlnIyIleuAlaGlyIySerGlnLeuGlnMet 270
DB 895 CTCACCACTCAAGATCCCACTACTCCAGGAACCTGTGGGACAGTCCCAATGCAAGTTG 954
QY 271 GlnIyIyIlePheIyIyIyLeuProGlyIyPheIyIyIleIyValIleuGlyIyPheArgPro 290
DB 955 CAAGAAGATTTTAAGAAACTTCAGAGATTCGAGAAATCCGCGTGTAGATTTAGACCA 1014
QY 291 IyIyIyGluIyAspGlyIySerSerThrgIuMetGlnLeuThraIleIlePheIyArg 310
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QY 311 HisSerAlaGluAlaIySerProAlaSerAspLeuSerPheAspSerAsnIyIle 330
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QY 331 GluSerGluGluValTYrHisGlyThrMetGluIyAspIyGlnProGluIleTYrLeu 350
DB 1135 GAACGTGAAGAAATCCATCAAGAGACATA---GAGACAAACCAACGAGAGCTTACTTC 1191
QY 351 ThrAlaThrAspLeuIyAspGluIleSerIyAlaIleuGluGluGlnIyGlnSerIleuAsp 370
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QY 371 ValGlyThrIleGlnPheThraspGluIleAlaGlySerIleuProAlaPheGlyIyProAsp 390
DB 1252 GAGAGACAGTTCCATTCAGATGATAGCTT-----ACTGAGCCACTTTCAAGACTGTC 1305
QY 391 ThrGlnSerGluLeuProThrasPheAlaValIleThrgIuAspAlaThrLeuSerPro 410
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QY 411 GluLeuProProValGluProGlnIyGluThryValAspGlyAlaGlnHisGlyLeuPro 430
DB 1366 GAGCTTCTCTTCAAGTGAACCTGAGCTTGAAGTGTGACATATATGTCCTGACTGCTCT 1425
QY 431 AspThrSerTrpSerProProAlaMetAlaSerThrSer---LeuSerGluAlaIyProPro 449
DB 1426 GACAGTTCTTGTCTCTGCTCTGTAACAGCTTCGACTTCGAGAGTGGAAATCTACCTTCC 1485
QY 450 PhePheMetAlaSerSerIlePheSerIyThraspGlnIyThrThraspThrMetAla 469
DB 1486 TTT-----ACGCTAGATCTTGCCTCTGATGATCACTCAAACTCCCTCCCTTAGAGCC 1539
QY 470 ThrAspGlnThrMetLeuValIyProGlyLeuThrIleProThrasPTrpSerAlaIle 489
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DB 1600 CGCCATAGCCGCTAGAGATGTCACATYGCTGAGCTTCTCAAGTGAACAGAGAGTTCG 1659
QY 509 SerAlaGlyIyGluAspMetValArgHisIleuAspGluMetAspLeuSerAspThrPro 528
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QY 529 AlaProSerGluValIyProGluLeuSerGluIyTYrValSerValIyProAspHisPheLeuGlu 548
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 QY 559 IlyGlyIlyrGluValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAen 588  
 DB 1840 AAGGGCAAGAGCTAGTGTATTTCTTCACTTGGCGGTCTTAACATGGCGTTCTCTAT 1899  
 QY 588 AapLeuPheAsnLysSerSerLeuGluIlyrArgAlaLeuGlnGlnPheThrGlnLeu 608  
 DB 1900 GACTTGTCATATAGAGTTCCTCGAGTACCAAGCCTTGAAACAAGATTACAGACTG 1959  
 QY 609 LeuValProTyrLeuArgSerAsnLeuThrGlyPheIlyGlnLeuGlnIleLeuAsnPe 628  
 DB 1960 TTGGTTCATATCTATCGATCGAATCTTACGGGCTTTAACAACCTGAAATACCTCACTTC 2019  
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 QY 649 LeuThrLysAlaValAlaIleGlyValLeuGlnLysPheArgSerAlaAlaIleGlnGlnLeu 668  
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 ACCESSION AF229929  
 VERSION AF229929.1 GI:11177167  
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 ORGANISM  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciromachti; Murioidea; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Lee,J.W., Chen,Q., Rayborn,M.E., Shadach,K.G., Crabbs,J.W.,  
 Rodriguez,I.R. and Hollyfield,J.G.  
 TITLE SPACR in the interphotoreceptor matrix of the mouse retina:  
 molecular and biochemical characterization  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 3675)

AUTHORS Rodriguez,I.R., Lee,J.W. and Hollyfield,J.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JAN-2000) LRCMB, NEI-NIH, 6 Center Drive MSC2740  
 6/304, Bethesda, MD 20892, USA  
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 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGlnIlyrLysAspIleAspAsnProPro 40  
 DB 185 ATCAACA-ATT----- 195  
 QY 41 ArgAsnGlnIlyrThrGlnSerThrGlnLysMetTyrLysMetSerThrMetArgArgIle 60  
 DB 196 -----GAAAGTACTTCAACAGTGCACAAAGTGTCAACATGAAGAAAGATA 240  
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 QY 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430  
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 QY 431 ---AspThrSerTyrSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
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 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.





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Db	1594	ACATCTGAACCTGCATTCCTTACCAAACTCCAGAGAACCACTCAACAGACAGATCTCCA	1653
Oy	400	-----	400
Db	1654	GACACAGAAATATCACTACTGATTACCAAAAGATTACAGTGCCTTTCAGTGTCTGGTT	1713
Oy	403	ThrgluAepAlaThrLeuSerProGlu-----LeuProProValGluProLeu	419
Db	1714	AGCACGAGACAGTCTGCAAAACGAGAGATTCTTACCTGCTCTCCACAGATGAGTCA	1773
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Oy	440	AlaSerThrSerLeuSerGluAlaProProPheMetAlaSerSer-----	455
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Oy	463	-----	463
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Oy	468	MetAlaThr-----	475
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Oy	476	ValProGlyLeuThrIleProThrSerAspTrpSerAlaIleSerIleuAlaLeuGly	495
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Oy	506	SerArgSerSerAlaGlyGlyLeuAepMetValArgHisLeuAepGluMetAepLeuSer	525
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Oy	526	AspThrProAlaProSerGlyValProGluLeuSerGlyTrpValSerValProAepHis	545
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Oy	586	PheSerAanAepLeuPheAanLeuIlySerSerLeuGlnTrpArgAlaLeuGluGlnPhe	605
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Oy		Acharya,S., Fioletta,V.C., Lee,J.W., Raybourn,M.B., Rodriguez,I.R.,	
Db	TITLE	Young,W.S., III and Holleyfield,J.G.	
Oy		SPACRCAN, a novel human interphotoreceptor matrix	
Db		hyaluronan-binding proteoglycan synthesized by photoreceptors and	
Oy	JOURNAL	pinelalocytes	
Db	PUBMED	J. Biol. Chem. 275 (10), 6945-6955 (2000)	
Oy	REFERENCE		
Db	AUTHORS	2 (bases 1 to 3989)	
Oy	TITLE	Fioletta,V.C. and Young,W.S.	
Db	JOURNAL	Direct Submission	
Oy		Submitted (09-UDN-1999) SNGE, NIMH, 36 Convent Dr, MSC 4068,	
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## ORIGIN

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Percent Similarity:	39.62%	Conservative:	145
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US-10-007-270-2 (1-797) x AF157624 (1-3989)

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QY	40	-----ProArgAsnGluThr-----	ThrGluSerThrIuLysMetIyr	52
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DB	264	CTGTTTCTTAATGAGTGAATAATCTGCCAGATGAAGTGTTCAGAGGCTGTGGCAAT		323
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DB	324	CATGTGAAGTATTTTAAAGTCCGAGTGTTCAGAAAGCTGTCTGGAAACCTTCAGGACT		383
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DB	384	TTTTGGGAACTGACTTCTGGGGGTAGAGAAATATCATTAAGTAATTTGTGTAGAGAT		443
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QY	217	ThrIlyMetProThrThyGluArgGluThrGluPheAlaValLeuGlnGlnArgVal		236
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QY	237	GluLeuSerValSerLeuValAsnGlnIlyAspPheValIleGluLeuAlaAspSerGlnSer		256
DB	750	-----AGATTCACACCTTTTGGGGAAGCAGTACAGAGAAAGTACAGGATTCCTCAGC		803
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QY	356	LysArgLeuIleSerLysAlaLeuGlnGlu-----		365
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VERSION CQ870600.1 GI:52000111
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Homnidae; Homo.
REFERENCE
1. Aziz,N., Gish,K.C., Wilson,K.B. and Zlotnick,A.
Method of diagnosis of cancer, composition and methods of
screening for modulators of cancer
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 Homiidae; Homo.  
 REFERENCE Kuehn, M.H. and Hageman, G.S.  
 1 (bases 1 to 4165)  
 TITLE Molecular characterization and genomic mapping of human IPM 200, a  
 second member of a novel family of proteoglycans  
 Mol. Cell Biol. Res. Commun. 2 (2), 103-110 (1999)  
 JOURNAL  
 PUBMED 10542133  
 REFERENCE Kuehn, M.H. and Hageman, G.S.  
 2 (bases 1 to 4165)  
 TITLE Direct Submission  
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## ORIGIN

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## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3,52e-50	927.00	39.71%	26.68%	22.52%	4165	297	145	267	405	36

US-10-007-270-2 (1-797) x AF173155 (1-4165)

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QY      68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGlnSerMetLys 87
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QY      88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGlnAlaValTyr 107
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QY      185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200
Db      768 TTGGAGAGACATACTCTCAGTGT-----CCATCCACAGAGGTGAGCCCTTAGAA 818
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Db      819 GGTGCTCAGAGAGCAGCTTGAAAGCCAGAGAGAGATATTGACATGAATTT---GAG 875
QY      212 AsnThrLeuAsnAspThrLysMetProThrThrGluArgIleThrGlnPheAlaValLeu 231
Db      876 AATGTGATGAAGAACCCACAAACAGCAGTGAAACAGATTGCAAAATTC----- 926
QY      232 GluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeu 251

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Db      966 CAGGATTCCTCCAGCTTTCACACACAGCAGCTTGAAAGAAATTTATTTCAAGAGTTGAA 1025
QY      272 LysIlePheLysLeuLeuProGlyPheLysValIleValLeuGlyPheArgProLys 291
Db      1026 AATGCATTTTACTGGTTTACAGGCTTACAGGAAATTCGTGTACTTGATTTAGTCCCC 1085
QY      292 LysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHis 311
Db      1086 AAGGAAGATGAC-----AGTGGCGTGAATGTTTACTATGACATTAACCTTC----- 1130
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QY      351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGlu----- 365
Db      1239 ACAATCAGTAATTCAGAGATTAATATGTGTGACATTCACAGCAATTTTGTGCGGG 1298
QY      365 ----- 365
Db      1299 AACTCTTCTTGATATCCAGATCCTGATTCCTGACAGTTATGCAATGTGAGAGAGTTTGG 1358
QY      366 ---GluGlnSerLeuAspVal-----GlyThrIleGlnPheThr--- 377
Db      1359 CGTCAACAACTGAAAGATCTAGTTTGGAACACCCAAAGTTCAAGTCTTAGCGCAACGCCG 1418
QY      378 -----AspGluIleAla 381
Db      1419 TCATCATTTCTGGATATATACCTTTCAAGCTGATGAGCCCTCAGAGATGAATCATCAC 1478
QY      382 GlySerLeuPro-----AlaPheGlyProAspThr 391
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QY      392 GlnSerGluLeuPro----- 396
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QY      396 ----- 396
Db      1599 ATGGGCTCAGCTTTCGCCAAGGTTTAAAGTTAGAGCTTGAACCTTTCATTTCTGTC 1658
QY      397 -----ThreSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410
Db      1659 ACCCGGCGAGTCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1718
QY      411 GluLeuProProValGluProGlnLeuGlnIleThrValAspGlyAlaGlu----- 426
Db      1719 CACTTG-----GTGAAGATGAGATTTAGCAATGTGGAAGTCAAGAAATTTCTTCT 1772
QY      427 ---HisGlyLeuProAspThrSerThrSerProAlaMetAlaSerThr----- 442
Db      1773 ATTGATTCATTCCTTCAAGTTCATCTCACTCAACTGCTGCCAAGAAACAAATACATCC 1832
QY      443 -----SerLeuSerGluAlaPro-----ProPhe 450
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QY      451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470
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Qy 495 GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGlyIle 514
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Qy 527 -----ThrProAlaProSerGlyValPro----- 534
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Qy 535 -----GluLeuSerGlyTyrValSerValProAspHisAspHe 546
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Qy 547 LeuGlu-----AspThr 550
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Qy 551 ThrProValSerAla----- 555
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Qy 556 LeuGlnTyrIleThrThrSerSer----- 563
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Qy 564 -----MetThrIleAlaProValSerGlyArgGlu----- 572
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Qy 661 ArgSerAlaAlaValGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680
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Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln--- 719
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Qy 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735
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Qy 736 GluCysGluValLeuGlnGlyLysGlyValAspProCysArg 748
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RESULT 12
AY174061 4010 bp mRNA linear ROD 27-MAR-2003
LOCUS AY174061
DEFINITION Mus musculus sialoprotein associated with cones and rods
ACCESSION AY174061
VERSION AY174061.1 GI:27802104
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
1 Chen, Q., Lee, J.W., Nishiyama, K., Shadreh, K.G., Rayborn, M.E. and
Hollyfield, J.G.
SPACRCAN in the interphotoreceptor matrix of the mouse retina:
molecular, developmental and promoter analysis
Exp. Eye Res. 76 (1), 1-14 (2003)
2 (bases 1 to 4010)
Chen, Q. and Hollyfield, J.G.
Direct Submission
Submitted (06-NOV-2002)
JOURNAL Foundation, 131, 9500 Euclid Ave., Cleveland, OH 44195, USA
FEATURES
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## ORIGIN

Alignment Scores: 3,37e-49 Length: 4010  
 Pred. No.: 911,50 Matches: 279  
 Score: 42.43% Conservative: 136  
 Percent Similarity: 42.43% Mismatches: 272  
 Best Local Similarity: 28.53% Indels: 291  
 Query Match: 22.14% Gaps: 35  
 DB: 9  
 US-10-007-270-2 (1-797) x AY174061 (1-4010)

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 QY 51 MetYrIlyMetSer-----ThreCArgArgIlePheAspLeuAlaIysHis--- 66  
 DB TCACAGACCTTTCCTGCTTACAGAGAGAGCTTCGCTTCGCTTCCTCACCTTCAAG 414  
 QY 67 -----ArgThrIlyAspSerAlaPhePheProThrGIuValIyValCys 81  
 DB AGAGAGGCTGCTTACAGAGAGGCGGATTAATTCCTCCAAAGAGATAAATTTGC 474  
 QY 82 ProGIuIlySerMetIySerIleIleuAspSerIleuGlnAlaIyTyrArgLeuArgVal 101  
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 QY 179 Pro-----GlyGIuThrIleValIleSerThrAspValAlaAsnValSerLeuGIu 195  
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 QY 196 ProPhePro-----LeuThrProAspAspThrLeuLeuAsn 207  
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 DB TTC-----AGATTCCAACTTCGAGGAGAGGATTC 969

QY 248 LysAlaGIuLeuAlaAspSerGlnSerProTyrTyrGIuIuLeuAlaGIuIySerGln 267  
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 QY 412 -----LeuProValGIu--- 416  
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      1 (bases 1 to 816)
      Felbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,
      Schmid,M. and Weber,B.H.F.
      Genomic organization and chromosomal localization of the
      interphotoreceptor matrix proteoglycan-1 (IMP1) gene: a candidate
      for 6q-linked retinopathies
      Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
      9691169
      JOURNAL PUBMED
      2 (bases 1 to 816)
      Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Huelsen,I.B.
      and Weber,B.H.F.
      Assessment of a novel interphotoreceptor matrix gene (IPM150)
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      macular dystrophy, progressive bilateral choriorretinal atrophy
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      3 (bases 1 to 816)
      Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
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      Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am
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ACCESSION	AL392166			
VERSION	AL392166.19	GI:13396652		
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ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 90766) Clark,S.			
REFERENCE	Submitted Direct Submission			
AUTHORS	Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,			
TITLE	Cambridgehire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk			
JOURNAL	Clone requests: clonerequest@sanger.ac.uk			
COMMENT	On Mar 20, 2001 this sequence version replaced gi:133934983. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMEP; Information on the WOMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 Rpl1-758j17 is from the library RPc1-11.3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAC3.6			
	----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: vegas@sanger.ac.uk			
	----- This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. location/Qualifiers 1..90766 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6"			
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US-10-007-270-2 (1-797) x AL392166 (1-90766)

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Hominoidea; Homo.
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AUTHORS McJarry, K.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT Requesters: clonerequest@sanger.ac.uk
On Jan 14, 2001 this sequence version replaced gi:12214326.
Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
Center project name: BA505B21
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Chemistry: Dye-terminator Big Dye; 100% of reads
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Consensus quality: 126505 bases at least Q20
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coverage: 2.65x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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